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(54) Title: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

(57) Abstract: The present invention provides novel isolated polynucleotides and small molecule target polypeptides encoded by the polynucleotides. Antibodies that immunospecifically bind to a novel small molecule target polypeptide or any derivative, variant, mutant or fragment of that polypeptide, polynucleotide or antibody are disclosed, as are methods in which the small molecule target polypeptide, polynucleotide and antibody are utilized in the detection and treatment of a broad range of pathological states. More specifically, the present invention discloses methods of using recombinantly expressed and/or endogenously expressed proteins in various screening procedures for the purpose of identifying therapeutic antibodies and therapeutic small molecules associated with diseases.



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Novel Proteins and Nucleic Acids Encoding Same

Field of the Invention

The present invention relates to novel polypeptides that are targets of small molecule drugs and that have properties related to stimulation of biochemical or physiological responses in a cell, a tissue, an organ or an organism. More particularly, the novel polypeptides are gene products of novel genes, or are specified biologically active fragments or derivatives thereof. Methods of use encompass diagnostic and prognostic assay procedures as well as methods of treating diverse pathological conditions. The present invention discloses novel associations of proteins and polypeptides and the nucleic acids that encode them with various diseases or pathologies. The proteins and related proteins that are similar to them, are encoded by a cDNA and/or by genomic DNA. The proteins, polypeptides and their cognate nucleic acids were identified by Curagen Corporation in certain cases. The XYZase-encoded protein and any variants, thereof, are suitable as diagnostic markers, targets for an antibody therapeutic and targets for small molecule drugs. As such the current invention embodies the use of recombinantly expressed and/or endogenously expressed protein in various screens to identify such therapeutic antibodies and/or therapeutic small molecules.

Background

Eukaryotic cells are characterized by biochemical and physiological processes which under normal conditions are exquisitely balanced to achieve the preservation and propagation of the cells. When such cells are components of multicellular organisms such as vertebrates, or more particularly organisms such as mammals, the regulation of the biochemical and physiological processes involves intricate signaling pathways. Frequently, such signaling pathways are constituted of extracellular signaling proteins, cellular receptors that bind the signaling proteins and signal transducing components located within the cells.

Signaling proteins may be classified as endocrine effectors, paracrine effectors or autocrine effectors. Endocrine effectors are signaling molecules secreted by a given organ into the circulatory system, which are then transported to a distant target organ or tissue. The target cells include the receptors for the endocrine effector, and when the endocrine effector binds, a signaling cascade is induced. Paracrine effectors involve secreting cells and receptor cells in close proximity to each other, for example two different classes of cells in the same tissue or organ. One class of cells secretes the paracrine effector, which then reaches the second class of cells, for example by diffusion through the extracellular fluid. The second class of cells contains the receptors for the paracrine effector; binding of the effector results in induction of the signaling cascade that elicits the corresponding biochemical or physiological effect. Autocrine effectors are highly analogous to paracrine effectors, except that the same cell type that secretes the autocrine effector also contains the receptor. Thus the autocrine effector binds to receptors on the same cell, or on identical neighboring cells. The binding process then elicits the characteristic biochemical or physiological effect.

Signaling processes may elicit a variety of effects on cells and tissues including by way of nonlimiting example induction of cell or tissue proliferation, suppression of growth or proliferation, induction of differentiation or maturation of a cell or tissue, and suppression of differentiation or maturation of a cell or tissue.

Many pathological conditions involve dysregulation of expression of important effector proteins. In certain classes of pathologies the dysregulation is manifested as diminished or suppressed level of synthesis and secretion protein effectors. In a clinical setting a subject may be suspected of suffering from a condition brought on by diminished or suppressed levels of a protein effector of interest. Therefore there is a need to be able to assay for the level of the protein effector of interest in a biological sample from such a subject, and to compare the level with that characteristic of a nonpathological condition. There further is a

need to provide the protein effector as a product of manufacture. Administration of the effector to a subject in need thereof is useful in treatment of the pathological condition, or the protein effector deficiency or suppression may be favorably acted upon by the administration of another small molecule drug product. Accordingly, there is a need for a method of treatment of a pathological condition brought on by a diminished or suppressed levels of the protein effector of interest.

Small molecule targets have been implicated in various disease states or pathologies. These targets may be proteins, and particularly enzymatic proteins, which are acted upon by small molecule drugs for the purpose of altering target function and achieving a desired result. Cellular, animal and clinical studies can be performed to elucidate the genetic contribution to the etiology and pathogenesis of conditions in which small molecule targets are implicated in a variety of physiologic, pharmacologic or native states. These studies utilize the core technologies at CuraGen Corporation to look at differential gene expression, protein-protein interactions, large-scale sequencing of expressed genes and the association of genetic variations such as, but not limited to, single nucleotide polymorphisms (SNPs) or splice variants in and between biological samples from experimental and control groups. The goal of such studies is to identify potential avenues for therapeutic intervention in order to prevent, treat the consequences or cure the conditions.

In order to treat diseases, pathologies and other abnormal states or conditions in which a mammalian organism has been diagnosed as being, or as being at risk for becoming, other than in a normal state or condition, it is important to identify new therapeutic agents. Such a procedure includes at least the steps of identifying a target component within an affected tissue or organ, and identifying a candidate therapeutic agent that modulates the functional attributes of the target. The target component may be any biological macromolecule implicated in the disease or pathology. Commonly the target is a polypeptide or protein with specific functional attributes. Other classes of macromolecule may be a nucleic acid, a polysaccharide, a lipid such as a complex lipid or a glycolipid; in addition a target may be a sub-cellular structure or extra-cellular structure that is comprised of more than one of these classes of macromolecule. Once such a target has been identified, it may be employed in a screening assay in order to identify favorable candidate therapeutic agents from among a large population of substances or compounds.

In many cases the objective of such screening assays is to identify small molecule candidates; this is commonly approached by the use of combinatorial methodologies to develop the population of substances to be tested. The implementation of high throughput

screening methodologies is advantageous when working with large, combinatorial libraries of compounds.

It is an objective of this invention to provide at least one target biopolymer that is intended to serve as the macromolecular component in a screening assay for identifying candidate pharmaceutical agents.

It is another objective of the present invention to provide screening assays that positively identify candidate pharmaceutical agents from among a combinatorial library of low molecular weight substances or compounds.

It is still a further objective of this invention to employ the candidate pharmaceutical agents in any of a variety of in vitro, ex vivo and in vivo assays in order to identify pharmaceutical agents with advantageous therapeutic applications in the treatment of a disease, pathology, or abnormal state or condition in a mammal.

Summary Of The Invention

The invention is based in part upon the discovery of nucleic acid sequences encoding novel polypeptides. These nucleic acids and polypeptides, as well as derivatives, homologs, analogs and fragments thereof, will hereinafter be collectively designated as "NOVX" nucleic acid, which represents the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or polypeptide sequences, which represents the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178.

In one aspect, the invention provides an isolated polypeptide comprising a mature form of a NOVX amino acid. One example is a variant of a mature form of a NOVX amino acid sequence, wherein any amino acid in the mature form is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed. The amino acid can be, for example, a NOVX amino acid sequence or a variant of a NOVX amino acid sequence, wherein any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed. The invention also includes fragments of any of these. In another aspect, the invention also includes an isolated nucleic acid that encodes a NOVX polypeptide, or a fragment, homolog, analog or derivative thereof.

Also included in the invention is a NOVX polypeptide that is a naturally occurring allelic variant of a NOVX sequence. In one embodiment, the allelic variant includes an amino acid sequence that is the translation of a nucleic acid sequence differing by a single nucleotide

from a NOVX nucleic acid sequence. In another embodiment, the NOVX polypeptide is a variant polypeptide described therein, wherein any amino acid specified in the chosen sequence is changed to provide a conservative substitution. In one embodiment, the invention discloses a method for determining the presence or amount of the NOVX polypeptide in a sample. The method involves the steps of: providing a sample; introducing the sample to an antibody that binds immunospecifically to the polypeptide; and determining the presence or amount of antibody bound to the NOVX polypeptide, thereby determining the presence or amount of the NOVX polypeptide in the sample. In another embodiment, the invention provides a method for determining the presence of or predisposition to a disease associated with altered levels of a NOVX polypeptide in a mammalian subject. This method involves the steps of: measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and comparing the amount of the polypeptide in the sample of the first step to the amount of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, the disease, wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

In a further embodiment, the invention includes a method of identifying an agent that binds to a NOVX polypeptide. This method involves the steps of: introducing the polypeptide to the agent; and determining whether the agent binds to the polypeptide. In various embodiments, the agent is a cellular receptor or a downstream effector.

In another aspect, the invention provides a method for identifying a potential therapeutic agent for use in treatment of a pathology, wherein the pathology is related to aberrant expression or aberrant physiological interactions of a NOVX polypeptide. The method involves the steps of: providing a cell expressing the NOVX polypeptide and having a property or function ascribable to the polypeptide; contacting the cell with a composition comprising a candidate substance; and determining whether the substance alters the property or function ascribable to the polypeptide; whereby, if an alteration observed in the presence of the substance is not observed when the cell is contacted with a composition devoid of the substance, the substance is identified as a potential therapeutic agent. In another aspect, the invention describes a method for screening for a modulator of activity or of latency or predisposition to a pathology associated with the NOVX polypeptide. This method involves the following steps: administering a test compound to a test animal at increased risk for a pathology associated with the NOVX polypeptide, wherein the test animal recombinantly expresses the NOVX polypeptide. This method involves the steps of measuring the activity of

the NOVX polypeptide in the test animal after administering the compound of step; and comparing the activity of the protein in the test animal with the activity of the NOVX polypeptide in a control animal not administered the polypeptide, wherein a change in the activity of the NOVX polypeptide in the test animal relative to the control animal indicates the test compound is a modulator of latency of, or predisposition to, a pathology associated with the NOVX polypeptide. In one embodiment, the test animal is a recombinant test animal that expresses a test protein transgene or expresses the transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein the promoter is not the native gene promoter of the transgene. In another aspect, the invention includes a method for modulating the activity of the NOVX polypeptide, the method comprising introducing a cell sample expressing the NOVX polypeptide with a compound that binds to the polypeptide in an amount sufficient to modulate the activity of the polypeptide.

The invention also includes an isolated nucleic acid that encodes a NOVX polypeptide, or a fragment, homolog, analog or derivative thereof. In a preferred embodiment, the nucleic acid molecule comprises the nucleotide sequence of a naturally occurring allelic nucleic acid variant. In another embodiment, the nucleic acid encodes a variant polypeptide, wherein the variant polypeptide has the polypeptide sequence of a naturally occurring polypeptide variant. In another embodiment, the nucleic acid molecule differs by a single nucleotide from a NOVX nucleic acid sequence. In one embodiment, the NOVX nucleic acid molecule hybridizes under stringent conditions to the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a complement of the nucleotide sequence. In another aspect, the invention provides a vector or a cell expressing a NOVX nucleotide sequence.

In one embodiment, the invention discloses a method for modulating the activity of a NOVX polypeptide. The method includes the steps of: introducing a cell sample expressing the NOVX polypeptide with a compound that binds to the polypeptide in an amount sufficient to modulate the activity of the polypeptide. In another embodiment, the invention includes an isolated NOVX nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising a NOVX amino acid sequence or a variant of a mature form of the NOVX amino acid sequence, wherein any amino acid in the mature form of the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed. In another embodiment, the invention includes an amino acid sequence that is a variant of the NOVX amino acid sequence, in which any amino acid specified in the chosen sequence is changed to a different

amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed.

In one embodiment, the invention discloses a NOVX nucleic acid fragment encoding at least a portion of a NOVX polypeptide or any variant of the polypeptide, wherein any amino acid of the chosen sequence is changed to a different amino acid, provided that no more than 10% of the amino acid residues in the sequence are so changed. In another embodiment, the invention includes the complement of any of the NOVX nucleic acid molecules or a naturally occurring allelic nucleic acid variant. In another embodiment, the invention discloses a NOVX nucleic acid molecule that encodes a variant polypeptide, wherein the variant polypeptide has the polypeptide sequence of a naturally occurring polypeptide variant. In another embodiment, the invention discloses a NOVX nucleic acid, wherein the nucleic acid molecule differs by a single nucleotide from a NOVX nucleic acid sequence.

In another aspect, the invention includes a NOVX nucleic acid, wherein one or more nucleotides in the NOVX nucleotide sequence is changed to a different nucleotide provided that no more than 15% of the nucleotides are so changed. In one embodiment, the invention discloses a nucleic acid fragment of the NOVX nucleotide sequence and a nucleic acid fragment wherein one or more nucleotides in the NOVX nucleotide sequence is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed. In another embodiment, the invention includes a nucleic acid molecule wherein the nucleic acid molecule hybridizes under stringent conditions to a NOVX nucleotide sequence or a complement of the NOVX nucleotide sequence. In one embodiment, the invention includes a nucleic acid molecule, wherein the sequence is changed such that no more than 15% of the nucleotides in the coding sequence differ from the NOVX nucleotide sequence or a fragment thereof.

In a further aspect, the invention includes a method for determining the presence or amount of the NOVX nucleic acid in a sample. The method involves the steps of: providing the sample; introducing the sample to a probe that binds to the nucleic acid molecule; and determining the presence or amount of the probe bound to the NOVX nucleic acid molecule, thereby determining the presence or amount of the NOVX nucleic acid molecule in the sample. In one embodiment, the presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.

In another aspect, the invention discloses a method for determining the presence of or predisposition to a disease associated with altered levels of the NOVX nucleic acid molecule of in a first mammalian subject. The method involves the steps of: measuring the amount of

NOVX nucleic acid in a sample from the first mammalian subject; and comparing the amount of the nucleic acid in the sample of step (a) to the amount of NOVX nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease; wherein an alteration in the level of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

Detailed Description Of The Invention

The present invention provides novel nucleotides and polypeptides encoded thereby. Included in the invention are the novel nucleic acid sequences, their encoded polypeptides, antibodies, and other related compounds. The sequences are collectively referred to herein as "NOVX nucleic acids" or "NOVX polynucleotides" and the corresponding encoded polypeptides are referred to as "NOVX polypeptides" or "NOVX proteins." Unless indicated otherwise, "NOVX" is meant to refer to any of the novel sequences disclosed herein. Table 1 provides a summary of the NOVX nucleic acids and their encoded polypeptides.

TABLE 1. Sequences and Corresponding SEQ ID Numbers

NOVX No.	Internal Acc. No.	Nucleic Acid SEQ ID NO.	Amino Acid SEQ ID NO.	Homology
1a	CG58522-01	1	2	human platelet activating factor acetylhydrolase
2a	CG58520-01	3	4	GABA(A) receptor
2b	CG58520-02	5	6	GABA(A) receptor
2c	CG58520-03	7	8	GABA(A) receptor

3a	CG58518-01	9	10	GABA(A) receptor
4a	CG58516-01	11	12	Beta transducin
5a	CG58473-01	13	14	Protein kinase
6a	CG58470-01	15	16	UDP-N-acetylhexosamine pyrophosphorylase
7a	CG58593-01	17	18	ubiquitin 52 like
8a	CG57871-01	19	20	tousled like kinase like
9a	CG58590-01	21	22	guanylate kinase like
9b	CG58590-02	23	24	guanylate kinase like
10a	CG58572-01	25	26	glucosamine phosphate N acetyltransferase like
10b	CG58572-02	27	28	glucosamine phosphate N acetyltransferase like
11a	CG58564-01	29	30	Protein tyrosine phosphatase like
11b	CG58564-02	31	32	Protein tyrosine phosphatase like
11c	CG58564-03	33	34	Dual-Specificity phosphatase like
11d	CG58564-04	35	36	Dual-Specificity phosphatase like
12a	CG57819-01	37	38	RPGR interacting protein 1 like
13a	CG57789-01	39	40	RAS like protein RRP22 like
13b	CG57789-02	41	42	RAS like protein RRP22 like
14a	CG57758-01	43	44	sodium/lithium dependent dicarboxylate transporter like
14b	CG57758-02	45	46	sodium/lithium dependent dicarboxylate transporter like
14c	CG57758-03	47	48	sodium/lithium dependent dicarboxylate transporter like
14d	CG57758-04	49	50	sodium/lithium dependent dicarboxylate transporter like
14e	CG57758-05	51	52	sodium/lithium dependent dicarboxylate transporter like
15a	CG57732-01	53	54	Ca 2+ calmodulin dependent protein kinase IV kinase like
15b	CG57732-02	55	56	Ca 2+ calmodulin dependent protein kinase IV kinase like

15c	CG57732-03	57	58	Ca 2+ calmodulin dependent protein kinase IV kinase like
16a	CG57709-01	59	60	TCE2 like
17a	CG57700-01	61	62	hydroxyacylglutathione hydrolase like
17b	CG57700-02	63	64	hydroxyacylglutathione hydrolase like
17c	CG57700-03	65	66	hydroxyacylglutathione hydrolase like
17d	CG57700-04	67	68	hydroxyacylglutathione hydrolase like
18a	CG58553-01	69	70	vasopressin receptor like
19a	CG58626-01	71	72	phosphatidic acid preferring phospholipase A1 like
20a	CG57597-01	73	74	hypothetical protein like
21a	CG57804-01	75	76	Talin like
22a	CG57551-01	77	78	NAC-1 like
23a	CG57411-01	79	80	Kelch like
24a	CG57399-01	81	82	phospholipase ADRA-B precursor like
24b	CG57399-02	83	84	phospholipase ADRA-B precursor like
24c	CG57399-03	85	86	phospholipase ADRA-B precursor like
25a	CG59311-01	87	88	acyl-coenzyme A thioester hydrolase
25b	CG59311-02	89	90	peroxisomal acyl-coenzyme A thioester hydrolase like
25c	CG59311-03	91	92	peroxisomal acyl-coenzyme A thioester hydrolase like
26a	CG59309-01	93	94	acyl-coenzyme A thioester hydrolase
27a	CG57364-01	95	96	CG6896
28a	CG59348-01	97	98	cytoplasmic protein (patent calls this Cyclin L-like)
29a	CG59245-01	99	100	glucose 6-phosphatase
29b	CG59245-02	101	102	glucose 6-phosphatase
30a	CG59241-01	103	104	Amiloride-sensitive sodium channel
31a	CG58602-01	105	106	FAD binding domain containing protein
32a	CG58468-01	107	108	Serum Amyloid Protein
33a	CG58183-01	109	110	N-Methyl-D-Aspartate receptor

34a	CG59315-01	111	112	Connexin
35a	CG59203-01	113	114	lysozyme C
35b	CG59203-02	115	116	lysozyme C
36a	CG58662-01	117	118	cytoplasmic protein
36b	CG58662-02	119	120	cytoplasmic protein
37a	CG58584-01	121	122	40S ribosomal protein S29 like
38a	CG58538-01	123	124	Histone deacetylase complex protein 66 like
39a	CG59371-01	125	126	expressed cytoplasmic protein like
40a	CG59346-01	127	128	cortactin binding protein 1 like
41a	CG57814-01	129	130	Basic I 19 like homo sapiens
41b	CG57814-02	131	132	Basic I 19 like homo sapiens
42a	CG59327-01	133	134	Monocarboxylate transporter 1 like
43a	CG59494-01	135	136	myelin P2 like
44a	CG59432-01	137	138	chloride channel like
44b	CG59432-02	139	140	chloride channel like
45a	CG59394-01	141	142	GPCR like
46a	CG59383-01	143	144	D6MM5E PROTEIN like
46b	CG59383-02	145	146	D6MM5E PROTEIN like
47a	CG58526-01	147	148	scramblase like
48a	CG57851-01	149	150	sulfotransferase like
49a	CG59377-01	151	152	epsin like
50a	CG59258-01	153	154	transcriptional activator like
51a	CG59492-01	155	156	Myosin Head (Motor Domain) like
52a	CG59564-01	157	158	Sorting nexin 6 like
53a	CG59553-01	159	160	Secretory protein SEC8 like
54a	CG59545-01	161	162	Placental protein 13 like
55a	CG59435-01	163	164	Nedd-1 like
55b	CG59435-02	165	166	Nedd-1 like
56a	CG59439-01	167	168	Xenobiotic/medium-chain fatty acid:CoA ligase form XL-III like
56b	CG59439-02	169	170	Xenobiotic/medium-chain fatty acid:CoA ligase form XL-III like
57a	CG59354-01	171	172	phosducin like
57b	CG59354-02	173	174	phosducin like
57c	CG59354-03	175	176	phosducin like
58a	CG59319-01	177	178	phosducin like
58b	CG59319-02	179	180	phosducin like
59a	CG59576-01	181	182	GPCR like
60a	CG59557-01	183	184	GPCR like

61a	CG59555-01	185	186	GPCR like
62a	CG59551-01	187	188	GPCR like
63a	CG59540-01	189	190	GPCR like
64a	CG59280-01	191	192	GPCR like
64b	CG59280-02	193	194	GPCR like
65a	CG59568-01	195	196	GPCR like
66a	CG59224-01	197	198	GPCR like
67a	CG59222-01	199	200	GPCR like
68a	CG59220-01	201	202	GPCR like
69a	CG59218-01	203	204	GPCR like
70a	CG59216-01	205	206	GPCR like
71a	CG59214-01	207	208	GPCR like
72a	CG59211-01	209	210	GPCR like
73a	CG59276-01	211	212	Dihydroorotate dehydrogenase like
74a	CG59268-01	213	214	monooxygenase like
75a	CG59549-01	215	216	H326 like (cytoplasmic protein with WD repeat domain)
76a	CG59641-01	217	218	Acetyl-CoA Carboxylase 2 like
77a	CG59630-01	219	220	Midnolin like
78a	CG59561-01	221	222	ACYL COENZYME A THIOESTER HYDROLASE like
79a	CG59452-01	223	224	CELL PROLIFERATION RELATED PROTEIN CAP like
80a	CG59572-01	225	226	Pseudouridine Synthase 3 like
80b	CG59572-02	227	228	Pseudouridine Synthase 3 like
81a	CG59522-01	229	230	Myosin like
82a	CG59520-01	231	232	Farnesyl- pyrophosphate synthetase like
83a	CG59758-01	233	234	UBIQUITIN like
83b	CG59758-02	235	236	UBIQUITIN like
84a	CG59586-01	237	238	glucokinase like
85a	CG59704-01	239	240	serine/threonine kinase like
86a	CG59628-01	241	242	Short-chain dehydrogenase like
87a	CG59516-01	243	244	Calponin like
87b	CG59516-02	245	246	Calponin like
88a	CG59671-02	247	248	acyl-coenzyme A thioester hydrolase
89a	CG56870-01	249	250	NDRG3 like
89b	CG56870-02	251	252	NDRG3 like
89c	CG56870-03	253	254	NDRG3 like
89d	CG56870-04	255	256	NDRG3 like
89e	CG56870-05	257	258	NDRG3 like
90a	CG59764-01	259	260	Ferritin like

91a	CG59710-01	261	262	P14 like
92a	CG59754-02	263	264	Downs syndrome cell adhesion molecule like
92b	CG59754-01	265	266	Downs syndrome cell adhesion molecule like
93a	CG59800-01	267	268	HEPARAN SULFATE D-GLUCOSAMINYL 3-O-SULFOTRANSFERASE-3B like
94a	CG59761-01	269	270	AXIN 1 (AXIS INHIBITION PROTEIN 1) (HAXIN) like
95a	CG59756-01	271	272	JUNCTOPHILIN TYPE 2 like
96a	CG59708-01	273	274	Ubiquitin carboxyl-terminal hydrolase 21 like
96b	CG59708-02	275	276	Ubiquitin carboxyl-terminal hydrolase 21 like
96c	CG59708-03	277	278	Ubiquitin carboxyl-terminal hydrolase 21 like
97a	CG59559-01	279	280	BA12M19.1.3 like
98a	CG59669-01	281	282	carbonyl reductase (called NADPH-dependent carbonyl reductase-like in patent)
99a	CG58624-01	283	284	metal transporter
100a	CG59679-01	285	286	carbonyl reductase
101a	CG59644-01	287	288	CG12091 (putative protein phosphatase)
102a	CG59662-01	289	290	Cyclophilin
103a	CG59773-01	291	292	Myomegalin
103b	CG59773-02	293	294	Myomegalin
103c	CG59773-03	295	296	Myomegalin
104a	CG57460-01	297	298	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE like
105a	CG57464-01	299	300	N-ACETYLTRANSFERASE like
106a	CG57466-01	301	302	Acetylglucosaminyltransferase like
107a	CG57468-01	303	304	ABC transporter like homo sapiens
108a	CG59609-01	305	306	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A like
109a	CG59613-01	307	308	Proliferating cell nuclear antigen like

110a	CG59619-01	309	310	CYTOPLASMIC ACTIN 2 like
111a	CG59621-01	311	312	SELENOPHOSPHAT E SYNTHETASE like
112a	CG59625-01	313	314	glucose transporter like
113a	CG59887-01	315	316	Amino Acid/Metabolite Permease like
113b	CG59887-02	317	318	Amino Acid/Metabolite Permease like
114a	CG59861-01	319	320	RIBULOSE-5- PHOSPHATE- EPIMERASE like
114b	CG59861-02	321	322	RIBULOSE-5- PHOSPHATE- EPIMERASE like
115a	CG59857-01	323	324	Rhotekin like homo sapiens
116a	CG59855-01	325	326	ATP SYNTHASE SUBUNIT C lik
116b	CG59855-02	327	328	ATP SYNTHASE SUBUNIT C like
117a	CG59807-01	329	330	Zinc finger like
118a	CG59805-01	331	332	Zinc finger like
119a	CG59928-01	333	334	Universal Stress (USP) Domain Containing Protein like
120a	CG59947-01	335	336	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) like
121a	CG59938-01	337	338	arylsulfatase like homo sapiens
122a	CG59746-01	339	340	ubiquitin-specific processing protease like homo sapiens
123a	CG88613-01	341	342	INOSITOL 1,4,5- TRISPHOSPHATE 3- KINASE ISOENZYME like
124a	CG59993-01	343	344	synaptotagmin II like
124b	CG59993-02	345	346	synaptotagmin II like
125a	CG59991-01	347	348	ooplasm specific protein like
126a	CG59987-01	349	350	GTP-RHO binding protein 1 (rhopilin) like
126b	CG59987-02	351	352	GTP-RHO binding protein 1 (rhopilin) like
127a	CG59971-01	353	354	Leucine rich repeat (LRR) like
127b	CG59971-02	355	356	Leucine rich repeat (LRR) like

Table 1 indicates homology of NOVX nucleic acids to known protein families. Thus, the nucleic acids and polypeptides, antibodies and related compounds according to the invention corresponding to a NOVX as identified in column 1 of Table 1 will be useful in therapeutic and diagnostic applications implicated in, for example, pathologies and disorders associated with the known protein families identified in column 5 of Table 1.

NOVX nucleic acids and their encoded polypeptides are useful in a variety of applications and contexts. The various NOVX nucleic acids and polypeptides according to the invention are useful as novel members of the protein families according to the presence of domains and sequence relatedness to previously described proteins. Additionally, NOVX nucleic acids and polypeptides can also be used to identify proteins that are members of the family to which the NOVX polypeptides belong.

Consistent with other known members of the family of proteins, identified in column 5 of Table 1, the NOVX polypeptides of the present invention show homology to, and contain domains that are characteristic of, other members of such protein families. Details of the sequence relatedness and domain analysis for each NOVX are presented in Example A.

The NOVX nucleic acids and polypeptides can also be used to screen for molecules, which inhibit or enhance NOVX activity or function. Specifically, the nucleic acids and polypeptides according to the invention may be used as targets for the identification of small molecules that modulate or inhibit diseases associated with the protein families listed in Table 1.

The NOVX nucleic acids and polypeptides are also useful for detecting specific cell types. Details of the expression analysis for each NOVX are presented in Example C. Accordingly, the NOVX nucleic acids, polypeptides, antibodies and related compounds according to the invention will have diagnostic and therapeutic applications in the detection of a variety of diseases with differential expression in normal vs. diseased tissues, e.g. a variety of cancers.

Additional utilities for NOVX nucleic acids and polypeptides according to the invention are disclosed herein.

The present invention is based on the identification of biological macromolecules differentially modulated in a pathologic state, disease, or an abnormal condition or state. Among the pathologies or diseases of present interest include metabolic diseases including those related to endocrinologic disorders, cancers, various tumors and neoplasias, inflammatory disorders, central nervous system disorders, and similar abnormal conditions or

states. In very significant embodiments of the present invention, the biological macromolecules implicated in the pathologies and conditions are proteins and polypeptides, and in such cases the present invention is related as well to the nucleic acids that encode them. Methods that may be employed to identify relevant biological macromolecules include any procedures that detect differential expression of nucleic acids encoding proteins and polypeptides associated with the disorder, as well as procedures that detect the respective proteins and polypeptides themselves. Significant methods that have been employed by the present inventors, include GeneCalling® technology and SeqCalling™ technology, disclosed respectively, in U. S. Patent No. 5,871,697, and in U. S. Ser. No. 09/417,386, filed Oct. 13, 1999, each of which is incorporated herein by reference in its entirety. GeneCalling® is also described in Shimkets, et al., "Gene expression analysis by transcript profiling coupled to a gene database query" *Nature Biotechnology* 17:198-803 (1999).

The invention provides polypeptides and nucleotides encoded thereby that have been identified as having novel associations with a disease or pathology, or an abnormal state or condition, in a mammal. The present invention further identifies a set of proteins and polypeptides, including naturally occurring polypeptides, precursor forms or proproteins, or mature forms of the polypeptides or proteins, which are implicated as targets for therapeutic agents in the treatment of various diseases, pathologies, abnormal states and conditions. A target may be employed in any of a variety of screening methodologies in order to identify candidate therapeutic agents which interact with the target and in so doing exert a desired or favorable effect. The candidate therapeutic agent is identified by screening a large collection of substances or compounds in an important embodiment of the invention. Such a collection may comprise a combinatorial library of substances or compounds in which, in at least one subset of substances or compounds, the individual members are related to each other by simple structural variations based on a particular canonical or basic chemical structure. The variations may include, by way of nonlimiting example, changes in length or identity of a basic framework of bonded atoms; changes in number, composition and disposition of ringed structures, bridge structures, alicyclic rings, and aromatic rings; and changes in pendent or substituents atoms or groups that are bonded at particular positions to the basic framework of bonded atoms or to the ringed structures, the bridge structures, the alicyclic structures, or the aromatic structures.

A polypeptide or protein described herein, and that serves as a target in the screening procedure, includes the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, e.g., the

full-length gene product, encoded by the corresponding gene. The naturally occurring polypeptide also includes the polypeptide, precursor or proprotein encoded by an open reading frame described herein. A "mature" form of a polypeptide or protein arises as a result of one or more naturally occurring processing steps as they may occur within the cell, including a host cell. The processing steps occur as the gene product arises, e.g., via cleavage of the amino-terminal methionine residue encoded by the initiation codon of an open reading frame, or the proteolytic cleavage of a signal peptide or leader sequence. Thus, a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an amino-terminal signal sequence from residue 1 to residue M is cleaved, includes the residues from residue M+1 to residue N remaining. A "mature" form of a polypeptide or protein may also arise from non-proteolytic post-translational modification. Such non-proteolytic processes include, e.g., glycosylation, myristylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or the combination of any of them.

As used herein, "identical" residues correspond to those residues in a comparison between two sequences where the equivalent nucleotide base or amino acid residue in an alignment of two sequences is the same residue. Residues are alternatively described as "similar" or "positive" when the comparisons between two sequences in an alignment show that residues in an equivalent position in a comparison are either the same amino acid or a conserved amino acid as defined below.

As used herein, a "chemical composition" relates to a composition including at least one compound that is either synthesized or extracted from a natural source. A chemical compound may be the product of a defined synthetic procedure. Such a synthesized compound is understood herein to have defined properties in terms of molecular formula, molecular structure relating the association of bonded atoms to each other, physical properties such as chromatographic or spectroscopic characterizations, and the like. A compound extracted from a natural source is advantageously analyzed by chemical and physical methods in order to provide a representation of its defined properties, including its molecular formula, molecular structure relating the association of bonded atoms to each other, physical properties such as chromatographic or spectroscopic characterizations, and the like.

As used herein, a "candidate therapeutic agent" is a chemical compound that includes at least one substance shown to bind to a target biopolymer. In important embodiments of the

invention, the target biopolymer is a protein or polypeptide, a nucleic acid, a polysaccharide or proteoglycan, or a lipid such as a complex lipid. The method of identifying compounds that bind to the target effectively eliminates compounds with little or no binding affinity, thereby increasing the potential that the identified chemical compound may have beneficial therapeutic applications. In cases where the "candidate therapeutic agent" is a mixture of more than one chemical compound, subsequent screening procedures may be carried out to identify the particular substance in the mixture that is the binding compound, and that is to be identified as a candidate therapeutic agent.

As used herein, a "pharmaceutical agent" is provided by screening a candidate therapeutic agent using models for a disease state or pathology in order to identify a candidate exerting a desired or beneficial therapeutic effect with relation to the disease or pathology. Such a candidate that successfully provides such an effect is termed a pharmaceutical agent herein. Nonlimiting examples of model systems that may be used in such screens include particular cell lines, cultured cells, tissue preparations, whole tissues, organ preparations, intact organs, and nonhuman mammals. Screens employing at least one system, and preferably more than one system, may be employed in order to identify a pharmaceutical agent. Any pharmaceutical agent so identified may be pursued in further investigation using human subjects.

NOVX Nucleic Acids and Polypeptides

NOVX clones

NOVX nucleic acids and their encoded polypeptides are useful in a variety of applications and contexts. The various NOVX nucleic acids and polypeptides according to the invention are useful as novel members of the protein families according to the presence of domains and sequence relatedness to previously described proteins. Additionally, NOVX nucleic acids and polypeptides can also be used to identify proteins that are members of the family to which the NOVX polypeptides belong.

The NOVX genes and their corresponding encoded proteins are useful for preventing, treating or ameliorating medical conditions, *e.g.*, by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the NOVX genes, based on the tissues in which they are most highly expressed. Uses include developing products for the diagnosis or treatment of a variety of diseases and disorders.

The NOVX nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications and as a research tool. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed, as well as potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), and (v) a composition promoting tissue regeneration *in vitro* and *in vivo* (vi) biological defense weapon.

In one specific embodiment, the invention includes an isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178; (b) a variant of a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178, wherein any amino acid in the mature form is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed; (c) an amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178; (d) a variant of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178 wherein any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed; and (e) a fragment of any of (a) through (d).

In another specific embodiment, the invention includes an isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of: (a) a mature form of the amino acid sequence given SEQ ID NO: 2n, wherein n is an integer between 1 and 178; (b) a variant of a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178 wherein any amino acid in the mature form of the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed; (c) the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178; (d) a variant of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178, in which any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed; (e) a nucleic acid

fragment encoding at least a portion of a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 178 or any variant of said polypeptide wherein any amino acid of the chosen sequence is changed to a different amino acid, provided that no more than 10% of the amino acid residues in the sequence are so changed; and (f) the complement of any of said nucleic acid molecules.

In yet another specific embodiment, the invention includes an isolated nucleic acid molecule, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178; (b) a nucleotide sequence wherein one or more nucleotides in the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed; (c) a nucleic acid fragment of the sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178; and (d) a nucleic acid fragment wherein one or more nucleotides in the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed.

One aspect of the invention pertains to isolated nucleic acid molecules that encode NOVX polypeptides or biologically active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify NOVX-encoding nucleic acids (*e.g.*, NOVX mRNAs) and fragments for use as PCR primers for the amplification and/or mutation of NOVX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule may be single-stranded or double-stranded, but preferably is comprised double-stranded DNA.

An NOVX nucleic acid can encode a mature NOVX polypeptide. As used herein, a "mature" form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full-length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the

polypeptide, precursor or proprotein encoded by an ORF described herein. The product "mature" form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a "mature" form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an ORF, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

The term "probes", as utilized herein, refers to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as approximately, *e.g.*, 6,000 nt, depending upon the specific use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are generally obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

The term "isolated" nucleic acid molecule, as utilized herein, is one, which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated NOVX nucleic acid molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, etc.). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by

recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a complement of this aforementioned nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 as a hybridization probe, NOVX molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, *et al.*, (eds.), MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to NOVX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue.

Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a portion of this nucleotide sequence (*e.g.*, a fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an NOVX polypeptide). A nucleic acid molecule that is

complementary to the nucleotide sequence from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 is one that is sufficiently complementary to the nucleotide sequence from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 that it can hydrogen bond with little or no mismatches to the nucleotide sequence from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, thereby forming a stable duplex.

As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

A full-length NOVX clone is identified as containing an ATG translation start codon and an in-frame stop codon. Any disclosed NOVX nucleotide sequence lacking an ATG start codon therefore encodes a truncated C-terminal fragment of the respective NOVX polypeptide, and requires that the corresponding full-length cDNA extend in the 5' direction of the disclosed sequence. Any disclosed NOVX nucleotide sequence lacking an in-frame stop codon similarly encodes a truncated N-terminal fragment of the respective NOVX

polypeptide, and requires that the corresponding full-length cDNA extend in the 3' direction of the disclosed sequence.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. *See e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below.

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of NOVX polypeptides. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the invention, homologous nucleotide sequences include nucleotide sequences encoding for an NOVX polypeptide of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the exact nucleotide sequence encoding human NOVX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, as well as a polypeptide possessing NOVX biological activity. Various biological activities of the NOVX proteins are described below.

An NOVX polypeptide is encoded by the open reading frame ("ORF") of an NOVX nucleic acid. An ORF corresponds to a nucleotide sequence that could potentially be translated into a polypeptide. A stretch of nucleic acids comprising an ORF is uninterrupted by a stop codon. An ORF that represents the coding sequence for a full protein begins with an ATG "start" codon and terminates with one of the three "stop" codons, namely, TAA, TAG, or

TGA. For the purposes of this invention, an ORF may be any part of a coding sequence, with or without a start codon, a stop codon, or both. For an ORF to be considered as a good candidate for coding for a *bona fide* cellular protein, a minimum size requirement is often set, *e.g.*, a stretch of DNA that would encode a protein of 50 amino acids or more.

The nucleotide sequences determined from the cloning of the human NOVX genes allows for the generation of probes and primers designed for use in identifying and/or cloning NOVX homologues in other cell types, *e.g.* from other tissues, as well as NOVX homologues from other vertebrates. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178; or an anti-sense strand nucleotide sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178.

Probes based on the human NOVX nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues which mis-express an NOVX protein, such as by measuring a level of an NOVX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting NOVX mRNA levels or determining whether a genomic NOVX gene has been mutated or deleted.

"A polypeptide having a biologically-active portion of an NOVX polypeptide" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically-active portion of NOVX" can be prepared by isolating a portion SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, that encodes a polypeptide having an NOVX biological activity (the biological activities of the NOVX proteins are described below), expressing the encoded portion of NOVX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of NOVX.

NOVX Nucleic Acid and Polypeptide Variants

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown in SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178

due to degeneracy of the genetic code and thus encode the same NOVX proteins as that encoded by the nucleotide sequences shown in SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NO: 2n, wherein n is an integer between 1 and 178.

In addition to the human NOVX nucleotide sequences shown in SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the NOVX polypeptides may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the NOVX genes may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an NOVX protein, preferably a vertebrate NOVX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the NOVX genes. Any and all such nucleotide variations and resulting amino acid polymorphisms in the NOVX polypeptides, which are the result of natural allelic variation and that do not alter the functional activity of the NOVX polypeptides, are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding NOVX proteins from other species, and thus that have a nucleotide sequence that differs from the human SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the NOVX cDNAs of the invention can be isolated based on their homology to the human NOVX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500, 750, 1000, 1500, or 2000 or more nucleotides in length. In yet another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding NOVX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5 °C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions are hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C, followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequences SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well-known within the art. *See, e.g.*, Ausubel, et al. (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990; GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequences SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). *See, e.g.*, Ausubel, et al. (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981. *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative Mutations

In addition to naturally-occurring allelic variants of NOVX sequences that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, thereby leading to changes in the amino acid sequences of the encoded NOVX proteins, without altering the functional ability of said NOVX proteins. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence SEQ ID NO: 2n, wherein n is an integer between 1 and 178. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the NOVX proteins without altering their biological activity, whereas an

"essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the NOVX proteins of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known within the art.

Another aspect of the invention pertains to nucleic acid molecules encoding NOVX proteins that contain changes in amino acid residues that are not essential for activity. Such NOVX proteins differ in amino acid sequence from SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45% homologous to the amino acid sequences SEQ ID NO: 2n, wherein n is an integer between 1 and 178. Preferably, the protein encoded by the nucleic acid molecule is at least about 60% homologous to SEQ ID NO: 2n, wherein n is an integer between 1 and 178; more preferably at least about 70% homologous SEQ ID NO: 2n, wherein n is an integer between 1 and 178; still more preferably at least about 80% homologous to SEQ ID NO: 2n, wherein n is an integer between 1 and 178; even more preferably at least about 90% homologous to SEQ ID NO: 2n, wherein n is an integer between 1 and 178; and most preferably at least about 95% homologous to SEQ ID NO: 2n, wherein n is an integer between 1 and 178.

An isolated nucleic acid molecule encoding an NOVX protein homologous to the protein of SEQ ID NO: 2n, wherein n is an integer between 1 and 178 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted, non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined within the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side

chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted non-essential amino acid residue in the NOVX protein is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an NOVX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for NOVX biological activity to identify mutants that retain activity. Following mutagenesis SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

The relatedness of amino acid families may also be determined based on side chain interactions. Substituted amino acids may be fully conserved "strong" residues or fully conserved "weak" residues. The "strong" group of conserved amino acid residues may be any one of the following groups: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW, wherein the single letter amino acid codes are grouped by those amino acids that may be substituted for each other. Likewise, the "weak" group of conserved residues may be any one of the following: CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK, NEQHRK, HFY, wherein the letters within each group represent the single letter amino acid code.

In one embodiment, a mutant NOVX protein can be assayed for (i) the ability to form protein:protein interactions with other NOVX proteins, other cell-surface proteins, or biologically-active portions thereof, (ii) complex formation between a mutant NOVX protein and an NOVX ligand; or (iii) the ability of a mutant NOVX protein to bind to an intracellular target protein or biologically-active portion thereof; (*e.g.* avidin proteins).

In yet another embodiment, a mutant NOVX protein can be assayed for the ability to regulate a specific biological function (*e.g.*, regulation of insulin release).

Antisense Nucleic Acids

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein (*e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence). In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire NOVX coding strand, or to only a portion thereof. Nucleic acid molecules

encoding fragments, homologs, derivatives and analogs of an NOVX protein of SEQ ID NO: 2n, wherein n is an integer between 1 and 178, or antisense nucleic acids complementary to an NOVX nucleic acid sequence of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an NOVX protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding the NOVX protein. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding the NOVX protein disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of NOVX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of NOVX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of NOVX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally-occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids (*e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used).

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxymethylaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil,

2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an NOVX protein to thereby inhibit expression of the protein (*e.g.*, by inhibiting transcription and/or translation). The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface (*e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens). The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient nucleic acid molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other. *See, e.g.*, Gaultier, *et al.*, 1987. *Nucl. Acids Res.* **15**: 6625-6641. The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (*See, e.g.*, Inoue, *et al.* 1987. *Nucl. Acids Res.* **15**: 6131-6148) or a chimeric RNA-DNA analogue (*See, e.g.*, Inoue, *et al.*, 1987. *FEBS Lett.* **215**: 327-330).

Ribozymes and PNA Moieties

Nucleic acid modifications include, by way of non-limiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In one embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes as described in Haselhoff and Gerlach 1988. *Nature* 334: 585-591) can be used to catalytically cleave NOVX mRNA transcripts to thereby inhibit translation of NOVX mRNA. A ribozyme having specificity for an NOVX-encoding nucleic acid can be designed based upon the nucleotide sequence of an NOVX cDNA disclosed herein (*i.e.*, SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an NOVX-encoding mRNA. *See, e.g.*, U.S. Patent 4,987,071 to Cech, *et al.* and U.S. Patent 5,116,742 to Cech, *et al.* NOVX mRNA can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. *See, e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, NOVX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the NOVX nucleic acid (*e.g.*, the NOVX promoter and/or enhancers) to form triple helical structures that prevent transcription of the NOVX gene in target cells. *See, e.g.*, Helene, 1991. *Anticancer Drug Des.* 6: 569-84; Helene, *et al.* 1992. *Ann. N.Y. Acad. Sci.* 660: 27-36; Maher, 1992. *Bioassays* 14: 807-15.

In various embodiments, the NOVX nucleic acids can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids. *See, e.g.*, Hyrup, *et al.*, 1996. *Bioorg Med Chem* 4: 5-23. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (*e.g.*, DNA mimics) in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using

standard solid phase peptide synthesis protocols as described in Hyrup, *et al.*, 1996. *supra*; Perry-O'Keefe, *et al.*, 1996. *Proc. Natl. Acad. Sci. USA* 93: 14670-14675.

PNAs of NOVX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of NOVX can also be used, for example, in the analysis of single base pair mutations in a gene (*e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S₁ nucleases (*See*, Hyrup, *et al.*, 1996.*supra*); or as probes or primers for DNA sequence and hybridization (*See*, Hyrup, *et al.*, 1996, *supra*; Perry-O'Keefe, *et al.*, 1996. *supra*).

In another embodiment, PNAs of NOVX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of NOVX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (*e.g.*, RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (*see*, Hyrup, *et al.*, 1996. *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, *et al.*, 1996. *supra* and Finn, *et al.*, 1996. *Nucl Acids Res* 24: 3357-3363. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA. *See, e.g.*, Mag, *et al.*, 1989. *Nucl Acid Res* 17: 5973-5988. PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment. *See, e.g.*, Finn, *et al.*, 1996. *supra*. Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. *See, e.g.*, Petersen, *et al.*, 1975. *Bioorg. Med. Chem. Lett.* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (*see, e.g.*, Letsinger, *et al.*, 1989. *Proc. Natl. Acad. Sci. U.S.A.* 86: 6553-6556; Lemaitre, *et al.*, 1987. *Proc. Natl. Acad. Sci.* 84: 648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (*see, e.g.*, PCT Publication No. WO 89/10134). In

addition, oligonucleotides can be modified with hybridization triggered cleavage agents (*see, e.g., Krol, et al., 1988. BioTechniques 6:958-976*) or intercalating agents (*see, e.g., Zon, 1988. Pharm. Res. 5: 539-549*). To this end, the oligonucleotide may be conjugated to another molecule, *e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.*

NOVX Polypeptides

A polypeptide according to the invention includes a polypeptide including the amino acid sequence of NOVX polypeptides whose sequences are provided in SEQ ID NO: 2n, wherein n is an integer between 1 and 178. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in SEQ ID NO: 2n, wherein n is an integer between 1 and 178 while still encoding a protein that maintains its NOVX activities and physiological functions, or a functional fragment thereof.

In general, an NOVX variant that preserves NOVX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

One aspect of the invention pertains to isolated NOVX proteins, and biologically-active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-NOVX antibodies. In one embodiment, native NOVX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, NOVX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, an NOVX protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" polypeptide or protein or biologically-active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the NOVX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of NOVX proteins in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly-produced. In

one embodiment, the language "substantially free of cellular material" includes preparations of NOVX proteins having less than about 30% (by dry weight) of non-NOVX proteins (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-NOVX proteins, still more preferably less than about 10% of non-NOVX proteins, and most preferably less than about 5% of non-NOVX proteins. When the NOVX protein or biologically-active portion thereof is recombinantly-produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the NOVX protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins having less than about 30% (by dry weight) of chemical precursors or non-NOVX chemicals, more preferably less than about 20% chemical precursors or non-NOVX chemicals, still more preferably less than about 10% chemical precursors or non-NOVX chemicals, and most preferably less than about 5% chemical precursors or non-NOVX chemicals.

Biologically-active portions of NOVX proteins include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of the NOVX proteins (*e.g.*, the amino acid sequence shown in SEQ ID NO: 2n, wherein n is an integer between 1 and 178) that include fewer amino acids than the full-length NOVX proteins, and exhibit at least one activity of an NOVX protein. Typically, biologically-active portions comprise a domain or motif with at least one activity of the NOVX protein. A biologically-active portion of an NOVX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acid residues in length. Moreover, other biologically-active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native NOVX protein.

In an embodiment, the NOVX protein has an amino acid sequence shown SEQ ID NO: 2n, wherein n is an integer between 1 and 178. In other embodiments, the NOVX protein is substantially homologous to SEQ ID NO: 2n, wherein n is an integer between 1 and 178, and retains the functional activity of the protein of SEQ ID NO: 2n, wherein n is an integer between 1 and 178, yet differs in amino acid sequence due to natural allelic variation or

mutagenesis, as described in detail, below. Accordingly, in another embodiment, the NOVX protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino acid sequence SEQ ID NO: 2n, wherein n is an integer between 1 and 178, and retains the functional activity of the NOVX proteins of SEQ ID NO: 2n, wherein n is an integer between 1 and 178.

Determining Homology Between Two or More Sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. *See*, Needleman and Wunsch, 1970. *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178.

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a

polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region.

Chimeric and Fusion Proteins

The invention also provides NOVX chimeric or fusion proteins. As used herein, an NOVX "chimeric protein" or "fusion protein" comprises an NOVX polypeptide operatively-linked to a non-NOVX polypeptide. An "NOVX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an NOVX protein SEQ ID NO: 2n, wherein n is an integer between 1 and 178, whereas a "non-NOVX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the NOVX protein, *e.g.*, a protein that is different from the NOVX protein and that is derived from the same or a different organism. Within an NOVX fusion protein the NOVX polypeptide can correspond to all or a portion of an NOVX protein. In one embodiment, an NOVX fusion protein comprises at least one biologically-active portion of an NOVX protein. In another embodiment, an NOVX fusion protein comprises at least two biologically-active portions of an NOVX protein. In yet another embodiment, an NOVX fusion protein comprises at least three biologically-active portions of an NOVX protein. Within the fusion protein, the term "operatively-linked" is intended to indicate that the NOVX polypeptide and the non-NOVX polypeptide are fused in-frame with one another. The non-NOVX polypeptide can be fused to the N-terminus or C-terminus of the NOVX polypeptide.

In one embodiment, the fusion protein is a GST-NOVX fusion protein in which the NOVX sequences are fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant NOVX polypeptides.

In another embodiment, the fusion protein is an NOVX protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of NOVX can be increased through use of a heterologous signal sequence.

In yet another embodiment, the fusion protein is an NOVX-immunoglobulin fusion protein in which the NOVX sequences are fused to sequences derived from a member of the immunoglobulin protein family. The NOVX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit

an interaction between an NOVX ligand and an NOVX protein on the surface of a cell, to thereby suppress NOVX-mediated signal transduction *in vivo*. The NOVX-immunoglobulin fusion proteins can be used to affect the bioavailability of an NOVX cognate ligand. Inhibition of the NOVX ligand/NOVX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the NOVX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-NOVX antibodies in a subject, to purify NOVX ligands, and in screening assays to identify molecules that inhibit the interaction of NOVX with an NOVX ligand.

An NOVX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (*see, e.g.*, Ausubel, *et al.* (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An NOVX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the NOVX protein.

NOVX Agonists and Antagonists

The invention also pertains to variants of the NOVX proteins that function as either NOVX agonists (*i.e.*, mimetics) or as NOVX antagonists. Variants of the NOVX protein can be generated by mutagenesis (*e.g.*, discrete point mutation or truncation of the NOVX protein). An agonist of the NOVX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the NOVX protein. An antagonist of the NOVX protein can inhibit one or more of the activities of the naturally occurring form of the NOVX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the NOVX protein. Thus, specific

biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the NOVX proteins.

Variants of the NOVX proteins that function as either NOVX agonists (*i.e.*, mimetics) or as NOVX antagonists can be identified by screening combinatorial libraries of mutants (*e.g.*, truncation mutants) of the NOVX proteins for NOVX protein agonist or antagonist activity. In one embodiment, a variegated library of NOVX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of NOVX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential NOVX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of NOVX sequences therein. There are a variety of methods which can be used to produce libraries of potential NOVX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential NOVX sequences. Methods for synthesizing degenerate oligonucleotides are well-known within the art. *See, e.g.*, Narang, 1983. *Tetrahedron* 39: 3; Itakura, *et al.*, 1984. *Annu. Rev. Biochem.* 53: 323; Itakura, *et al.*, 1984. *Science* 198: 1056; Ike, *et al.*, 1983. *Nucl. Acids Res.* 11: 477.

Polypeptide Libraries

In addition, libraries of fragments of the NOVX protein coding sequences can be used to generate a variegated population of NOVX fragments for screening and subsequent selection of variants of an NOVX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an NOVX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double-stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S_1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, expression libraries can

be derived which encodes N-terminal and internal fragments of various sizes of the NOVX proteins.

Various techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of NOVX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify NOVX variants. See, e.g., Arkin and Yourvan, 1992. *Proc. Natl. Acad. Sci. USA* 89: 7811-7815; Delgrave, *et al.*, 1993. *Protein Engineering* 6:327-331.

NOVX Antibodies

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, antibody molecules obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated protein of the invention intended to serve as an antigen, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 2n, wherein n is an

integer between 1 and 178, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of NOVX that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human NOVX protein sequence will indicate which regions of a NOVX polypeptide are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each incorporated herein by reference in their entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a

recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to

elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., **133**:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., **107**:220 (1980). It is an objective, especially important in therapeutic applications of monoclonal antibodies, to

identify antibodies having a high degree of specificity and a high binding affinity for the target antigen.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods (Goding, 1986). Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature **368**, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-

binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

Human Antibodies

Fully human antibodies essentially relate to antibody molecules in which the entire sequence of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon

challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab')₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab')₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit. Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of

immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific

antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994). Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic

agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active

toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

Immunoliposomes

The antibodies disclosed herein can also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon et al., J. National Cancer Inst., 81(19): 1484 (1989).

Diagnostic Applications of Antibodies Directed Against the Proteins of the Invention

Antibodies directed against a protein of the invention may be used in methods known within the art relating to the localization and/or quantitation of the protein (e.g., for use in measuring levels of the protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies against the proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antigen binding domain, are utilized as pharmacologically-active compounds (see below).

An antibody specific for a protein of the invention can be used to isolate the protein by standard techniques, such as immunoaffinity chromatography or immunoprecipitation. Such an antibody can facilitate the purification of the natural protein antigen from cells and of recombinantly produced antigen expressed in host cells. Moreover, such an antibody can be used to detect the antigenic protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the antigenic protein. Antibodies directed against the protein can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include

luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

Antibody Therapeutics

Antibodies of the invention, including polyclonal, monoclonal, humanized and fully human antibodies, may be used as therapeutic agents. Such agents will generally be employed to treat or prevent a disease or pathology in a subject. An antibody preparation, preferably one having high specificity and high affinity for its target antigen, is administered to the subject and will generally have an effect due to its binding with the target. Such an effect may be one of two kinds, depending on the specific nature of the interaction between the given antibody molecule and the target antigen in question. In the first instance, administration of the antibody may abrogate or inhibit the binding of the target with an endogenous ligand to which it naturally binds. In this case, the antibody binds to the target and masks a binding site of the naturally occurring ligand, wherein the ligand serves as an effector molecule. Thus the receptor mediates a signal transduction pathway for which ligand is responsible.

Alternatively, the effect may be one in which the antibody elicits a physiological result by virtue of binding to an effector binding site on the target molecule. In this case the target, a receptor having an endogenous ligand which may be absent or defective in the disease or pathology, binds the antibody as a surrogate effector ligand, initiating a receptor-based signal transduction event by the receptor.

A therapeutically effective amount of an antibody of the invention relates generally to the amount needed to achieve a therapeutic objective. As noted above, this may be a binding interaction between the antibody and its target antigen that, in certain cases, interferes with the functioning of the target, and in other cases, promotes a physiological response. The amount required to be administered will furthermore depend on the binding affinity of the antibody for its specific antigen, and will also depend on the rate at which an administered antibody is depleted from the free volume of the subject to which it is administered. Common ranges for therapeutically effective dosing of an antibody or antibody fragment of the invention may be, by way of nonlimiting example, from about 0.1 mg/kg body weight to about 50 mg/kg body weight. Common dosing frequencies may range, for example, from twice daily to once a week.

Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a protein of the invention, as well as other molecules identified by the screening assays disclosed herein, can be administered for the treatment of various disorders in the form of pharmaceutical compositions. Principles and considerations involved in preparing such compositions, as well as guidance in the choice of components are provided, for example, in Remington : The Science And Practice Of Pharmacy 19th ed. (Alfonso R. Gennaro, et al., editors) Mack Pub. Co., Easton, Pa. : 1995; Drug Absorption Enhancement : Concepts, Possibilities, Limitations, And Trends, Harwood Academic Publishers, Langhorne, Pa., 1994; and Peptide And Protein Drug Delivery (Advances In Parenteral Sciences, Vol. 4), 1991, M. Dekker, New York.

If the antigenic protein is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, e.g., Marasco et al., Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein can also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition can comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients can also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions.

The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations can be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules.

Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOTTM (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods.

ELISA Assay

An agent for detecting an analyte protein is an antibody capable of binding to an analyte protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, F_{ab} or $F_{(ab)_2}$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. Included within the usage of the term "biological sample", therefore, is blood and a fraction or component of blood including blood serum, blood plasma, or lymph. That is, the detection method of the invention can be used to detect an analyte mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of an analyte mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of an analyte protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of an analyte genomic DNA include Southern hybridizations. Procedures for conducting immunoassays are described, for example in "ELISA: Theory and Practice: Methods in Molecular Biology", Vol. 42, J. R. Crowther (Ed.) Human Press, Totowa, NJ, 1995; "Immunoassay", E. Diamandis and T. Christopoulos, Academic Press, Inc., San Diego, CA, 1996; and "Practice and Theory of Enzyme Immunoassays", P. Tijssen, Elsevier Science Publishers, Amsterdam, 1985. Furthermore, *in*

vivo techniques for detection of an analyte protein include introducing into a subject a labeled anti-analyte protein antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

NOVX Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an NOVX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably-linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell).

The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, NOVX proteins, mutant forms of NOVX proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of NOVX proteins in prokaryotic or eukaryotic cells. For example, NOVX proteins can be expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase. Expression of proteins in prokaryotes is most often carried out in *Escherichia coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (i) to increase expression of recombinant protein; (ii) to increase the solubility of the recombinant protein; and (iii) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, e.g., Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (see, e.g., Wada, *et al.*, 1992. *Nucl. Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the NOVX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerevisiae* include pYepSec1 (Baldari, *et al.*, 1987. *EMBO J.* 6: 229-234), pMFa (Kurjan and Herskowitz, 1982. *Cell* 30: 933-943), pJRY88 (Schultz *et al.*, 1987. *Gene* 54: 113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, NOVX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., SF9 cells) include the pAc series (Smith, *et al.*, 1983. *Mol. Cell. Biol.* 3: 2156-2165) and the pVL series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987. *Nature* 329: 840) and pMT2PC (Kaufman, *et al.*, 1987. *EMBO J.* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see, e.g., Chapters 16 and 17 of Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, *et al.*, 1987. *Genes Dev.* 1:

268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43: 235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8: 729-733) and immunoglobulins (Banerji, *et al.*, 1983. *Cell* 33: 729-740; Queen and Baltimore, 1983. *Cell* 33: 741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477), pancreas-specific promoters (Edlund, *et al.*, 1985. *Science* 230: 912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss, 1990. *Science* 249: 374-379) and the α -fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3: 537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively-linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to NOVX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes *see, e.g.*, Weintraub, *et al.*, "Antisense RNA as a molecular tool for genetic analysis," *Reviews-Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, NOVX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as

Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding NOVX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) NOVX protein. Accordingly, the invention further provides methods for producing NOVX protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding NOVX protein has been introduced) in a suitable medium such that NOVX protein is produced. In another embodiment, the method further comprises isolating NOVX protein from the medium or the host cell.

Transgenic NOVX Animals

The host cells of the invention can also be used to produce non-human transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which NOVX protein-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous

NOVX sequences have been introduced into their genome or homologous recombinant animals in which endogenous NOVX sequences have been altered. Such animals are useful for studying the function and/or activity of NOVX protein and for identifying and/or evaluating modulators of NOVX protein activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous NOVX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing NOVX-encoding nucleic acid into the male pronuclei of a fertilized oocyte (*e.g.*, by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal. The human NOVX cDNA sequences SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a non-human homologue of the human NOVX gene, such as a mouse NOVX gene, can be isolated based on hybridization to the human NOVX cDNA (described further *supra*) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably-linked to the NOVX transgene to direct expression of NOVX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan, 1986. In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the NOVX transgene in its genome and/or expression of NOVX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene-

encoding NOVX protein can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of an NOVX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the NOVX gene. The NOVX gene can be a human gene (*e.g.*, the cDNA of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178), but more preferably, is a non-human homologue of a human NOVX gene. For example, a mouse homologue of human NOVX gene of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 can be used to construct a homologous recombination vector suitable for altering an endogenous NOVX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous NOVX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous NOVX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous NOVX protein). In the homologous recombination vector, the altered portion of the NOVX gene is flanked at its 5'- and 3'-termini by additional nucleic acid of the NOVX gene to allow for homologous recombination to occur between the exogenous NOVX gene carried by the vector and an endogenous NOVX gene in an embryonic stem cell. The additional flanking NOVX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector. *See, e.g.*, Thomas, *et al.*, 1987. *Cell* 51: 503 for a description of homologous recombination vectors. The vector is then introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced NOVX gene has homologously-recombined with the endogenous NOVX gene are selected. *See, e.g.*, Li, *et al.*, 1992. *Cell* 69: 915.

The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras. *See, e.g.*, Bradley, 1987. In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for

constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, 1991. *Curr. Opin. Biotechnol.* 2: 823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, See, e.g., Lakso, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae*. See, O'Gorman, *et al.*, 1991. *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut, *et al.*, 1997. *Nature* 385: 810-813. In brief, a cell (e.g., a somatic cell) from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell (e.g., the somatic cell) is isolated.

Pharmaceutical Compositions

The NOVX nucleic acid molecules, NOVX proteins, and anti-NOVX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field,

which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (*i.e.*, topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic

acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, an NOVX protein or anti-NOVX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid

derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see, e.g.*, U.S. Patent No. 5,328,470) or by stereotactic injection (*see, e.g.*, Chen, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced

intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Screening and Detection Methods

The isolated nucleic acid molecules of the invention can be used to express NOVX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect NOVX mRNA (*e.g.*, in a biological sample) or a genetic lesion in an NOVX gene, and to modulate NOVX activity, as described further, below. In addition, the NOVX proteins can be used to screen drugs or compounds that modulate the NOVX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of NOVX protein or production of NOVX protein forms that have decreased or aberrant activity compared to NOVX wild-type protein (*e.g.*; diabetes (regulates insulin release); obesity (binds and transport lipids); metabolic disturbances associated with obesity, the metabolic syndrome X as well as anorexia and wasting disorders associated with chronic diseases and various cancers, and infectious disease (possesses anti-microbial activity) and the various dyslipidemias. In addition, the anti-NOVX antibodies of the invention can be used to detect and isolate NOVX proteins and modulate NOVX activity. In yet a further aspect, the invention can be used in methods to influence appetite, absorption of nutrients and the disposition of metabolic substrates in both a positive and negative fashion.

The invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described, *supra*.

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs) that bind to NOVX proteins or have a stimulatory or inhibitory effect on, *e.g.*, NOVX protein expression or NOVX protein activity. The invention also includes compounds identified in the screening assays described herein. In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of an NOVX protein or polypeptide or biologically-active portion thereof. The test compounds of the invention can be

obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds. *See, e.g., Lam, 1997. Anticancer Drug Design 12: 145.*

A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be, *e.g.,* nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention.

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt, *et al.*, 1993. *Proc. Natl. Acad. Sci. U.S.A.* 90: 6909; Erb, *et al.*, 1994. *Proc. Natl. Acad. Sci. U.S.A.* 91: 11422; Zuckermann, *et al.*, 1994. *J. Med. Chem.* 37: 2678; Cho, *et al.*, 1993. *Science* 261: 1303; Carrell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2059; Carell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2061; and Gallop, *et al.*, 1994. *J. Med. Chem.* 37: 1233.

Libraries of compounds may be presented in solution (*e.g.,* Houghten, 1992. *Biotechniques* 13: 412-421), or on beads (Lam, 1991. *Nature* 354: 82-84), on chips (Fodor, 1993. *Nature* 364: 555-556), bacteria (Ladner, U.S. Patent No. 5,223,409), spores (Ladner, U.S. Patent 5,233,409), plasmids (Cull, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 1865-1869) or on phage (Scott and Smith, 1990. *Science* 249: 386-390; Devlin, 1990. *Science* 249: 404-406; Cwirla, *et al.*, 1990. *Proc. Natl. Acad. Sci. U.S.A.* 87: 6378-6382; Felici, 1991. *J. Mol. Biol.* 222: 301-310; Ladner, U.S. Patent No. 5,233,409.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to an NOVX protein determined. The cell, for example, can be of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the NOVX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the NOVX protein or biologically-active portion thereof can be determined by detecting the labeled compound in a complex. For

example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically-labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a known compound which binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX protein or a biologically-active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of NOVX or a biologically-active portion thereof can be accomplished, for example, by determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule. As used herein, a "target molecule" is a molecule with which an NOVX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses an NOVX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. An NOVX target molecule can be a non-NOVX molecule or an NOVX protein or polypeptide of the invention. In one embodiment, an NOVX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.* a signal generated by binding of a compound to a membrane-bound NOVX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with NOVX.

Determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the NOVX protein to bind to or interact with an NOVX target molecule can be accomplished by determining the activity of the

target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising an NOVX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the invention is a cell-free assay comprising contacting an NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to bind to the NOVX protein or biologically-active portion thereof. Binding of the test compound to the NOVX protein can be determined either directly or indirectly as described above. In one such embodiment, the assay comprises contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX or biologically-active portion thereof as compared to the known compound.

In still another embodiment, an assay is a cell-free assay comprising contacting NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.* stimulate or inhibit) the activity of the NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of NOVX can be accomplished, for example, by determining the ability of the NOVX protein to bind to an NOVX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of NOVX protein can be accomplished by determining the ability of the NOVX protein further modulate an NOVX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as described, *supra*.

In yet another embodiment, the cell-free assay comprises contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an NOVX protein, wherein determining the ability of the test compound to interact with an NOVX protein comprises determining the

ability of the NOVX protein to preferentially bind to or modulate the activity of an NOVX target molecule.

The cell-free assays of the invention are amenable to use of both the soluble form or the membrane-bound form of NOVX protein. In the case of cell-free assays comprising the membrane-bound form of NOVX protein, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of NOVX protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the invention, it may be desirable to immobilize either NOVX protein or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to NOVX protein, or interaction of NOVX protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-NOVX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or NOVX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described, *supra*. Alternatively, the complexes can be dissociated from the matrix, and the level of NOVX protein binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either the NOVX protein or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated NOVX protein or target molecules can be prepared from biotin-NHS

(N-hydroxy-succinimide) using techniques well-known within the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with NOVX protein or target molecules, but which do not interfere with binding of the NOVX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or NOVX protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the NOVX protein or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the NOVX protein or target molecule.

In another embodiment, modulators of NOVX protein expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of NOVX mRNA or protein in the cell is determined. The level of expression of NOVX mRNA or protein in the presence of the candidate compound is compared to the level of expression of NOVX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of NOVX mRNA or protein expression based upon this comparison. For example, when expression of NOVX mRNA or protein is greater (*i.e.*, statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of NOVX mRNA or protein expression. Alternatively, when expression of NOVX mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of NOVX mRNA or protein expression. The level of NOVX mRNA or protein expression in the cells can be determined by methods described herein for detecting NOVX mRNA or protein.

In yet another aspect of the invention, the NOVX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (*see, e.g.*, U.S. Patent No. 5,283,317; Zervos, *et al.*, 1993. *Cell* 72: 223-232; Madura, *et al.*, 1993. *J. Biol. Chem.* 268: 12046-12054; Bartel, *et al.*, 1993. *Biotechniques* 14: 920-924; Iwabuchi, *et al.*, 1993. *Oncogene* 8: 1693-1696; and Brent WO 94/10300), to identify other proteins that bind to or interact with NOVX ("NOVX-binding proteins" or "NOVX-bp") and modulate NOVX activity. Such NOVX-binding proteins are also likely to be involved in the propagation of signals by the NOVX proteins as, for example, upstream or downstream elements of the NOVX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes

two different DNA constructs. In one construct, the gene that codes for NOVX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming an NOVX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with NOVX.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. By way of example, and not of limitation, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Some of these applications are described in the subsections, below.

Chromosome Mapping

Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. This process is called chromosome mapping. Accordingly, portions or fragments of the NOVX sequences, SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or fragments or derivatives thereof, can be used to map the location of the NOVX genes, respectively, on a chromosome. The mapping of the NOVX sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Briefly, NOVX genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the NOVX sequences. Computer analysis of the NOVX sequences can be used to rapidly select primers that do not span more than one exon in the

genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the NOVX sequences will yield an amplified fragment.

Somatic cell hybrids are prepared by fusing somatic cells from different mammals (*e.g.*, human and mouse cells). As hybrids of human and mouse cells grow and divide, they gradually lose human chromosomes in random order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow, because they lack a particular enzyme, but in which human cells can, the one human chromosome that contains the gene encoding the needed enzyme will be retained. By using various media, panels of hybrid cell lines can be established. Each cell line in a panel contains either a single human chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, allowing easy mapping of individual genes to specific human chromosomes. *See, e.g.*, D'Eustachio, *et al.*, 1983. *Science* 220: 919-924. Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human chromosomes with translocations and deletions.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using a single thermal cycler. Using the NOVX sequences to design oligonucleotide primers, sub-localization can be achieved with panels of fragments from specific chromosomes.

Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step.

Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical like colcemid that disrupts the mitotic spindle. The chromosomes can be treated briefly with trypsin, and then stained with Giemsa. A pattern of light and dark bands develops on each chromosome, so that the chromosomes can be identified individually. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases, will suffice to get good results at a reasonable amount of time. For a review of this technique, *see*, Verma, *et al.*, HUMAN CHROMOSOMES: A MANUAL OF BASIC TECHNIQUES (Pergamon Press, New York 1988).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for

marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, *e.g.*, in McKusick, MENDELIAN INHERITANCE IN MAN, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, *e.g.*, Egeland, *et al.*, 1987. *Nature*, 325: 783-787.

Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the NOVX gene, can be determined. If a mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

Tissue Typing

The NOVX sequences of the invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Patent No. 5,272,057). Furthermore, the sequences of the invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the NOVX sequences described herein can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such

DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The NOVX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining NOVX protein and/or nucleic acid expression as well as NOVX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant NOVX expression or activity. The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with NOVX protein, nucleic acid expression or activity. For example, mutations in an NOVX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby

prophylactically treat an individual prior to the onset of a disorder characterized by or associated with NOVX protein, nucleic acid expression, or biological activity.

Another aspect of the invention provides methods for determining NOVX protein, nucleic acid expression or activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics").

Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of NOVX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

An exemplary method for detecting the presence or absence of NOVX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting NOVX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes NOVX protein such that the presence of NOVX is detected in the biological sample. An agent for detecting NOVX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to NOVX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length NOVX nucleic acid, such as the nucleic acid of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 178, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to NOVX mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

An agent for detecting NOVX protein is an antibody capable of binding to NOVX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and

end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect NOVX mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of NOVX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of NOVX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of NOVX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of NOVX protein include introducing into a subject a labeled anti-NOVX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting NOVX protein, mRNA, or genomic DNA, such that the presence of NOVX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of NOVX protein, mRNA or genomic DNA in the control sample with the presence of NOVX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of NOVX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting NOVX protein or mRNA in a biological sample; means for determining the amount of NOVX in the sample; and means for comparing the amount of NOVX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect NOVX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant NOVX expression or activity. For example, the assays described herein, such as the preceding

diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with NOVX protein, nucleic acid expression or activity. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the invention provides a method for identifying a disease or disorder associated with aberrant NOVX expression or activity in which a test sample is obtained from a subject and NOVX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of NOVX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant NOVX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant NOVX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. Thus, the invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant NOVX expression or activity in which a test sample is obtained and NOVX protein or nucleic acid is detected (*e.g.*, wherein the presence of NOVX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant NOVX expression or activity).

The methods of the invention can also be used to detect genetic lesions in an NOVX gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell proliferation and/or differentiation. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding an NOVX-protein, or the misexpression of the NOVX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of: (i) a deletion of one or more nucleotides from an NOVX gene; (ii) an addition of one or more nucleotides to an NOVX gene; (iii) a substitution of one or more nucleotides of an NOVX gene, (iv) a chromosomal rearrangement of an NOVX gene; (v) an alteration in the level of a messenger RNA transcript of an NOVX gene, (vi) aberrant modification of an NOVX gene, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild-type splicing pattern

of a messenger RNA transcript of an NOVX gene, (viii) a non-wild-type level of an NOVX protein, (ix) allelic loss of an NOVX gene, and (x) inappropriate post-translational modification of an NOVX protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in an NOVX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (*see, e.g.*, U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (*see, e.g.*, Landegran, *et al.*, 1988. *Science* 241: 1077-1080; and Nakazawa, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 360-364), the latter of which can be particularly useful for detecting point mutations in the NOVX-gene (*see*, Abravaya, *et al.*, 1995. *Nucl. Acids Res.* 23: 675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to an NOVX gene under conditions such that hybridization and amplification of the NOVX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (*see*, Guatelli, *et al.*, 1990. *Proc. Natl. Acad. Sci. USA* 87: 1874-1878), transcriptional amplification system (*see*, Kwoh, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA* 86: 1173-1177); Q β Replicase (*see*, Lizardi, *et al.*, 1988. *BioTechnology* 6: 1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in an NOVX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (*see, e.g.*, U.S. Patent

No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in NOVX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotide probes. *See, e.g.*, Cronin, *et al.*, 1996. *Human Mutation* 7: 244-255; Kozal, *et al.*, 1996. *Nat. Med.* 2: 753-759. For example, genetic mutations in NOVX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin, *et al.*, *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the NOVX gene and detect mutations by comparing the sequence of the sample NOVX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert, 1977. *Proc. Natl. Acad. Sci. USA* 74: 560 or Sanger, 1977. *Proc. Natl. Acad. Sci. USA* 74: 5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (*see, e.g.*, Naeve, *et al.*, 1995. *Biotechniques* 19: 448), including sequencing by mass spectrometry (*see, e.g.*, PCT International Publication No. WO 94/16101; Cohen, *et al.*, 1996. *Adv. Chromatography* 36: 127-162; and Griffin, *et al.*, 1993. *Appl. Biochem. Biotechnol.* 38: 147-159).

Other methods for detecting mutations in the NOVX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes. *See, e.g.*, Myers, *et al.*, 1985. *Science* 230: 1242. In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type NOVX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S₁

nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. *See, e.g., Cotton, et al., 1988. Proc. Natl. Acad. Sci. USA 85: 4397; Saleeba, et al., 1992. Methods Enzymol. 217: 286-295.* In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in NOVX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches. *See, e.g., Hsu, et al., 1994. Carcinogenesis 15: 1657-1662.* According to an exemplary embodiment, a probe based on an NOVX sequence, *e.g., a wild-type NOVX sequence*, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. *See, e.g., U.S. Patent No. 5,459,039.*

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in NOVX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids. *See, e.g., Orita, et al., 1989. Proc. Natl. Acad. Sci. USA: 86: 2766; Cotton, 1993. Mutat. Res. 285: 125-144; Hayashi, 1992. Genet. Anal. Tech. Appl. 9: 73-79.*

Single-stranded DNA fragments of sample and control NOVX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. *See, e.g., Keen, et al., 1991. Trends Genet. 7: 5.*

In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). *See, e.g., Myers, et al., 1985. Nature 313: 495.* When DGGE is

used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. *See, e.g., Rosenbaum and Reissner, 1987. Biophys. Chem. 265: 12753.*

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. *See, e.g., Saiki, et al., 1986. Nature 324: 163; Saiki, et al., 1989. Proc. Natl. Acad. Sci. USA 86: 6230.* Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization; *see, e.g., Gibbs, et al., 1989. Nucl. Acids Res. 17: 2437-2448*) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (*see, e.g., Prossner, 1993. Tibtech. 11: 238*). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. *See, e.g., Gasparini, et al., 1992. Mol. Cell Probes 6: 1.* It is anticipated that in certain embodiments amplification may also be performed using *Taq* ligase for amplification. *See, e.g., Barany, 1991. Proc. Natl. Acad. Sci. USA 88: 189.* In such cases, ligation will occur only if there is a perfect match at the 3'-terminus of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.,* in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an NOVX gene.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which NOVX is expressed may be utilized in the prognostic assays described herein. However, any

biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on NOVX activity (*e.g.*, NOVX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.) In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996. *Clin. Exp. Pharmacol. Physiol.*, 23: 983-985; Linder, 1997. *Clin. Chem.*, 43: 254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome PREGNANCY ZONE PROTEIN PRECURSOR enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an NOVX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of NOVX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase NOVX gene expression, protein levels, or upregulate NOVX activity, can be monitored in clinical trials of subjects exhibiting decreased NOVX gene expression, protein

levels, or downregulated NOVX activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease NOVX gene expression, protein levels, or downregulate NOVX activity, can be monitored in clinical trials of subjects exhibiting increased NOVX gene expression, protein levels, or upregulated NOVX activity. In such clinical trials, the expression or activity of NOVX and, preferably, other genes that have been implicated in, for example, a cellular proliferation or immune disorder can be used as a "read out" or markers of the immune responsiveness of a particular cell.

By way of example, and not of limitation, genes, including NOVX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates NOVX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of NOVX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of NOVX or other genes. In this manner, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of an NOVX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the pre-administration sample with the NOVX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of NOVX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased

administration of the agent may be desirable to decrease expression or activity of NOVX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant NOVX expression or activity. The disorders include cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm; adenocarcinoma, lymphoma, uterus cancer, fertility, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial asthma, Crohn's disease; multiple sclerosis, treatment of Albright Hereditary Osteodystrophy, and other diseases, disorders and conditions of the like.

These methods of treatment will be discussed more fully, below.

Disease and Disorders

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to: (i) an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to an aforementioned peptide; (iii) nucleic acids encoding an aforementioned peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to an aforementioned peptide) that are utilized to "knockout" endogenous function of an aforementioned peptide by homologous recombination (*see, e.g.*, Capecchi, 1989. *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between an aforementioned peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of an aforementioned peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, and the like).

Prophylactic Methods

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant NOVX expression or activity, by administering to the subject an agent that modulates NOVX expression or at least one NOVX activity. Subjects at risk for a disease that is caused or contributed to by aberrant NOVX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the NOVX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending upon the type of NOVX aberrancy, for example, an NOVX agonist or NOVX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein. The prophylactic methods of the invention are further discussed in the following subsections.

Therapeutic Methods

Another aspect of the invention pertains to methods of modulating NOVX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of NOVX protein activity associated with the cell. An agent that modulates NOVX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate

ligand of an NOVX protein, a peptide, an NOVX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more NOVX protein activity. Examples of such stimulatory agents include active NOVX protein and a nucleic acid molecule encoding NOVX that has been introduced into the cell. In another embodiment, the agent inhibits one or more NOVX protein activity. Examples of such inhibitory agents include antisense NOVX nucleic acid molecules and anti-NOVX antibodies. These modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an NOVX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g., up-regulates or down-regulates) NOVX expression or activity. In another embodiment, the method involves administering an NOVX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant NOVX expression or activity.

Stimulation of NOVX activity is desirable *in situations* in which NOVX is abnormally downregulated and/or in which increased NOVX activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant cell proliferation and/or differentiation (e.g., cancer or immune associated disorders). Another example of such a situation is where the subject has a gestational disease (e.g., preeclampsia).

Determination of the Biological Effect of the Therapeutic

In various embodiments of the invention, suitable *in vitro* or *in vivo* assays are performed to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Prophylactic and Therapeutic Uses of the Compositions of the Invention

The NOVX nucleic acids and proteins of the invention are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders including, but not limited to: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.

As an example, a cDNA encoding the NOVX protein of the invention may be useful in gene therapy, and the protein may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the invention will have efficacy for treatment of patients suffering from: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias.

Both the novel nucleic acid encoding the NOVX protein, and the NOVX protein of the invention, or fragments thereof, may also be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. A further use could be as an anti-bacterial molecule (*i.e.*, some peptides have been found to possess anti-bacterial properties). These materials are further useful in the generation of antibodies, which immunospecifically-bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

Sequence Analyses

The sequence of NOVX was derived by laboratory cloning of cDNA fragments, by *in silico* prediction of the sequence. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, were cloned. *In silico* prediction was based on sequences available in CuraGen's proprietary sequence databases or in the public human sequence databases, and provided either the full length DNA sequence, or some portion thereof.

The laboratory cloning was performed using one or more of the methods summarized below:

SeqCalling™ Technology: cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then sequenced using CuraGen Corporation's SeqCalling technology which is disclosed in full in U. S. Ser. Nos. 09/417,386 filed Oct. 13, 1999, and 09/614,505 filed July 11, 2000. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatics programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

Variant sequences are also included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, when a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern. Examples include alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, and stability of transcribed message.

Presented information includes that associated with genomic clones, public genes and ESTs sharing sequence identity with the disclosed sequence and CuraGen Corporation's Electronic Northern bioinformatic tool.

Examples

Example A: Sequence related information

The NOV1 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 1A.

Table 1A. NOV1 Sequence Analysis			
	SEQ ID NO: 1	711 bp	
NOV1a, CG58522-01 DNA Sequence	TGCAGAATGAACCAAGGAGACTCAAACCCAGCAGCTACTCCGCATGCGGCAGAAGAC TTCAAGGAGATGACAGATGGATGTGTGTCAGCACAAACAGATTGTTTGGACTGTAAAG CAAACAGCCTGATGTACCATTTGCGGGAGGCTCCGTGGTGCACTTACTGCAGCCATA GAGATATGGCGAGAGCTTTTTTCCCCTTCATGCACTGAATTTTGGAACTGGGGGAG ATACAACAAGACATGTTTGTGGAGACTAAAGAGCGGAGAACTGGGGAATACTAAGCC TAAGGTCATTGTTTTCTGGCTAGGAAGAAACAACCATGAAAATATGGCAGAAGAGGT GCAGGTGGTATGGCGGCCATCGTACAACCTTATCAACACAAGGCAGCCACAGGCCAA TCATTGTATTGTATCTGTTACCTCAAGGTGAGAAACCAACCTTTGAGGCAAAAGAA CGCCAAGGTGAACCCACTCGTCAAGATTTCGCTGCTGAACTTACCAACGTGCAGCT CTGGATACTGACAGGGGTTTCGTGCACTCCGACCGTGCCATCTCCTGCCACGACATG TTGATTTTCTGCATTGTGACAGGAGGTGGCTACTCAAAGGTCTGCAACCTTGAATGA ACTGATCATGCAGTTGTTGGAGGAAACACCTGAGGAGAGAAACAAACCACCATGTGCTG <u>CTGGCTCCCATGAGT</u>		
	ORF Start: ATG at 7	ORF Stop: TGA at 694	
	SEQ ID NO: 2	229 aa	MW at 25656.2kD
NOV1a, CG58522-01 Protein Sequence	MNQGDSNPAATPHAEDIQGDDRWMCQHNRFLDCKDKQPDVPFAGGSVVQLLPYEI WRELFSPLHALNFTGGDTTRHVLWRLKSGELGNTKPKVIVFWLGRNNHENMAEEVAG GMAAIVQLINTRQPAKIIIVFDLLPQGEKPNPLRQKNAKVNPLVKISLLKLTNVQLLD TDRGFVHSDRAISCHDMFDLHLTGGGYSKVCKPLNELIMQLEETPEEKQTTIA		

Further analysis of the NOV1a protein yielded the following properties shown in Table 1B.

Table 1B. Protein Sequence Properties NOV1a	
Psort analysis:	0.6500 probability located in cytoplasm; 0.2340 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space; 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV1a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 1C.

Table 1C. Geneseq Results for NOV1a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV1a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB49433	Human beta platelet activating factor acetylhydrolase - Homo sapiens, 229 aa. [US6146868-A, 14-NOV-2000]	1..229 1..229	196/229 (85%) 209/229 (90%)	e-114
AAB49432	Rat beta platelet activating factor acetylhydrolase - Rattus norvegicus, 229 aa. [US6146868-A, 14-NOV-2000]	1..229 1..229	195/229 (85%) 208/229 (90%)	e-114
AAB49434	Murine beta platelet activating factor acetylhydrolase - Mus musculus, 229 aa. [US6146868-A, 14-NOV-2000]	1..229 1..229	192/229 (83%) 205/229 (88%)	e-111
AAB49436	Bovine gamma platelet activating factor acetylhydrolase - Bos taurus, 232 aa. [US6146868-A, 14-NOV-2000]	4..219 3..218	124/216 (57%) 165/216 (75%)	5e-74
AAB49435	Human gamma platelet activating factor acetylhydrolase - Homo sapiens, 231 aa. [US6146868-A, 14-NOV-2000]	4..219 3..218	124/216 (57%) 164/216 (75%)	2e-73

In a BLAST search of public sequence databases, the NOV1a protein was found to have homology to the proteins shown in the BLASTP data in Table 1D.

Table 1D. Public BLASTP Results for NOV1a				
Protein Accession Number	Protein/Organism/Length	NOV1a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q29459	Platelet-activating factor acetylhydrolase IB beta subunit (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH beta subunit) (PAFAH beta subunit) - Homo sapiens (Human), and, 229 aa.	1..229 1..229	196/229 (85%) 209/229 (90%)	e-114
O35264	Platelet-activating factor acetylhydrolase IB beta subunit (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH beta subunit) (PAFAH beta subunit) (Platelet-activating factor acetylhydrolase alpha 2 subunit) (PAF-AH alpha 2) - Rattus norvegicus (Rat), 229 aa.	1..229 1..229	195/229 (85%) 208/229 (90%)	e-113
Q61206	Platelet-activating factor acetylhydrolase IB beta subunit (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH beta subunit) (PAFAH beta subunit) - Mus musculus (Mouse), 229 aa.	1..229 1..229	192/229 (83%) 205/229 (88%)	e-111
Q29460	Platelet-activating factor acetylhydrolase IB gamma subunit (EC 3.1.1.47) (PAF acetylhydrolase 29 kDa subunit) (PAF-AH 29 kDa subunit) (PAF-AH gamma subunit) (PAFAH gamma subunit) - Bos taurus (Bovine), 232 aa.	4..219 3..218	125/216 (57%) 165/216 (75%)	8e-74
Q15102	Platelet-activating factor acetylhydrolase IB gamma subunit (EC 3.1.1.47) (PAF acetylhydrolase 29 kDa subunit) (PAF-AH 29 kDa subunit) (PAF-AH gamma subunit) (PAFAH gamma subunit) - Homo sapiens (Human), 231 aa.	4..219 3..218	124/216 (57%) 164/216 (75%)	7e-73

PFam analysis predicts that the NOV1a protein contains the domains shown in the Table 1E.

Table 1E. Domain Analysis of NOV1a

Pfam Domain	NOV1a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PAF-AH: domain 1 of 1	7..221	150/215 (70%) 186/215 (87%)	6e-147

Example 2.

The NOV2 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 2A.

Table 2A. NOV2 Sequence Analysis			
	SEQ ID NO: 3	1457 bp	
NOV2a, CG58520-01 DNA Sequence	CGATTCCGATGGGTCCTTTGAAAGCTTTTCTCTCTCCCTTTTCTTCTGCGGAGTCA AAGTAGAGGGGTGAGGTTGGTCTTCTTGTACTGACCCTGCATTGGGAAACGTTGAT AAGGCAGATGATGAAGATGATGAGGATTTAACGGTGAACAAAACCTGGGTCTTGGCCC CAAAAATTCATGAAGGAGATATCACAAAATTCGAATTCATTGCTTCAAGGCTATGA CAATAAACTTCGTCCAGATATAGGAGTGAGGCCACAGTAATTGAACTGATGTTTAT GTAAACAGCATTGGACCAGTTGATCCAATTAATATGGAATATACAATAGATATAATT TTGCCCAAACCTGGTTTGACAGTCGTTTAAATTCATAGTACCATGAAAGTGCTTAT GCTTAACAGTAATATGGTTGGAAAAATTTGGATTCTGACACTTCTTCAGAACTCA AGAAAATCTGATGCTCACTGGATAACAACCTCTAATCGTCTGCTTCGAATTTGGAATG ATGGACGAGTTCTGTATACTCTAAGGAGATTGACAATTAATGCAGAATGTTATCTTCA GCTTCATAACTTTCCCATGGATGAACATTCTGTCCACTGGAATTTCAAGCTTCTCT ATAGATGGATACCCATAAAATGAAATTGAGTTATCAATGGAAGCGAAGTTCTGTGGAA GTGGCGCACACAAGATCCGGAGATTATATCAGTTTGCATTTTGAGGGTTACGGAACCT AACTGAAATCACTCACACGATCTCTGGGGATTATGTTATCATGACAATTTTTTTTGAC CTGAGCAGAAGAATGGGATATTTCACTATTGACACTACATTCCATGCATTCTGACAG TTGTTCTTTTCTGGGTGTCTTTTGGATCAATAAAGATGCAGTGCCTGCAAGAACATC GTTGGGTATGACATCTATAGGTATCACTACAGTTCTGACTATGACAACCTGAGTACA ATTGCCAGGAAGTCTTTACCTAAGGTTTCTTATGTGACTGCGATGGATCTCTTGTGTT CTGTTTGTGTTTCATTTTGTGTTTTGTCAGCCTTGATGGAATATGGAACCTTGCAATATT TACCAGCAACCAAAAGGAAAGACTGCTACTAAAGACAGAAAGCTAAAAATAAAGCC TCGACTCCTGGTCTCCATCCTGGATCCACTCTGATTCCAATGAATAATATTTCTGTGC CGCAAGAAGATGATTATGGGTATCAGTGTTTGGAGGGCAAGATTGTGCCAGCTTCTT CTGTGTGCTTTGAAGACTGCAGAACAGGATCTTGGAGGGAAGGAAGGATACACATACGC ATTGCCAAAATGACTCTTATTCTAGAATATTTTCCCAACCGCTTTTGCCTGTTC ACTTGGTTTATTGGGTTGGCTATCTTACTTATAAAATCTACTTCATAAGCAAAAATC AAAAGAA		
	ORF Start: ATG at 9	ORF Stop: TAA at 1425	
	SEQ ID NO: 4	472 aa	MW at 54100.9kD
NOV2a, CG58520-01 Protein Sequence	MGPLKAFLEFSPFLRLRSQSRGVRLVFLLLTLHLGNVDKADDEDEDLTVNKTWVLPKFI HEGDIQTILNSLLQGYDNKLRPDIGVRPTVIETDVVNSIGPVPDINMEYTDIIIFAQ TWFDRLKFNSTMKVLMNSNMVGIWIPDTFFRNSRKSDAHWITTPNRLRLRIWINDGR VLYTLRRLTINAECYLQHNPFMDHESCPLEFSSFSIDGYPKNEIELSMEAKFCGSGR HKIRRLYQFAFVGLRNSTEIHTISGDYVIMTIFDLSRRMGYFTIQTQYIPICLTVVL SWVSFWINKDAVPARTSLGMTSIGITTVLTMSTLTIARKSLPKVSYVTAMDLFVSVC FIFVFAALMEYGLTHYFTSNQKGKTATKDRKLKNKASTPGLHPGSTLIIPMNNISVPQE DDYGYQCLEGGKDCASFFCCFEDCRTGSWREGRIHIRIAKIDSYSRIFFPTAFALFNLV YWVGYLYL		
	SEQ ID NO: 5	1521 bp	
NOV2b, CG58520-02 DNA Sequence	CAACCAAGAGGCAAGAGGCGAGAGAAGGAAAAAAAAAAGCGATGAGTTCGCCAAAT ATATGGAGCACAGGAAGCTCAGTCTACTCGACTCCTGTATTTTACAGAAAATGACGG TGTGGATTCTGCTCCTGCTGTGCTCTACCTGGCTTCACTAGCCAGAAATCTGATGA TGACTATGAAGATTATGCTTCTAACAAAACATGGGTCTTGACTCCAAAAGTTCTGAG GGTGATGTCACTGTCTATCTTAAACAACCTGCTGGAAGGATATGACAATAAACTTCGGC CTGATATAGGAGTGAAGCCAACGTTAATTCACACAGACATGTATGTGAATAGCATTGG TCCAGTGAACGCTATCAATATGGAATACACTATTGATATATTTTTTGGCGAAACGTGG TATGACAGACGTTTGAAATTTAACAGCACCATTAAAGTCTCCGATTGAACAGCAACA TGGTGGGAAAACTGGATTCCAGACACTTTCTTCAGAAATTCAAAAAAGCTGATGC ACACTGGATCACCAACCCCAACAGGATGCTGAGAATTTGGAATGATGGTCGAGTGCTC TACACCCTAAGGTTGACAATTGATGCTGAGTGCCAATTACAATTGCACAACCTTCCAA TGGATGAACACTCCTGCCCTTGGAGTTCTCCAGTTATGGCTATCCACGTGAAGAAAT		

	TGTATTATCAATGGAAGCGAAGTTCTGTTGAAGTGGGCGACACAAGATCCTGGAGGCTT TATCAATTCTCATTGTTGGTCTAAGAAATACCACCGAAGTAGTGAAGACAACCTCCG GAGATTATGTGGTCATGTCTGTCTACTTTGATCTGAGCAGAAGAATGGGATACTTTAC CATCCAGACCTATATCCCTGCACACTCATTGTCGTCTATCCTGGGTGTCTTTCTGG ATCAATAAGGATGCTGTTCCAGCCAGAACATCTTTAGGTATCACCAGTGTCTCTGACAA TGACCACCTCAGCACCATTTGCCCGGAAATCGCTCCCCAAGGTCTCCTATGTCACAGC GATGGATCTCTTTGTATCTGTTTGTTCATCTTTGTCTCTCTGCTCTGGTGGAGTAT GGCACCTTGCAATTATTTGTGAGCAACCGGAAACCAAGCAAGGACAAAGATAAAAAAGA AGAAAAACCTCTCTCGGATGTTTCTTCAAGGCCCTACCATTGATATCCGCCCT AAGATCAGCAACCATTCAAATGAATAATGTACACACCTTCAAGAGAGAGATGAAGAG TACGGCTATGAGTGTCTGGACGGCAAGGACTGTGCCAGTTTTTCTGCTGTTTGAAG ATTGTGCAACAGGAGCTTGGAGACATGGGAGGATACATATCCGCAATTGCCAAATGGA CTCCTATGCTCGGATCTTCTTCCCCACTGCCTTCTGCTGTTTAATCTGGTCTATTGG GTCTCTACCTCTACCTGTGAGGAGGTATGGGTTTTACTGATATGGTCTTATTCACT GAGTCTCATGGAG		
	ORF Start: ATG at 44	ORF Stop: TGA at 1469	
	SEQ ID NO: 6	475 aa	MW at 55184.9kD
NOV2b, CG58520-02 Protein Sequence	MSSPNIWSTGSSVYSTPVFSQKMTVWILLLSLYPGFTSQKSDDDYEDYASNKTWVLT PKVPEGDVTVILNLLLEGYDNKLRPDIGVKPTLIHDMYVNSIGPVNAINMEYITIDIF FAQTWYDRRLKFNSTIKVLRNLNSNMVGKIWI PDTFFRNSKKADAHWITTPNRLRIWN DGRVLYTLRLTIDAECQLQLHNFPMDEHSCPLEFSSYGYPREIEVYQWRSSVEVGDT RSWRLYQFSFVGLRNTTEVVKTTSGDYVVMVYFDLSRRMGYFTIQTYPICTLIIVLS WVSFWINKDAVPARTSLGITTTLMTLSTIARKSLPKVSVYTAMDLFVSVCFIFVFS ALVEYGLHYFVSNRKPSKDKDKKKKNP LLRMFSFKAPTIDIRPSATIQMNNATHLQ ERDEEYGYECLDGKDCASFFCCFEDCRTGAWRHGRIHIRIAKMDSYARIFPPTAFCLF NLVYVWSYLYL		
	SEQ ID NO: 7	1455 bp	
NOV2c, CG58520-03 DNA Sequence	TAGTGCAGCACAGTAAAAAGCGATTCCGATGGGTCTTTGAAAGCTTTTCTCTTCT CCCCTTTTCTCTCGCGAGTCAAAGTAGAGGGGTGAGGTTGGTCTTCTTGTACTGAC CCTGCATTTGGGAACTGGGTGTGATAAGGCAGATGATGAAGATGATGAGGATTAAAGC GTGAACAAAACTGGGTCTTGGCCCCAAAAATTCATGAAGGAGATATCACAAATTC TGAATTCATTGCTTCAAGGCTATGACAATAAACTTCGTCCAGATATAGGAGTGAGGCC CACAGTAATTGAACTGATGTTTATGTAACAGCATTGGACCAGTTGATCCAATTAAT ATGGAATATACAATAGATATAAATTTTGCCCAAACTGGTTTGACAGTCGTTTAAAT TCAATAGTACCATGAAAGTGCTTATGCTTAACAGTAATATGGTTGGAAAAATTTGGAT TCCTGACACTTTCTTCAGAACTCAAGAAAATCTGATGCTCACTGGATAACAACTCCT AATCGTCTGCTTCGAATTTGGAATGATGGACGAGTCTGTATACTCTAAGGTGACAA TTAATGCAGAAATGTTATCTTCAGCTTCATAACTTTCCCATGGATGAACATTCCTGTCC ACTGGAATTTTCAAGCGATGGATACCTTAAAAATGAAATTGAGTATAAGTGGAAAAAG CCCTCCGTAGAAGTGGCTGATCCTAAATACTGGAGATTATATCAGTTTGCATTTGTAG GGTTACGGAACTCAACTGAAATCACTCACACGATCTCTGGTGATTATGTTATCATGAC AATTTTTTTGACCTGAGCAGAAGAATGGGATATTTCACTATTGACACTACATCCA TGCATTCTGACAGTTGTTCTTTCTTGGGTGTCTTTTGGATCAATAAAGATGCAGTGC CTGCAAGAACATCGTTGGGTATCACTACAGTTCGACTATGACAACCTTGAGTACAAT TGCCAGGAAGTCTTTACCTAAGGTTTCTTATGTGACTGCGATGGATCTCTTTGTTCT GTTTGTTTCATTTTGTTTTTCAGCCTTGATGGAATATGGAACCTTGCATTATTTTA CCAGCAACCAAAAAGGAAAGACTGCTACTAAAGACAGAAAGCTAAAAAATAAGCCTC GGTAACTCCTGGTCTCCATCCTGGATCCACTCTGATTCCAATGAATAATATTTCTGTG CCGCAAGAAGATGATTATGGGTATCAGTGTGAGGGGCAAGATTGTGCCAGCTTCT TCTGTTGCTTTGAAGACTGCAGAACAGGATCTTGAGGGAAGGAAGGATACACATACG CATTGCCAAAATGACTCTTATTCTAGAATATTTTCCCAACCGCTTTTGCCCTGTTC AACTTGGTTTATTGGGTGGCTATCTTTACTTATAAAATCTACTTCATAAGCAAAAT CAAAA		
	ORF Start: ATG at 31	ORF Stop: TAA at 1426	
	SEQ ID NO: 8	465 aa	MW at 53597.3kD
NOV2c, CG58520-03 Protein Sequence	MGPLKAFLESPFLRSQSRGVRLVFLLTLHLGNWVDKADDEDDEDLTVNKTWVLAPK IHEGDITQILNSLLQGYDNKLRPDIGVRPTVIE TDVYVNSIGPVDPIINMEYITIDIFA QTWFSRLKFNSTMKVLMNSNMVGKIWI PDTFFRNSRKSDAHWITTPNRLRIWNDG RVLVTLRLTINAECYLQLHNFPMDEHSCPLEFSSDGYPKNEIEYKWKPKSVEVADPKY WRLYQFAFVGLRNSTEITHITISGDYVIMTIFFDLSRRMGYFTIQTYPICTLIIVLSW SFWINKDAVPARTSLGITTTLMTLSTIARKSLPKVSVYTAMDLFVSVCFIFVFAAL MEYGT LHYFTSNQKGTATKDRKLKNKASVTPLHPGSTLIPMNNISVPQEDDYGYQC LEGKDCASFFCCFEDCRTGSWREGRIHIRIAKIDSYSRIFFPTAFALFNLVYVWGVL L		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 2B.

Table 2B. Comparison of NOV2a against NOV2b through NOV2c.		
Protein Sequence	NOV2a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV2b	24..472	311/458 (67%)
	27..475	352/458 (75%)
NOV2c	1..472	414/474 (87%)
	1..465	415/474 (87%)

Further analysis of the NOV2a protein yielded the following properties shown in Table 2C.

Table 2C. Protein Sequence Properties NOV2a	
Psort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 38 and 39

A search of the NOV2a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 2D.

Table 2D. Geneseq Results for NOV2a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV2a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41007	Human polypeptide SEQ ID NO 5938 - Homo sapiens, 489 aa. [WO200153312-A1, 26-JUL-2001]	24..472 49..489	334/451 (74%) 379/451 (83%)	0.0
AAM39221	Human polypeptide SEQ ID NO 2366 - Homo sapiens, 467 aa. [WO200153312-A1, 26-JUL-2001]	24..472 27..467	334/451 (74%) 379/451 (83%)	0.0
AAR83968	GABA-A receptor gamma-3 subunit - Homo sapiens, 467 aa. [WO9529234-A1, 02-NOV-1995]	24..472 5..467	300/472 (63%) 356/472 (74%)	e-169

AAW59048	GABA-A receptor epsilon subunit related protein - Mammalia, 506 aa. [DE19644501-A1, 30-APR-1998]	62..472 70..506	193/448 (43%) 274/448 (61%)	e-102
AAW61045	Human GABA receptor epsilon subunit - Homo sapiens, 506 aa. [WO9823742-A1, 04-JUN-1998]	62..472 70..506	193/448 (43%) 274/448 (61%)	e-102

In a BLAST search of public sequence databases, the NOV2a protein was found to have homology to the proteins shown in the BLASTP data in Table 2E.

Table 2E. Public BLASTP Results for NOV2a				
Protein Accession Number	Protein/Organism/Length	NOV2a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P23574	Gamma-aminobutyric-acid receptor gamma-1 subunit precursor (GABA(A) receptor) - Rattus norvegicus (Rat), 465 aa.	1..472 1..465	426/475 (89%) 440/475 (91%)	0.0
Q9R0Y8	Gamma-aminobutyric-acid receptor gamma-1 subunit precursor (GABA(A) receptor) - Mus musculus (Mouse), 465 aa.	1..472 1..465	420/477 (88%) 434/477 (90%)	0.0
JH0824	gamma-aminobutyric acid A receptor gamma 1 chain precursor - chicken, 464 aa.	16..472 12..464	390/463 (84%) 416/463 (89%)	0.0
JH0316	gamma-aminobutyric acid A receptor gamma 2 chain alternatively spliced precursor - mouse, 466 aa.	24..472 26..466	336/451 (74%) 380/451 (83%)	0.0
P18508	Gamma-aminobutyric-acid receptor gamma-2 subunit precursor (GABA(A) receptor) - Rattus norvegicus (Rat), 466 aa.	24..472 26..466	335/451 (74%) 379/451 (83%)	0.0

PFam analysis predicts that the NOV2a protein contains the domains shown in the Table 2F.

Table 2F. Domain Analysis of NOV2a			
Pfam Domain	NOV2a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Neur_chan_LBD: domain 1 of 1	63..273	66/271 (24%) 162/271 (60%)	2.7e-56
Cys-protease-3C: domain 1 of 1	363..369	4/7 (57%) 6/7 (86%)	5.2
Neur_chan_memb: domain 1 of 1	280..466	44/297 (15%) 164/297 (55%)	1.2e-60

Example 3.

The NOV3 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 3A.

Table 3A. NOV3 Sequence Analysis			
	SEQ ID NO: 9	1440 bp	
NOV3a, CG58518-01 DNA Sequence	GAAGAGATGGTCCTGGCTTTCAGTTAGTCTCCTTCACCTACATCTGGATCATATTGA AACCAAATGTTTGTGCTGCTTCTAACATCAAGATGACACACCAGCGGTGCTCCTCTT AATGAAACAAACCTGGAAAACAAGAACTAGAATGAAGAAAGATGACAGTACCAAAGCG CGGCCTCAGAAATATGAGCAACTTCTCCATATAGAGGACAACGATTTCCGCAATGAGA CTGGATTGGAGGTGAGTATTATCCTCTCAAAATTGGGTCTCCAGTGCCAGTAGGTAT AGATGTCCATGTTGAAAGCATTGACAGCATTTCAGAGACTAACATGGTAAGTTTCTTC ATGGGATATGACTTTACAATGACTTTTTATCTCAGGCATTACTGGAAAGACGAGAGG TCTCCTTTCTAGCACAGCAACAAAGCATGACATTTGATCATAGATTGACCAGAA GATCTGGGTGCTGATATCTTTTGTCCACTCTAAAAGATCCTTCATCCATGATACA ACTATGGAGAAATATCATGCTGCGCGTACACCTGATGGAAACGTCCTCCCTAAGTCTCA GGAGGATAACGGTTTCGGCCATGTGCTTTATGGATTTCAGCAGGTTTCTCTTGACAG TCAAAATTGTTCTCTTGAAGTGGAAAGCGCCTACAATGAGGATGACCTAATGCTATAC TGGAAACACGGAACAAGTCCCTTAAATACTGAAGAACATATGTCCTTCTCAGTTCT TCATTGAAGACTTCAGTGCATCTAGTGGATTAGCTTCTATAGCAGCACAGGTTGGTA CAATAGGCTTTTCATCACTTTGTGCTAAGGAGGCATGTTTTCTTCTTGTGCTGCA ACCTATTTCCAGCCATATTGATGGTGATGCTTTCATGGGTTTCATTTGGATTGAC GAAGAGCTGTCTGCAAGAGTTTCCCTGGGTGGAATCACCACAGTCTGACCATGTG CACAATCATCACTGCTGTGAGCGCCTCCATGCCCCAGGTGTCTACCTCAAGGCTGT GATGTGTACCTGTGGGTGAGCTCCCTCTTTGTGTTCTGTGTCAGTCATTGATGTCAG CTGTGAACCTACCTACCCACAGTGGAAAGAGCGGAACAATTCAAGAAGACAGGAAAGGT ACAGATTTCTAGGATGTACAATATTGATGCAGTTCAAGCTATGGCCTTTGATGGTTGT TACCATGACAGCGAGATTGACATGGACCAGACTTCCCTCTCTCTAAACTCAGAAGACT TCATGAGAAGAAAATCGATATGCAGCCCCAGCACCAGATTCACTCGGATAAAGAGAA AAAATCCCTAGGAGGACATGTTGGTAGAATCATTCTGAAAAACAACCATGTCAATGAC ACCTATTCTAGGATTTTATCCCATGTGTATATCTTTATTTAATT		
	ORF Start: ATG at 7	ORF Stop: TAA at 1435	
	SEQ ID NO: 10	476 aa	MW at 55285.2kD
NOV3a, CG58518-01 Protein Sequence	MVLAPQLVSFTYIWIILKPNVCAASNIKMTQRCSSSMKQTKWQETRMKKDDSTKARP QKYEQLLHIEDNDFAMRPGFGGEYYPKIGSPVPVGIDVHVESIDSISETNMVSFFMG YDFTMTFYLRHWKDERLSFPSTANKSMTFDHRLTRKIWVPDIFVHSHKRSFIHDTTM ENIMLRVHPDGNVLLSLRRI TVSAMCFMDFSRFLDTQNCSELESAYNEDDLMLYWK HGNKSLNTEEHMSLSQFFIEDFSASSGLAFYSSTGWYNRLF INFVLRHRVFFVFLQTY FPAILMVMLSWSVFWIDRRVAPARVSLGGITTVLTMSTIITAVSASMPQVSYLKAVDV YLWVSSLFVFLSVIEYAAVNYLTVEERKQFKKTGKVQISRMYNIDAVQAMAFDGCYH DSEIDMDQTSLSLNSDFMRKRSICSPSTDSSRIKRRKSLGGHVGRILENNHVIDTY SRILFPPIVYIFI		

Further analysis of the NOV3a protein yielded the following properties shown in Table 3B.

Table 3B. Protein Sequence Properties NOV3a	
PSort analysis:	0.6850 probability located in endoplasmic reticulum (membrane); 0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.2400 probability located in nucleus
SignalP analysis:	Likely cleavage site between residues 25 and 26

A search of the NOV3a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 3C.

Table 3C. Geneseq Results for NOV3a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV3a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU04467	Human gamma-amino butyric acid (GABA) receptor protein #1 - Homo sapiens, 467 aa. [WO200153489-A1, 26-JUL-2001]	1..474 1..456	454/475 (95%) 454/475 (95%)	0.0
AAU04470	Human gamma-amino butyric acid (GABA) receptor protein #4 - Homo sapiens, 420 aa. [WO200153489-A1, 26-JUL-2001]	48..474 1..409	408/428 (95%) 408/428 (95%)	0.0
AAU04468	Human gamma-amino butyric acid (GABA) receptor protein #2 - Homo sapiens, 392 aa. [WO200153489-A1, 26-JUL-2001]	1..393 1..377	370/394 (93%) 370/394 (93%)	0.0
AAU04471	Human gamma-amino butyric acid (GABA) receptor protein #5 - Homo sapiens, 345 aa. [WO200153489-A1, 26-JUL-2001]	48..393 1..330	324/347 (93%) 324/347 (93%)	e-180
AAU04469	Human gamma-amino butyric	1..192 1..177	176/192	2e-96

	Homo sapiens, 180 aa. [WO200153489-A1, 26-JUL-2001]		176/192 (91%)	
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In a BLAST search of public sequence databases, the NOV3a protein was found to have homology to the proteins shown in the BLASTP data in Table 3D.

Table 3D. Public BLASTP Results for NOV3a				
Protein Accession Number	Protein/Organism/Length	NOV3a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P50573	Gamma-aminobutyric-acid receptor rho-3 subunit precursor (GABA(A) receptor) - Rattus norvegicus (Rat), 464 aa.	1..474 1..453	383/476 (80%) 407/476 (85%)	0.0
Q9YGQ2	GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-3 SUBUNIT - Morone americana (White perch), 470 aa.	1..474 4..459	293/485 (60%) 363/485 (74%)	e-153
P50572	Gamma-aminobutyric-acid receptor rho-1 subunit precursor (GABA(A) receptor) - Rattus norvegicus (Rat), 474 aa.	49..474 58..463	270/427 (63%) 317/427 (74%)	e-144
P56475	Gamma-aminobutyric-acid receptor rho-1 subunit precursor (GABA(A) receptor) - Mus musculus (Mouse), 474 aa.	49..474 58..463	270/427 (63%) 317/427 (74%)	e-143
P24046	Gamma-aminobutyric-acid receptor rho-1 subunit precursor (GABA(A) receptor) - Homo sapiens (Human), 473 aa.	49..474 57..462	268/427 (62%) 317/427 (73%)	e-143

PFam analysis predicts that the NOV3a protein contains the domains shown in the Table 3E.

Table 3E. Domain Analysis of NOV3a

Pfam Domain	NOV3a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Neur_chan_LBD: domain 1 of 1	88..282	70/250 (28%) 165/250 (66%)	1.2e- 54
Neur_chan_memb: domain 1 of 1	289..475	44/292 (15%) 141/292 (48%)	7.6e- 28

Example 4.

The NOV4 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 4A.

Table 4A. NOV4 Sequence Analysis			
	SEQ ID NO: 11	1587 bp	
NOV4a, CG58516-01 DNA Sequence	GAACAGAAATGAATAAAAGTCGCTGGCAGAGTAGAAGACGACATGGGAGAAGAAGCC CCAGCAGAACCCCTTGGTTTCAGACTCCGTGATTCTGAAGACAGGTCTGACTCCCGGGC GCACAGCCCCGCTCACGATTCCGGCCACGGTGATGACGAGTCTCCGTCAACCTCGTCTC GCACAGCTGGGACCTCCTCTGTGCCAGAGCTACCTGGGTTTACTTTGACCCTGAAAA GAAACGCTACTTCCGCTTGCTCCCTGGACATAACAACCTGCAACCCCTGACGAAAGAG AGCATCCGGCAGAAGGAGATGGAGAGCAAGAGACTGCGGCTGCTCCAGGAAGAAGACA GACGGAAAAAGATTGCCAGGATGGGATTTAATGCATCTTCCATGTCTACGAAAAAGCCA GCTGGGTTTTCTCAACGTCACCAATTACTGGCATTTAGCCCCACGAGCTGCGTCTCAGC TGCAATGGAGAGGAAAAAGGTCCAGATTGCAAGCATGGATCCCTCCGCCTTGGCAAGCG ACCGATTTAACCTCATACTGGCAGATACCAACAGTGACCGGCTCTTACAGTGAACG TGTTACAGTTGGAGGCTCCAAGTATGGTATCATCAACCTGCAAAGTCTGAAGACCCCT ACGCTCAAGGTGTTTCATGCCACGAAACCTCCGATTCTCACCAACCGGAAGGTGAACA CTTCGGTGTGCTGGGCCTCGCTGAATCACTTGGATTCCCACTTCTGCTATGCCTCAT GGGACTCGCAGAGACTCCAGGCTGTGCCACCTGCTCCCAGCATCACTGTTCTGCTCAAT AGTCCCCACCCAGGAATAGACCGGCTGGCATGCTCTGCAGTTTCCGGATCCCTGGGG GTGCCTGGTCTGTGCCCTGGTCCCTGAATATCCAAGCAAATAACTGCTTCAGTACAGG CTTGCTTCGGCGGGTCTCTGTTGACCAACGTGGTGACGGGACACCGGCAGTCCCTTGGG ACCAACAGTGATGCTTTGGCCAGCAGTTTGCTCTCATGGCTCCTCTGCTGTTTAATG GCTGCGCTCTGGGGAATCTTTGCCATTGATCTGCGTTGTGGAATCAAGGCAAGG ATGGAAGGCCACCCGCTGTTTCATGATTACGAGTGACCTCTGTGCGGATCCTCCAA GATGAGCAATACCTGATGGCTTCAGACATGGCTGGAAAGATCAAGCTGTGGGACCTGA GGACCACGAAGTGCCTAAGGCAGTACGAAGGCCACGTGAATGAGTAGCGCTACCTGCC CCTGCATGTGCACGAGGAAGAAGGAATCCTGGTGGCAGTGGGCCAGGACTGCTACACC AGAATCTGGAGCCTCCACGATGCCCGCTACTGAGAACCATAACCTCCCGTACCCTG CCTCCAAGGCCGACATTCCAGTGTGGCCTTCTCGTCGCGGCTGGGGGCTCCCGGGC GCGCGCCGGGGCTGCTCATGGCTGTGCGGCAGGACCTTTACTGTTACTCCTACAGT ATTCTGCAGGGCACAGCCAGAGCCATGTGGATTGACTTACGGGAGTAAAGCGTAA TTTTTACTGCATCTAATGAGG		
	ORF Start: ATG at 9	ORF Stop: TAA at 1563	
	SEQ ID NO: 12	518 aa	MW at 57769.3kD
NOV4a, CG58516-01 Protein Sequence	MNKSRWQSRRRHRRSHQNPWFRLRDSRSDSRAAQPAPDSDSHGDDSPSTSSGTA GTSSVPELPGFYFDEPKRYFRLLPGHNNCNPLTKESIRQKEMESKRLRLQEDRRK KIARMGFNASSMLRKSQGLFNVNTNYCHLAHELRLSCMERKKVQIRMDPSALASDR NLILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFMPPRPPILTNRKNTSV CWASLNHLDSHILCLMGLAETPGCATLLPASLFVNSPHPGIDRPGMLCSFRIPGGAW SCAWSLNIQANNCFSTGLSRRVLLTNVVTGHRQSFGTNSDVLAAQQFALMAPLLFNCR SGEIPAFIDLRGNQKGWKATRLFHDSAVTSVRILQDEQYLMASDMAGKIKLWDLRTT KCVRYEGHVNEYAYLPLHVHEEGILVAVGQDCYTRIWSLHDARLLRTIPSPYASK ADIPSVAFSSRLGSSRGRAGAAHGCRAGPLLLLLQLILQGTQASHVDLTYGSKA		

Further analysis of the NOV4a protein yielded the following properties shown in Table 4B.

Table 4B. Protein Sequence Properties NOV4a	
Psort analysis:	0.9600 probability located in nucleus; 0.4776 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1837 probability located in mitochondrial inner membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV4a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 4C.

Table 4C. Geneseq Results for NOV4a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV4a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABB11794	Human secreted protein homologue, SEQ ID NO:2164 - Homo sapiens, 500 aa. [WO200157188-A2, 09-AUG-2001]	1..484 5..485	470/484 (97%) 471/484 (97%)	0.0
AAM79804	Human protein SEQ ID NO 3450 - Homo sapiens, 500 aa. [WO200157190-A2, 09-AUG-2001]	1..484 5..485	470/484 (97%) 471/484 (97%)	0.0
AAM41122	Human polypeptide SEQ ID NO 6053 - Homo sapiens, 500 aa. [WO200153312-A1, 26-JUL-2001]	1..484 5..485	470/484 (97%) 471/484 (97%)	0.0
AAG67256	Amino acid sequence of a human liver-associated gene - Homo sapiens, 489 aa. [WO200109318-A1, 08-FEB-2001]	1..484 1..474	459/484 (94%) 462/484 (94%)	0.0
AAB94587	Human protein sequence SEQ ID NO:15389 - Homo sapiens, 489 aa. [EP1074617-A2, 07-FEB-2001]	1..484 1..474	459/484 (94%) 462/484 (94%)	0.0

In a BLAST search of public sequence databases, the NOV4a protein was found to have homology to the proteins shown in the BLASTP data in Table 4D.

Table 4D. Public BLASTP Results for NOV4a
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Protein Accession Number	Protein/Organism/Length	NOV4a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAH18979	HYPOTHETICAL 55.7 KDA PROTEIN - Homo sapiens (Human), 495 aa.	1..484 1..480	470/484 (97%) 471/484 (97%)	0.0
Q96K22	CDNA FLJ14839 FIS, CLONE OVARC1001791 - Homo sapiens (Human), 489 aa.	1..484 1..474	459/484 (94%) 462/484 (94%)	0.0
Q9Y4P5	HYPOTHETICAL 48.5 KDA PROTEIN - Homo sapiens (Human), 430 aa (fragment).	5..435 2..428	420/431 (97%) 421/431 (97%)	0.0
Q99LF7	HYPOTHETICAL 58.1 KDA PROTEIN - Mus musculus (Mouse), 519 aa.	1..484 1..481	378/485 (77%) 423/485 (86%)	0.0
Q9UFI0	HYPOTHETICAL 26.0 KDA PROTEIN - Homo sapiens (Human), 234 aa (fragment).	269..483 4..217	175/215 (81%) 193/215 (89%)	4e-99

PFam analysis predicts that the NOV4a protein contains the domains shown in the Table 4E.

Table 4E. Domain Analysis of NOV4a			
Pfam Domain	NOV4a Match Region	Identities/ Similarities for the Matched Region	Expect Value
WD40: domain 1 of 3	281..316	2/37 (5%) 26/37 (70%)	5.8e+02
WD40: domain 2 of 3	367..402	10/37 (27%) 27/37 (73%)	6.1
WD40: domain 3 of 3	408..446	10/39 (26%) 23/39 (59%)	13

Example 5.

The NOV5 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 5A.

Table 5A. NOV5 Sequence Analysis

	SEQ ID NO: 13	1081 bp
NOV5a, CG58473-01 DNA Sequence	AGGATGGCCCAAGGAGAACAGTTATCCCTGGCCCTATGGCAAGCAGACGGCTCCAG CCGGCCTGAGTACCCCTGCTCCCGGAGTCCTCCCGAGGATCCCCACCGAAGCTGCGCG TGAGCTCCCGAGCTGCGCAGACCCACAGCCCGCAGCGGCCCTGGCCATGAGGTGGTA GAGAACAGTTGTGGGAAGCGCAGCATCTTAACGCGGCCCTTCTGGTCGACGACCTTG AGACTGGGCGTCCCTGGGCAAGACAAGTTTGTACATGTGTACTTGGCTCGAAAGAA GACAAGCCATTTCATCGTGGCCCTCAAGGCCTTCAAGTCTCAGATAGAGGAGGGCGTG GAGCACCAGATGCGCAGGCAGATGGAATCCAGGCCCTTTTTCAGCATCCCAACATAT TGAGTCTCTACAACCTATTTTATGACCTGAGAAAAATCTACTGGATTCTAGAGTACGC CCCGCCACCCCTACCCCGAGGAGCTGTACCAGGAGCTGCGAAAGAGCCGCACCTTT GACAAGAAGCCAACAGCCACCATCACGGGGGAGGTGGCAGATGCTCTGATGTACTGCC ACGGGAAGAAGGTGACTCCAGAGACATGAAGCCAGATAATCTACTCTCAGGGCTTGA GGGCGAGCTGAAAGTTGCGCACTCGGCTGCCCTGTGCACGCCCCCTCACTGAGGAGG AAGACAAGACAAATGTGTGGCACCCTGGACTACCTGTCCCAGAGACAATTGAGGGGC GCGCGCACACCAGAAAGGTGGATTGTGGTACATCGGAGCACTCGGCTATGAGCCGCT GGTGGGGAACCCACACACAATGAGGCCTATGGGCGAATCGTCAAGGTGGCCCTAAAA TTCCCCCTTCTGTGCCAGGAGAGCCCCAGGACCTCATCTCCAAGCTGCTTAGGCATA ACCCCTCAGAACGGCTGCCCTGGCCAGGTCTCAGCCCACCTGGGATCCTGGCCCA TTCTCGGAGGGTTTGCCTCCCTCTGCCCATCAGTCTGTCCCCTGGTGGTCCCTGACA TTCACCTCGGGGCGTCTGTGTTTGTAACTCTGCATAT	
	ORF Start: ATG at 4	ORF Stop: TAA at 1069
	SEQ ID NO: 14	355 aa MW at 40012.7kD
NOV5a, CG58473-01 Protein Sequence	MAQKENSYPWPYQKQAPAGLSTLLPRVLPRIPTAAARELPSCADPQPAAPGHEVVE NSCGKRSILTRPFLVDDLETGRPLGKDKFVHVYLARKKTSHFIVALKAFKSQIEEGVE HQMRRQMEIQAPFQHPNILLSLYNYFYDLRKIYWILEYAPATPTPEELYQELRKSRTPD KKPTATITGEVADALMYCHGKKVTPRDMKPDNLLSGLEGELEKVAIDFGCPVHAPSLRRK TRQMCGLDYLSPETIEGRAHTEKVDLWYIGALGYEPLVGNPHTNEAYGRIVKVALKF PLLCPEPQDLISKLLRHNPSERLPLAQVSAHPGILAHSSRRVLPSSAHQSVPPWWSLTF TRGRLCL	

Further analysis of the NOV5a protein yielded the following properties shown in Table 5B.

Table 5B. Protein Sequence Properties NOV5a	
Psort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1897 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV5a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 5C.

Table 5C. Geneseq Results for NOV5a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV5a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG67615	Amino acid sequence of a human protein - Homo sapiens, 344 aa. [WO200109316-A1, 08-FEB-2001]	1..341 1..343	247/349 (70%) 274/349 (77%)	e-129

AAG67436	Amino acid sequence of a human polypeptide - Homo sapiens, 344 aa. [WO200109345-A1, 08-FEB-2001]	1..341 1..343	247/349 (70%) 274/349 (77%)	e-129
AAY22475	Human AUR1 protein sequence - Homo sapiens, 344 aa. [WO9937788-A2, 29-JUL-1999]	1..341 1..343	247/349 (70%) 274/349 (77%)	e-129
AAW18083	Human Aurora-1 - Homo sapiens, 344 aa. [WO9722702-A1, 26-JUN-1997]	1..341 1..343	247/349 (70%) 274/349 (77%)	e-129
AAY27052	Human protein kinase (HPKM)-1 (clone ID 2940) - Homo sapiens, 347 aa. [WO9938981-A2, 05-AUG-1999]	1..341 1..346	246/352 (69%) 274/352 (76%)	e-127

In a BLAST search of public sequence databases, the NOV5a protein was found to have homology to the proteins shown in the BLASTP data in Table 5D.

Table 5D. Public BLASTP Results for NOV5a				
Protein Accession Number	Protein/Organism/Length	NOV5a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O60446	AURORA-RELATED KINASE 2 (SERINE/THREONINE KINASE 12) - Homo sapiens (Human), 344 aa.	1..341 1..343	247/349 (70%) 274/349 (77%)	e-128
Q96GD4	UNKNOWN (PROTEIN FOR MGC:11031) - Homo sapiens (Human), 344 aa.	1..341 1..343	247/349 (70%) 274/349 (77%)	e-128
Q96DV5	UNKNOWN (PROTEIN FOR MGC:4243) - Homo sapiens (Human), 345 aa.	1..341 1..344	247/350 (70%) 274/350 (77%)	e-126
Q9UQ46	AIK2 - Homo sapiens (Human), 343 aa.	1..341 1..342	245/348 (70%) 272/348 (77%)	e-126
O14630	PROTEIN KINASE - Homo sapiens (Human), 347 aa.	1..341 1..346	245/352 (69%) 272/352 (76%)	e-125

PFam analysis predicts that the NOV5a protein contains the domains shown in the Table 5E.

Table 5E. Domain Analysis of NOV5a

Pfam Domain	NOV5a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Pkinase: domain 1 of 1	76..325	81/293 (28%) 184/293 (63%)	6.5e-36

Example 6.

The NOV6 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 6A.

Table 6A. NOV6 Sequence Analysis			
	SEQ ID NO: 15	1524 bp	
NOV6a, CG58470-01 DNA Sequence	AGCATTATGAACACTAATGACCTTAACTCAGGTTGTCCAAAGCTGAGCAAGAACACC CACTACGTTTCTGGAATGAGCTTGAAGAAGCCCGACAGGTAGAACTTTATGCAGAGCT CCAGGCCATCGACTTTCAGGAAGTGAACCTCTTTTCCAAAGGCCATTGAAGGATTT AACCAGTCCTCTCATCAAGAAAAGGTGGATGCGGGAATGGAACCTGTCCTCGAGAAG TACTGGGCAGTGCTGCAGGGAAGCTAGATCAGCTCCAGGCTGGGAAAGCAAAGTTT CCAGATTTCTGAGAACAAAGTCACAGTTGTTCTAGCTGGTGGGCAGGGGACTAGACTC GTTGCATATCCAAAGGGGATGTATGATGTTGGTTTGCCATCCCATAGACACTTTTTC AGATTCAAGCAGAGCATATCCTGAAGCTACAACAGTTAGCTGAAAAATATTATGGCAA CAAATGCATTATTCCATATTACGTCATGACCAGCGAGTTCACTCTGGGGCCACCGGCC GAGTTCTTCAGGGAGCACAACCTTCTTCCACCTGGACCCGCCAACGTGGTCATGTTTG AGCAGCGCCTGCTGCCTGCTGTGACCTTTGATGGCAAGGTTATCTCGGAGCGGAAAGA CAAAGTTGCCATGGCCCCAGACGGCAACGGGGGCTCTACTGCGCGCTGGAGGACCAC AAGATCCTGGAGGACATGGAGCGCCGGGGAGTGGAGTTTGTGCACGTGTACTGTGTGG ACAACATCCTGGTGGCGCTGGCGGACCTGTCTTCATCGGCTTCTGTGTGTGTCAGGG CGCAGACTGTGGCGCCAAGGTGGTGGAAAAGGCATACCCCGAGGAGCCCGTGGGCGTG GTGTGCCAGGTGACCGGTGTCCCCAGGTGGTGGAGTACAGCGAGATCAGTCTGTGAGA CCGCACAGTACGTGTCTCCGACGGGAGCCTGCTGTACAATGCAGGCAACATCTGCAA CCACTTCTTCAACCGAGGCTTCCTTAAAGCGGTCACCAGGGAGTTTGAGCCTTTGCTG AAGCCACACGTGGCTGTGAAGAAGGTCCCGTATGTGGATGAGGAGGGAATCTGGTAA AGCCGCTAAACCGAACCGGATAAAGATGGAGAAGTTTGTGTTTGTATGTGTTCCGGTT TGCTAAGAACTTTGCTGCCTTGAAGTGCTGCGGGAGGAGGAATTTTCCCACTGAAG AACGCAGAGCCAGCCGACAGGACAGTCCCCGACCGCTCGCCAGGCCCTGCTCAGCC AGCACTACCGGTGGGCTCTGCGGGCCGGGCCGCTTCTGTGATGCCATGGGSCCGG GCTCCCAGAGCTGCCAGCTTGCCCCAAATGGAGACCTCCGCCATCTGTGAGATA TCGCCCTTGGTGTCTTACTCTGGAGAGGGTTAGAAGGTACCTGCAAGGCCGGGAGT TCCAGTCCCCGCTCATCTCTGGATGAAGACCAGGCCAGGGAGCTGGGAAAAATGGTAT <u>ATGAACCTGATACCAA</u>		
	ORF Start: ATG at 7	ORF Stop: TGA at 1510	
	SEQ ID NO: 16	501 aa	MW at 56461.0kD
NOV6a, CG58470-01 Protein Sequence	MNTNDLKLRLSKAEQEHPLRFWNELEEARQVELYAELOAIDFQELNFFQKAIEGPNQ SSHQEKVDAGMEPVPREVLGSAAGKLDQLQAWESKVFQISENKVTVVLAGGQGRLLVA YPKGMVDVGLPSHKTLPQIAEHLKLQQLAEKYYGNKCIIPYYVMTSEFTLGPTAEF FREHNFFHLDPANVVMFEQRLPAVTFDGKVILERKDKVAMAPDNGGGLYCALEDHKKI LEDMERRGVFVHVYCDNILLRLADPVFIGFCVLQGADCGAKVVEKAYPEEPVGVVC QVDGVPQVVEYSEISPETAQLRVSDGSLLYNAGNICNHFFTRGFLKAVTREFEPLKLP HVAVKKVPYVDEEENLVKPLKPNGIKMEKFVDFVFRFAKNFAALEVLREEEFSPLKNA EPADRDSPTARQALLTQHYRWALRAGARFLDAHGARLPPLSLPNDPPAICEISP LVSYSGEGLEVYLGREFQSPLILDEDQARELVKNGI		

Further analysis of the NOV6a protein yielded the following properties shown in Table 6B.

Table 6B. Protein Sequence Properties NOV6a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3490 probability located in

	matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV6a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 6C.

Table 6C. Geneseq Results for NOV6a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV6a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB56960	Human prostate cancer antigen protein sequence SEQ ID NO:1538 - Homo sapiens, 524 aa. [WO200055174-A1, 21-SEP-2000]	1..501 3..524	353/522 (67%) 413/522 (78%)	0.0
AAG32392	Arabidopsis thaliana protein fragment SEQ ID NO: 39067 - Arabidopsis thaliana, 502 aa. [EP1033405-A2, 06-SEP-2000]	9..485 36..497	194/489 (39%) 275/489 (55%)	3e-84
AAG40236	Arabidopsis thaliana protein fragment SEQ ID NO: 49896 - Arabidopsis thaliana, 477 aa. [EP1033405-A2, 06-SEP-2000]	9..485 12..472	193/488 (39%) 272/488 (55%)	3e-82
AAG40235	Arabidopsis thaliana protein fragment SEQ ID NO: 49895 - Arabidopsis thaliana, 500 aa. [EP1033405-A2, 06-SEP-2000]	9..485 35..495	193/488 (39%) 272/488 (55%)	3e-82
AAG40234	Arabidopsis thaliana protein fragment SEQ ID NO: 49894 - Arabidopsis thaliana, 505 aa. [EP1033405-A2, 06-SEP-2000]	9..485 40..500	193/488 (39%) 272/488 (55%)	3e-82

In a BLAST search of public sequence databases, the NOV6a protein was found to have homology to the proteins shown in the BLASTP data in Table 6D.

Table 6D. Public BLASTP Results for NOV6a

Protein Accession Number	Protein/Organism/Length	NOV6a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96GM2	UDP-N-ACTEYLGLUCOSAMINE PYROPHOSPHORYLASE 1 - Homo sapiens (Human), 505 aa.	1..501 1..505	351/505 (69%) 412/505 (81%)	0.0
Q16222	UDP-N-acetylhexosamine pyrophosphorylase (Antigen X) (AGX) (Sperm- associated antigen 2) [Includes: UDP-N-acetylgalactosamine pyrophosphorylase (EC 2.7.7.-) (AGX-1); UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (AGX-2)] - Homo sapiens (Human), 522 aa.	1..501 1..522	352/522 (67%) 412/522 (78%)	0.0
Q91YN5	HYPOTHETICAL 58.6 KDA PROTEIN - Mus musculus (Mouse), 522 aa.	1..501 1..522	342/522 (65%) 407/522 (77%)	0.0
AAH17547	HYPOTHETICAL 58.5 KDA PROTEIN - Mus musculus (Mouse), 521 aa.	1..501 1..521	341/521 (65%) 407/521 (77%)	0.0
Q9Y0Z0	BCDNA:LD24639 PROTEIN - Drosophila melanogaster (Fruit fly), 520 aa.	6..492 44..513	236/491 (48%) 330/491 (67%)	e-124

PFam analysis predicts that the NOV6a protein contains the domains shown in the Table 6E.

Table 6E. Domain Analysis of NOV6a			
Pfam Domain	NOV6a Match Region	Identities/ Similarities for the Matched Region	Expect Value
UDPGP: domain 1 of 1	40..434	108/428 (25%) 324/428 (76%)	8.4e-111

Example 7.

The NOV7 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 7A.

Table 7A. NOV7 Sequence Analysis		
	SEQ ID NO: 17	461 bp
NOV7a, CG58593-01 DNA Sequence	ACGCAGAGATGCAGATCTTTGTGAAGACCCTCACGGGCAAGACCATCACCTTGGAGGT CAAGCCCACCGACACCATTTGAGAATGTCAAACCAAATTCAGGACAAGGAGGGTATC CCACCTGACCAGCAGCGTCTGATATTTGCTGGGAAACGGCTGGAGGATGGCCACATC TCTCAGGCTACAACATCCAGAAAGAGTCCACCTTAAACCTGGTGCTGCGCTGCGAGG TGGCATTACTGAGCCTTCCCTCCGCCAGCTCGTCCAGAAATACAACCTGCGACGAGATG ATCTGCTGCAAGTGCTATGCTTGCTGCACCCCGGTGCTATCAACTGCCACAAGAAGA	

	AATGCGGCCACACCAACACCTGTACCCAGGAAGAAGGTCAAATAAGGCTCTTCCTT CCTTGAAGGGCAGCAGCCTTCTGCCAGGCCCATGGCCCTGGGGCCTCAATAAA		
	ORF Start: ATG at 9	ORF Stop: TAA at 393	
	SEQ ID NO: 18	128 aa	MW at 14540.9kD
NOV7a, CG58593-01 Protein Sequence	MQIFVKLTGKTITLEVKPTDTIENVKTKIQDKEGIPPDQQLIFAGKRLEDGHTLSG YNIQKESTLNLVLRRLGGITEPSLRQLVQKYNCEMICCKCYACLHPGAINCHKKCG HTNNLYPRKKVK		

Further analysis of the NOV7a protein yielded the following properties shown in Table 7B.

Table 7B. Protein Sequence Properties NOV7a	
PSort analysis:	0.9800 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV7a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 7C.

Table 7C. Geneseq Results for NOV7a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV7a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB52080	Gene 16 human secreted protein homologous amino acid sequence #129 - <i>Sus scrofa</i> , 128 aa. [WO200061596-A1, 19-OCT-2000]	1..128 1..128	111/128 (86%) 118/128 (91%)	7e-61
AAG43861	<i>Arabidopsis thaliana</i> protein fragment SEQ ID NO: 54871 - <i>Arabidopsis thaliana</i> , 128 aa. [EP1033405-A2, 06-SEP-2000]	1..128 1..128	101/128 (78%) 113/128 (87%)	9e-55
AAG36188	<i>Arabidopsis thaliana</i> protein fragment SEQ ID NO: 44314 - <i>Arabidopsis thaliana</i> , 249 aa. [EP1033405-A2, 06-SEP-2000]	1..128 122..249	101/128 (78%) 113/128 (87%)	9e-55
AAG36187	<i>Arabidopsis thaliana</i> protein fragment	1..128 137..264	101/128 (78%) 113/128 (87%)	9e-55

	thaliana, 264 aa. [EP1033405-A2, 06-SEP-2000]			
AAG36186	Arabidopsis thaliana protein fragment SEQ ID NO: 44312 - Arabidopsis thaliana, 322 aa. [EP1033405-A2, 06-SEP-2000]	1..128 195..322	101/128 (78%) 113/128 (87%)	9e-55

In a BLAST search of public sequence databases, the NOV7a protein was found to have homology to the proteins shown in the BLASTP data in Table 7D.

Table 7D. Public BLASTP Results for NOV7a				
Protein Accession Number	Protein/Organism/Length	NOV7a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BX98	UBIQUITIN A-52 RESIDUE RIBOSOMAL PROTEIN FUSION PRODUCT 1 - Homo sapiens (Human), 141 aa (fragment).	1..128 14..141	111/128 (86%) 118/128 (91%)	3e-60
Q9UPK7	UBIQUITIN-52 AMINO ACID FUSION PROTEIN - Homo sapiens (Human), 128 aa.	1..128 1..128	111/128 (86%) 118/128 (91%)	3e-60
Q9PT09	UBIQUITIN - Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), 128 aa.	1..128 1..128	110/128 (85%) 118/128 (91%)	6e-60
O42388	UBIQUITIN-RIBOSOMAL PROTEIN FUSION PROTEIN - Gallus gallus (Chicken), 128 aa.	1..128 1..128	110/128 (85%) 117/128 (90%)	7e-60
Q9XSV1	UBIQUITIN-RIBOSOMAL PROTEIN L40 FUSION PROTEIN - Canis familiaris (Dog), 128 aa.	1..128 1..128	110/128 (85%) 117/128 (90%)	1e-59

PFam analysis predicts that the NOV7a protein contains the domains shown in the Table 7E.

Table 7E. Domain Analysis of NOV7a			
Pfam Domain	NOV7a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ubiquitin: domain 1 of 1	1..74	54/83 (65%) 72/83 (87%)	1.9e-38

Ribosomal L40e: domain 1 of 1	77..128	30/52 (58%) 42/52 (81%)	7.3e-20
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Example 8.

The NOV8 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 8A.

Table 8A. NOV8 Sequence Analysis			
	SEQ ID NO: 19	2296 bp	
NOV8a, CG57871-01 DNA Sequence	CGGCGGCGGCGGCGCAGTAGAAATGATGGAAGAATTGCATAGCCTGGACCCACGACGGCA GAAATTATTGGAGGCCAGGTTTACTGGAGTAGGTGTTAGTAAGGGACCCTTAATAGT GAGTCTTCCAACCAGAGCTTGTGCAGCGTCGGATCCTTGAGTGATAAAGAAGTAGAGA CTCCCAAGAAAAAGCAGAAATGACCAGCGGAAATCGGAAAAGAAAAGCTGAACCATATGA AAGTAGCCAAGGGAAGGCACTCCTAGGGGACATAAAATTAGTGATTACTTTGAGTTT GCTGGGGGAAGCGGGCCGGGAACCGCCTGGCAGAAGTGTTCCACCAGTTGCACGAT CCTCACTGCAACATTCTTTATCCAATCCCTTACCGGACGAGTAGAACAGCCCTCTA TGGTTTATAGATGGCAGTGCTGCAAAGGAGGCAACGGAGGAGCAGCTGCTCTGCCAAC CTCATGTCACTGATGCTAGCAAAACCTCGGCTTGACACAGAGCAGCTGGCGCAAAGGG GAGCTGGCCTCTGCTTCACTTTTGTTCAGCTCAGCAAAACAGTCCCTCATCTACGGG ATCTGGCAACACAGAGCATTCTGTCAGCTCCCAAAACAGATCTCCATCCAGCACAGA CAGACCCAGTCCGACCTCACAAATAGAAAAAATATCTGCCTAGAAAAACAGTAAGAATT CTGACTTAGAGAAGAAGGAGGGAAGAAATAGATGATTTATTAAGAGCCATCTGTGATTT GAGACGGCAGATTGATGAACAGCAAAAGATGCTAGAGAAATACAAGGAACGATTAAAT AGATGTGTGACAATGAGCAAGAACTCCTTATAGAAAAGTCAAAACAAGAGAAGATGG CGTGTAGAGATAAGAGCATGCAAGACCGCTTGAGACTGGGCCACTTTACTACGCTTGA CCACGGAGCCAAATTTACTGAGCAGTGGACAGATGGTTATGCTTTTCAGAATCTTATC AAGCAACAGGAAAGGATAAAATTCACAGAGGGAAGAGATAGAAAGCAACGGAAAAATGT TAGCAAAGCGGAAACCTCTGCCATGGGTGAGGCCCTCTCTGCAACCAATGAGCAGAA ACAGTGGAAAAAGCAAGACCAATGGAGCTGAAAATGAAACGTTAACGTTAAAAGAATAC CATGAACAAGAAGAAATCTTCAAACCTCAGATTAGGTCATCTTAAAGAGGAGGAAGCAG AGATCCAGGCAGAGCTGGAGAGGCTAGAAAGGGTTAGAAAACATACATATCAGGGAAGT AAAAAGGATACATAATGAAGATAATTACAATTTAAATATCATCCAACGCTAAATGAC AGATATTTGTTGTACATCTTTTGGGTAGAGGAGGTTTCAGTGAAGTTTACAAGGCAT TTGATCTAACAGAGCAAGATACGTAGCTGTGAAAATTCACAGTTAAATAAAAACTG GAGAGATGAGAAAAAGGAGAATTACCAACAGCATGCATGTAGGGAATACCGGATTCTAT AAAGAGCTGGACCATCCCAAGATAGTTAAGCTGTATGATTACTTTTCACTGGATACGT ACTCGTTTTGTACAGTATTAGAATACTGTGAGGGAATGATCTGGACTTCTACCTGAA ACAGCACAAATTAATGTCAGAGAAAGAGGCCCGGTCCATTATCATGCAGATTGTGAAT GCTTTAAAGTACTTTAAATGAAATAAAACCTCCCATCATACACTATGACCTCAAACAG GTAATATTCTTTTAGAAAATGGTACAGCGTGTGGAGAGATAAAAAATACAGATTTTGG TCTTTTCAAGATCATGGATGATGATAGCTACAATTCACTGAGTGGCATGGAGCTAACA TCACAAGGTGCTGGTACTTATTGGTATTTACCACCAGAGTGTTTTGTGGTTGGGAAG AACCACCAAAGATCTCAAATAAAGTTGATGTGTGGTGGTGGGTGTGATCTTCTATCA GTGTCTTTATGGAAGGAAGCCTTTTGGCCATAACCACTCTCAGCAAGACATCTCTACAA GAGAATACGATTCTTAAAGCTACTGAAAGTGCAGTTCCTCGCCAAAGCCGGTAGTAACAC CTGAAGCAAAGGCGTTGATTGACGATGCTTTGGCCTACCGAAAGGAGGACCGCATTGA TGTCACGACAGCTGGCCTGTGATCCCTACTTGTTCCTCACATCCGAAAGTCAGTCTCT ACGAGTAGCCCTGCTGGAGCTGCTATTGCATCAACCTCTGGGGCGTCCAATAACAGTT CTTCTAATTGAGACTGACTCCAAGGCCACAAACT		
	ORF Start: ATG at 24	ORF Stop: TGA at 2271	
	SEQ ID NO: 20	749 aa	MW at 85415.8kD
NOV8a, CG57871-01 Protein Sequence	MEELHSLDPRRQKLEARFTGVGVSKGPLNSESSNQSLCSVGSLSDEKVEVTPKKKQND QRNRKRKAEPYESSQKGTGRHKISDYFEPAGSGPGTSPGRSVPPVARSSIQHSLS NPLPRRVEQPLYLGDGSAAKEATEEQSALPTLMSVMLAKPRLDTEQLAQRGAGLCPTF VSAQQNSPSSSTGSGNTEHSCSSQKQISIQHRQTQSDLTIEKISALENSKNSDLEKKEG RIDDLRAICDLRRQIDEQKMLEKYKERLNRCVTMSKLLIEKSKQEKMACRDKSKQ DRLRLGHFTTSDHGAKFTEQWTDGYAFQNLIKQQRINSQREEIERQRKMLAKRKPPA MGQAPPATNEQKQWKSKTNGAENETLTKEYHEQEIEFKLRLGLHLKKEEAETQAELE LERVRKLHIREVKRIHNEDNSQFKYHPTLNDRYLLHLGRGGFSEVYKAFDTEQRY VAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKLYDYFSLDTSFCTVLE YCEGNDLDFYKQHKLMSEKEARSIMQIVNALKYLNEIKPPIHYDLKPGNILLENG TACGEIKITDFGLSKIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEPPKISNK VDVWSVGVIFYQCLYGRKPFQHNQSQDDILQENTILKATEVQFPKPVVTPKAKALIR RCLAYRKEDRIDVQQLACDPYLLPHIRKSVSTSSPAGAAIASTSGASNNSSN		

Further analysis of the NOV8a protein yielded the following properties shown in Table 8B.

Table 8B. Protein Sequence Properties NOV8a	
PSort analysis:	0.9600 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV8a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 8C.

Table 8C. Geneseq Results for NOV8a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV8a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM39278	Human polypeptide SEQ ID NO 2423 - Homo sapiens, 718 aa. [WO200153312-A1, 26-JUL-2001]	1..749 2..718	703/749 (93%) 707/749 (93%)	0.0
AAM41064	Human polypeptide SEQ ID NO 5995 - Homo sapiens, 809 aa. [WO200153312-A1, 26-JUL-2001]	1..749 92..809	695/750 (92%) 701/750 (92%)	0.0
AAR76062	Protein kinase PKU beta - Homo sapiens, 540 aa. [JP07132093-A, 23-MAY-1995]	210..749 1..540	525/540 (97%) 527/540 (97%)	0.0
AAR76061	Protein kinase PKU alpha - Homo sapiens, 787 aa. [JP07132093-A, 23-MAY-1995]	1..744 49..783	537/794 (67%) 592/794 (73%)	0.0
ABB20910	Protein #2909 encoded by probe for measuring heart cell gene expression - Homo sapiens, 404 aa. [WO200157274-A2, 09-AUG-2001]	346..749 1..404	404/404 (100%) 404/404 (100%)	0.0

In a BLAST search of public sequence databases, the NOV8a protein was found to have homology to the proteins shown in the BLASTP data in Table 8D.

Table 8D. Public BLASTP Results for NOV8a				
Protein Accession Number	Protein/Organism/Length	NOV8a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UKI7	TOUSLED-LIKE KINASE 2 - Homo sapiens (Human), 749 aa.	1..749 1..749	731/749 (97%) 736/749 (97%)	0.0
O55047	TOUSLED-LIKE KINASE - Mus musculus (Mouse), 717 aa.	1..749 1..717	699/749 (93%) 705/749 (93%)	0.0
Q9Y4F7	PKU-ALPHA - Homo sapiens (Human), 719 aa (fragment).	1..749 3..719	700/749 (93%) 705/749 (93%)	0.0
Q9D5Y5	TOUSLED-LIKE KINASE 2 (ARABIDOPSIS) - Mus musculus (Mouse), 696 aa.	1..656 1..656	629/656 (95%) 640/656 (96%)	0.0
Q90ZY7	PKU-ALPHA PROTEIN KINASE - Brachydanio rerio (Zebrafish) (Zebra danio), 697 aa.	1..749 2..697	580/753 (77%) 626/753 (83%)	0.0

PFam analysis predicts that the NOV8a protein contains the domains shown in the Table 8E.

Table 8E. Domain Analysis of NOV8a			
Pfam Domain	NOV8a Match Region	Identities/ Similarities for the Matched Region	Expect Value
A2M: domain 1 of 1	501..523	10/23 (43%) 20/23 (87%)	4.6
Pkinase: domain 1 of 1	439..718	96/316 (30%) 213/316 (67%)	5.4e-70

Example 9.

The NOV9 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 9A.

Table 9A. NOV9 Sequence Analysis		
	SEQ ID NO: 21	2060 bp
NOV9a, CG58590-01 DNA Sequence	GTTTTCATAGATAACCATGACAACATCCCATATGAATGGGCATGTTACAGAGGAATCA GACAGCGAAGTAAAAAATGTTGATCTTGATCATCACCAGAGGAACATCAGAAGCACCGAG AGATGGCTGTTGACTGCCCTGGAGATTTGGGCACCAGGATGATGCCAATACGTCGAAG TGCACAGTTGGAGCGTATTCGGCAACAACAGGAGGACATGAGGCGTAGGAGAGAGGAA GAAGGGAAAAAGCAAGAACTTGACCTTAATTCTTCCATGAGACTTAAGAACTAGCCC AAATTCCTCCAAGACCGGAATAGATAACCTATGTTTGATACAGAGGAAGGAATTGT CTTAGAAAGTCCTCATTATGCTGTGAAATATTAGAAATAGAAGACTGTTTTCTTCA CTTAAACATATCCAACATACTTTGGTAGATTCTCAGAGCCAGGAGGATATTTCACTGC TTTTACAACCTGTTCAAAATAAGGATTTCCAGAAATGCATTTAAGATACACAATGCCAT	

	CACAGTACACATGAACAAGGCCAGTCCTCCATTTCCTCTTATCTCCAACGCACAAGAT CTTGCTCAAGAGGTACAAACTGTTTTGAAGCCAGTTTCATCATAAGGAAGGACAAGAAC TAACTGCTTTGCTGAATACTCCACATATTAGGCACCTTTACTTGGCCACGATAAGGT TGCTGAGCAGGAAATGCAGCTAGAGCCCATACAGATGAGAGAGTTTATGAAAGTATT GGCCAGTATGGAGGAGAAACTGTAAAAATAGTTTCGTATAGAAAAGGCTCGTGATATTC CGTTGGGTGCTACAGTTCGTAATGAAATGGACTCTGTCATCATTAGCCGGATAGTAAA AGGGGGTGCTGCAGAGAAAAGTGGTCTGTTGCATGAAGGAGATGAAGTTCTAGAGATT AATGGCATTGAAATTCGGGGGAAAGATGTCAATGAGGTTTTTGACTTGTGTCTGATA TGCATGGTACTTTGACTTTTGTCTGATTCCCAGTCAACAGATCAAGCCGCTCCTGC CAAGGAAAACAGTAATCCATGTAAAAGCTCATTTTGACTATGACCCCTCAGATGACCT TATGTTCCATGTGAGAGTTAGGTCTGTCTTTTCAAAAAGGTGATATATCTCATGTGA TCAGTCAAGAAGATCCAACTGGTGGCAGCCTACAGGGAAGGGGACGAAGATAATCA ACCTCTAGCCGGCTTGTTCAGGGAAGGCTTTCAGCAGCAAAGGGAAGCCATGAA CAAACCATAGAGAAGATAAGGAGCCAGAAAAATCAGGTAAACTGTGGTGTGCAAGA AGAATAAAAAGAAGAGGAAAAAGGTTTTATATAATGCCAATAAAAAATGATGATTATGA CAACGAGGAGATCTTAACCTATGAGGAAATGTCACTTTATCATCAGCCAGCAATAGG AAGAGACCTATCATCTTGATTGGTCCACAGAAGCTGTGGCCAGAATGAATTGCGTCAGA GGCTCATGAACAAAGAAAAGGACCGCTTTGCATCTGCAGTTCTCTCGTACAACCCGGAG TAGGCGGAGACCAAGAAGTAGCCGGTAGAGATTACCACTTTGTTTCGCGGCAAGCAATC GAGGCAGACATAGCAGCTGGAAAGTTCATTGAGCATGGTGAATTTGAGAAGAATTTGT ATGGAACTAGCATAGATTCTGTACGGCAAGTGATCAACTCTGGCAAAATATGTCTTTT AAGTCTTCGTACACAGTCATTGAAGACTCTCCGGAATTTCAGATTTGAAACCATATATT ATCTTCTGCACCCCTTCAAGAAAGACTTCGGGCATTATTGGCCAAAGAAAGGCA AGAATCCAAAGCCTGAAGAGTTGAGAGAAATCATTGAGAAGACAAGAGAGATGGAGCA GAACAATGGCCACTACTTTGATACGGCAATTGTGAATTCCGATCTTGATAAAGCCTAT CAGGAATTGCTTAGGTTAATTAACTTGTACTGAACCTCAGTGGGTACCATCCA CTTGCGTGAGGTGAAAGAAACATCCATTCT		
	ORF Start: ATG at 17		ORF Stop: TGA at 2042
	SEQ ID NO: 22	675 aa	MW at 77311.8kD
NOV9a, CG58590-01 Protein Sequence	MTTSHMNGHVTEESDSEVKNVDLASPEEHQKHREMAVDCPGDLGRMPIRRSAQLER IRQQEDMRRRREEEGKKQELDLNSMRLKKLAQIPKGTGIDNPMFDTTEGIVLESPI YAVKILEIEDLFSSLLKHIQHTLVDSQSQEDISLLLQVLQNKDFQNAFKIHNAITVHMN KASPPFPLISNAQDLAQEVQTVLPVHHKEGQELTALLNTPHIQALLAHDKVAEQEM QLEPITDERVYESIGQYGGTGVKIVRIEKARDIPLGATVRNEMDSVIIISRVKGGAAE KSGLLHEGDEVLEINGIEIRGKDVNEVFDLLSDMHGTLTFVLIIPSQQIKPPPAKETVI HVKAHFDYDPSDDPYVPCRELGLSFQKGDILHVISQEDPNWWQAYREGDEDNQPLAGL VPGKSFQQQREAMKQTIIEEDKEPEKSGKLWCAKKNKKRKKVLYNANKNDYDNEEIL TYEEMSLYHQPANRKRPIILIGPQNCQNELRQLMNKEKDRFASAVPRTRSRRDQE VAGRDYHFVSRQAFADIAAGKFIHGEFEKNLYGTSIDSVRQVINSKICLLSLRTQ SLKTLRNSDLKPYIIFIAPPSQERLRALLAKEGKNPKPEELREIEKTRMEQNNGHY FDTAIVNSDLKAYQELLRLINKLDTEPQWVPSTWLR		
	SEQ ID NO: 23		2030 bp
NOV9b, CG58590-02 DNA Sequence	CCATGACAACATCCCATATGAATGGGCATGTTACAGAGGAATCAGACAGCGAAGTAAA AAATGTTGATCTTGCAATCACCAGAGGAACATCAGAAGCACCGAGAGATGGCTGTTGAC TGCCCTGGAGATTGGGCACCAGGATGATGCCAATACGTCGAAGTGACAGTTGGAGC GTATTCGGCAACCAACAGGAGGACATGAGGCGTAGGAGAGAGGAAGAGGAAAAAGCA AGAACTTGACCTTAATCTTCCATGAGACTTAAGAACTAGCCCAAATTCCTCCAAAG ACCGGAATAGATAACCCATATGTTGATACAGAGGAAGGAATTTGCTTAGAAAGTCCTC ATTATGCTGTGAAAATATTAGAAATAGAAGACTTGTTTTCTTCACTTAAACATATCCA ACATACTTTGGTAGATTCTCAGAGCCAGGAGGATATTTCACTGCTTTTACAACCTGTT CAAAATAGGATTTCAGAAATGCATTTAAGATACACAATGCCATCACAGTACATATGA ACAAAGGCCAGTCTCTCATTTCTCTTATCTCCAACGCACAAGATCTTGCTCAAGAGGT ACAAACTGTTTTGAAGCCAGTTCATCATAAGGAAGGACAAGAATCACTGCTTTGCTG AATACTCCACATATTAGGCACCTTTTACTGGCCACGATAAGGTTGGCTGAGCAGGAAA TGCAGCTAGAGCCCATACAGATGAGAGAGTTTATGAAAGTATTGCGTCAGATGGAGG AGAACTGTAAAAATAGTTTCGTATAGAAAAGGCTCGTGATATTCGTTGGGTGCTACA GTTTCGTAATGAAATGGACTCTGTCATCATTAGCCGGATAGTAAAAGGGGGTGCTGCAG AGAAAAGTGGTCTGTTGCATGAAGGAGATGAAGTTCTAGAGATTAAATGGCATTGAAAT TCGGGGGAAAGATGTCAATGAGGTTTTTGACCTGTTGTCTGATATGCATGGTACTTTG ACTTTTGTCTGATTCCCAGTCAACAGATCAAGCCGCTCCTGCCAAGGAAACAGTAA TCCATGTAAAAGCTCATTTTGACTATGACCCCTCAGATGACCCCTATGTTCCATGTGCG AGAGTTAGGTCTGCTCTTTTCAAAAAGGTGATATACTTCATGTGATCAGTCAAGAAGAT CCAACTGGTGGCAGGCCTACAGGGAAGGGGACGAAGATAATCAACCTCTAGCCGGGC TTGTTCCAGGGAAGGCTTTTCAGCAGCAAAGGGAAGCCATGAACAAACCATAGAAGA AGATAAGGAGCCAGAAAAATCAGGAAAACTGTGGTGTGCAAAAGAAATAAAAAGAAAG AGGAAAAAGGTTTTATATAATGCCAATAAAAATGATGATTATGACAACGAGGAGATCT TAACCTATGAGGAAATGTCACTTTATCATCAGCCAGCAAAATAGGAAGAGACCTATCAT CTTGATTGGTCCACAGAACTGTGGCCAGAATGAATTGCGTCAGAGGCTCATGAACAAA GAAAAGGACCGCTTTGCATCTGCAGTTCCTCATACAACCCGAGTAGGCGAGACCAAG AAGTAGCCGGTAGAGATTACCACTTTGTTTCGCGGCAAGCATTGAGGCAGACATAGC AGCTGGAAGATTCAATTGAGCATGGTGAATTTGAGAAGAATTTGTATGAACTAGCATA GATTCTGTACGGCAAGTGATCAACTCTGGCAAAATATGTCTTTAAGCTTCGTACAC AGTCATTGAAGACTCTCCGGAATTCAGATTGAAACCATATATTATCTTCATTGCACC		

	CCCTTCACAAGAAAGACTTCGGGCATTATTGGCCAAAGAAGGCAAGAATCCAAAGCCT GAAGAGTTGAGAGAAATCATTGAGAAGACAAGAGAGATGGAGCAGAACAAATGGCCACT ACTTTGATACGGCAATTGTGAATCCGATCTTGATAAAGCCTATCAGGAATTGCTTAG GTTAATTAACAAACTTGATACTGAACCTCAGTGGGTACCATCCACTTGGCTGAGGTGA		
	ORF Start: ATG at 3	ORF Stop: TGA at 2028	
	SEQ ID NO: 24	675 aa	MW at 77292.8kD
NOV9b, CG58590-02 Protein Sequence	MTTSHMNGHVTEESDSEVKNVDLASPEEHQKHREMAVDCPGDLGTRMMPIRRSAQLER IRQQQEDMRRRREEEGKKQELDLNSSMRLKKLAQIPPKTGIDNPMFDTEEGIVLES YAVKILEIEDLFSSSLKHIQHTLVDSQSQEDISLLLQLVQNKDFQNAFKIHNAITVHMN KASPPFPLISNAQDLAQEVQTVLKPVHHKEGQELTALLNTPHIQALLAHDKVAEQEM QLEPITDERVYESIGQYGGETVKIVRIEKARDIPLGATVRNEMDSVVISRIVKGGAAE KSGLLHEGDEVLEINGIEIRGKDVNEVFDLLSDMHGTLTFVLIPSQQIKPPPAKETVI HVKAHFDYDPSDDPYVPCRELGLSFQKGDILHVISQEDPNWWQAYREGDEDNQPLAGL VPGKSPQQQREAMQQTIEEDKEPEKSGKLWCAKKNKKRKKVLYNANKNDYDNEEIL TYEEMSLYHQPANRKRPIILIGPQNCGQNELRQLMNEKDRFASAVPHTRSRDQE VAGRDYHFVSRQAFEADIAAGKPIEHGEFEKNLYGTSIDSVRQVINSCKICLLSLRTQ SLKTLRNSDLKPYIIFIAPPSQERLRALLAKEGKNPKPEELREIIEKREMEQNNGHY FDTAIVNSDLKAYQELLRLINKLDTEPQWVPSTWLR		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 9B.

Table 9B. Comparison of NOV9a against NOV9b.		
Protein Sequence	NOV9a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV9b	1..675	636/675 (94%)
	1..675	636/675 (94%)

Further analysis of the NOV9a protein yielded the following properties shown in Table 9C.

Table 9C. Protein Sequence Properties NOV9a	
PSort analysis:	0.7000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV9a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 9D.

Table 9D. Geneseq Results for NOV9a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV9a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value

AAB94180	Human protein sequence SEQ ID NO:14494 - Homo sapiens, 503 aa. [EP1074617-A2, 07-FEB-2001]	173..675 1..503	501/503 (99%) 501/503 (99%)	0.0
AAB41921	Human ORFX ORF1685 polypeptide sequence SEQ ID NO:3370 - Homo sapiens, 269 aa. [WO200058473-A2, 05-OCT-2000]	406..675 1..269	261/270 (96%) 264/270 (97%)	e-147
AAU07123	Human novel human protein, NHP #23 - Homo sapiens, 576 aa. [WO200161016-A2, 23-AUG-2001]	143..674 31..574	224/564 (39%) 339/564 (59%)	e-109
AAU07119	Human novel human protein, NHP #19 - Homo sapiens, 560 aa. [WO200161016-A2, 23-AUG-2001]	143..654 31..554	213/544 (39%) 327/544 (59%)	e-102
AAU07115	Human novel human protein, NHP #15 - Homo sapiens, 520 aa. [WO200161016-A2, 23-AUG-2001]	143..606 31..495	196/481 (40%) 300/481 (61%)	5e-97

In a BLAST search of public sequence databases, the NOV9a protein was found to have homology to the proteins shown in the BLASTP data in Table 9E.

Table 9E. Public BLASTP Results for NOV9a				
Protein Accession Number	Protein/Organism/Length	NOV9a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JLB2	PALS1 - Mus musculus (Mouse), 675 aa.	1..675 1..675	652/675 (96%) 665/675 (97%)	0.0
Q9H9Q0	CDNA FLJ12615 FIS, CLONE NT2RM4001629, WEAKLY SIMILAR TO MAGUK P55 SUBFAMILY MEMBER 3 - Homo sapiens (Human), 503 aa.	173..675 1..503	501/503 (99%) 501/503 (99%)	0.0
AAL40935	STARDUST PROTEIN MAGUK1 ISOFORM - Drosophila melanogaster (Fruit fly), 1289 aa.	252..674 829..1282	252/460 (54%) 327/460 (70%)	e-140
Q9W3H6	CG1617 PROTEIN - Drosophila melanogaster (Fruit fly), 794 aa.	252..674 294..787	252/500 (50%) 327/500 (65%)	e-132
Q9W7F1	P55-RELATED MAGUK PROTEIN DLG3 - Brachydanio rerio (Zebrafish) (Zebra danio), 576 aa.	142..673 30..573	209/556 (37%) 335/556 (59%)	e-105

PFam analysis predicts that the NOV9a protein contains the domains shown in the Table 9F.

Table 9F. Domain Analysis of NOV9a			
Pfam Domain	NOV9a Match Region	Identities/ Similarities for the Matched Region	Expect Value
L27: domain 1 of 1	186..238	19/56 (34%) 39/56 (70%)	0.049
PDZ: domain 1 of 1	256..335	21/83 (25%) 58/83 (70%)	9.7e-12
SH3: domain 1 of 1	348..415	19/68 (28%) 46/68 (68%)	0.026
Guanylate_kin: domain 1 of 1	515..624	54/113 (48%) 87/113 (77%)	6.2e-38
Peptidase_S15: domain 1 of 1	642..658	6/17 (35%) 13/17 (76%)	8.2
Caulimo_mov: domain 1 of 1	420..673	59/335 (18%) 156/335 (47%)	6.1

Example 10.

The NOV10 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 10A.

Table 10A. NOV10 Sequence Analysis			
	SEQ ID NO: 25	576 bp	
NOV10a, CG58572-01 DNA Sequence	ACCTTACTAGAAAAATGAAACCTGATGAAACTCCTATGTTTGACCCAAGTCTACTCAA AGAAGTGGACTGGAGTCAGAATACAGCTACATTTTCTCCAGCCATTTCCCCAACACAT CCTGGAGAAGGCTTGGTTTGGAGGCCTCTTTGTACTGCTGACTTAAATAGAGGTTTTT TTAAGGTATTGGGTCAGCTAACAGAGACTGGAGTTGTGAGCCCTGAACAATTTATGGA ATCCTTTTGAGCATATGAAGAAATCTGGGGATTATTATGTTACAGTTGTAGAAGATGTG ACTCTAGGACAGATTGTTGCTACGGCAACTCTGATTATAGAACATAAATTCATCCATT CCTGTGCTAAGAGAGGAAGAGTAGAAGATGTTGTTGTTAGTGATGAATGCAGAGGAAA GCAGCTTGGCAAATGTTATTATCAACCCCTACTTTGCTAAGCAAGAAACTGAACTGT TACAAGATTACCCTTGAATGTCTACCACAAAATGTTGGTTTCTATAAAAAGTTGGAT ATACTGTATCTGAAGAAAACATACATGTGTGCGAGGTTTCTAAAGTAAAAATCTT		
	ORF Start: ATG at 15	ORF Stop: TAA at 567	
	SEQ ID NO: 26	184 aa	MW at 20749.9kD
NOV10a, CG58572-01 Protein Sequence	MKPDETPMFDPSLLKEVDWSQNTATFSPAISFTHPGEGLVLRPLCTADLNRGFFKVLG QLTETGVVVSPEQFMESFEHMKKSGDYVTVVVEDVTLGQIVATATLIIHKFIHSCAKR GRVEDVVVSDECRGKQLGKLLSTLTLLSKKLNCKITLCLPQNVGFYKFKGYTVSE ENYMCRRFLK		

	SEQ ID NO: 27	560 bp
NOV10b, CG58572-02 DNA Sequence	ATGAAACCTGATGAACTCCTATGTTTGACCCAAGTCTACTCAAAGAAGTGGACTGGA GTCAGAATACAGCTACATTTTCTCCAGCCATTTCCTCCACACATCCTGGAGAAGGCTT GGTTTTGGGGCCTCTTTGTACTGCTGACTTAAATAGAGGTTTTTTAAGGTATTGGGT CAGCTAACAGAGACTGGAGTTGTCAGCCCTGAACAATTTATGAAATCTTTGAGCATA TGAAGAAATCTGGGATTATTATGTTACAGTTGTAGAAGATGTGACTCTAGGACAGAT TGTTCCTACGGCAACTCTGATTATAGAACATAAATTCATCCATTCTGTGCTAAGAGA GGAAGAGTAGAAGATGTTGTTAGTGTGAATGCAGAGGAAAGCAGCTTGGCAAAT TGTATTATCAACCTTACTTTGCTAAGCAAGAACTGAACTGTTACAAGATTACCTT TGAATGTCTACCACAAATGTTGGTTTCTATAAAAAGTTTGGATATACTGTATCTGAA GAAACTACATGTGTCGGAGGTTCTAAAGTAAAAATC	
	ORF Start: ATG at 1	ORF Stop: TAA at 553
	SEQ ID NO: 28	184 aa MW at 20649.8kD
NOV10b, CG58572-02 Protein Sequence	MKPDETPMFDPSLLKEVDWSQNTATFSPAISPTHPEGGLVLGPLCTADLNRGFFKVLG QLTETGVVSPEQFMKSFHEMKKSGDYVTVVEDVTLGQIVATATLIEHKFIHSCAKR GRVEDVVVSDECRGKQLGKLLSTLTLLSKKLNCKITILECLPQNVGFYKFGYTVSE ENYMCRRFLK	

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 10B.

Table 10B. Comparison of NOV10a against NOV10b.		
Protein Sequence	NOV10a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV10b	1..184	163/184 (88%)
	1..184	164/184 (88%)

Further analysis of the NOV10a protein yielded the following properties shown in Table 10C.

Table 10C. Protein Sequence Properties NOV10a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.1206 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV10a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 10D.

Table 10D. Geneseq Results for NOV10a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV10a Residues/	Identities/ Similarities for	Expect Value

		Residues	Region	
AAG67123	Amino acid sequence of human 50287 transferase - Homo sapiens, 184 aa. [WO200164904-A2, 07-SEP-2001]	1..184 1..184	183/184 (99%) 184/184 (99%)	e-105
AAB73505	Human transferase HTFS-12, SEQ ID NO:12 - Homo sapiens, 184 aa. [WO200132888-A2, 10-MAY-2001]	1..184 1..184	183/184 (99%) 184/184 (99%)	e-105
AAB63700	Human gastric cancer associated antigen protein sequence SEQ ID NO:1062 - Homo sapiens, 200 aa. [WO200073801-A2, 07-DEC-2000]	1..184 17..200	183/184 (99%) 184/184 (99%)	e-105
AAU07779	Human novel transferase protein, NHP #22 - Homo sapiens, 184 aa. [WO200164903-A2, 07-SEP-2001]	1..184 1..184	182/184 (98%) 183/184 (98%)	e-104
AAM79992	Human protein SEQ ID NO 3638 - Homo sapiens, 206 aa. [WO200157190-A2, 09-AUG-2001]	1..184 23..206	181/184 (98%) 183/184 (99%)	e-104

In a BLAST search of public sequence databases, the NOV10a protein was found to have homology to the proteins shown in the BLASTP data in Table 10E.

Table 10E. Public BLASTP Results for NOV10a				
Protein Accession Number	Protein/Organism/Length	NOV10a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96EK6	SIMILAR TO GLUCOSAMINE-PHOSPHATE N-ACETYLTRANSFERASE - Homo sapiens (Human), 184 aa.	1..184 1..184	183/184 (99%) 184/184 (99%)	e-104
Q9JK38	EMEG32 PROTEIN (GLUCOSAMINE-PHOSPHATE N-ACETYLTRANSFERASE) - Mus musculus (Mouse), 184 aa.	1..184 1..184	180/184 (97%) 182/184 (98%)	e-102
Q9VAI0	Probable glucosamine-phosphate N-acetyltransferase (EC 2.3.1.4) (Phosphoglucosamine transacetylase) (Phosphoglucosamine acetylase) - Drosophila melanogaster (Fruit fly), 219 aa.	4..176 6..179	84/174 (48%) 123/174 (70%)	2e-43
Q17427	Probable glucosamine-phosphate N-acetyltransferase (EC 2.3.1.4) (Phosphoglucosamine transacetylase) (Phosphoglucosamine acetylase) - Caenorhabditis elegans, 165 aa.	32..182 15..165	65/152 (42%) 98/152 (63%)	1e-28
O45811	T23G11.2 PROTEIN - Caenorhabditis elegans, 347 aa.	42..184 201..340	63/143 (44%) 88/143 (61%)	3e-26

PFam analysis predicts that the NOV10a protein contains the domains shown in the Table 10F.

Table 10F. Domain Analysis of NOV10a			
Pfam Domain	NOV10a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Acetyltransf: domain 1 of 1	89..171	22/87 (25%) 62/87 (71%)	6.5e-13

Example 11.

The NOV11 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 11A.

Table 11A. NOV11 Sequence Analysis

	SEQ ID NO: 29	709 bp
NOV11a, CG58564-01 DNA Sequence	CCCGCGGGCCAGCACCATGGAGGACGTGAAGCTGGAGTTCCCTTCCCTTCCACAGTGC AAGGAAGACGCCGAGGAGTGGACCTACCCTATGAGACGAGAGATGCAGGAAATTTAC CTGGATTGTTCTTAGGCCCATATTCTGCTATGAAAAGCAAGTACCTGTACTACA GAAACATGGAATAACCCATATAATATGCATACGACAAAATATTGAAGCAAACCTTATT AAACCAAACCTTCAGCAGTTATTTAGGTATTTAGTCTGGATATTGCAGATAATCCAG TTGAAAATATAATACGTTTTTCCCTATGACTAAGGAATTTATTGATGGGAGCTTACA AATGGGAGGTAAAGTTCTGTGTCATGGAAATGCAGGGATCTCCAGAAGTGCAGCCTTT GTTATTGCATACATTATGGAACATTGGAATGAAGTACAGGGATGCTTTTGCTTATG TTCAAGAAAGAAGATTTGTATTAATCCTAATGCTGGATTGTCCATCAACTTCAGGA ATATGAAGCCATCTACCTAGCAAAATTAACAATACAGATGATGTCAACCTCCAGATA GAAAGGTCAATTATCTGTTCACTCTGGTACCACAGGTAGTTTGAAGAGAACACATGAAG AAGAGGATGATTTTGGAAACCATGCAAGTGGCGACTGCACAGAATGGCTGACTTGAAGA GCAACATCATAGA	
	ORF Start: ATG at 17	ORF Stop: TGA at 686
	SEQ ID NO: 30	223 aa MW at 25492.2kD
NOV11a, CG58564-01 Protein Sequence	MEDVKLEFPSPQCKEDAEWTPMRREMQEILPGLFLGYPYSSAMKSLPVLQKHGIT HIICIRQNIENFIKPNFQQLFRYLVLADIADNPVENIIRFFPMTKEFIDGSLQMGKV LVHGNAGISRSAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGFVHLQYEYAIY LAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHEEEDDFGTMQVATAQNG	
	SEQ ID NO: 31	724 bp
NOV11b, CG58564-02 DNA Sequence	ACTCTCCCACCCACCCACCAGAATGGCGGGCCAGCACCATGGAGGACGTGAAGCTGG AGTTCCCTTCCCTTCCACAGTGCAAGGAAGACGCCGAGGAGTGGACCTACCCTATGAG ACGAGAGATGCAGGAAATTTTATCTGGATTGTTCTTAGGCCCATATTCTGCTATG AAAAGCAAGCTACCTGTACTACAGAAACATGGAATAACCCATATAATATGTCATACGAC AAAATATTGAAGCAAACCTTTATTAACCAAACCTTTCAGCAGTTATTTAGATATTTAGT CCTGGATATTGCAGATAATCCAGTTGAAAATATAATACGTTTTTCCCTATGACTAAG GAATTTATTGATGGGAGCTTACAAATGGGAGGAAAAGTTCTGTGTCATGGAATGCAG GGATCTCCAGAAGTGCAGCCTTTGTTATTGCATACATTATGGAACATTGGAATGAA GTACAGAGATGCTTTTGCTTATGTTCAAGAAAGAAGATTTGTATTAATCCTAATGCT GGATTGTCCATCAACTTCAGGAATATGAAGCCATCTACCTAGCAAAATTAACAATAC AGATGATGTCAACCTCCAGATAGAAAGGTCATTATCTGTTCACTCTGGTACCACAGG CAGTTTGAAGAGAACACATGAAGAAGAGGATGATTTTGAACCCATGCAAGTGGCGACT GCACAGAATGGCTGACTTGAAGAGCAAC	
	ORF Start: ATG at 40	ORF Stop: TGA at 709
	SEQ ID NO: 32	223 aa MW at 25482.1kD
NOV11b, CG58564-02 Protein Sequence	MEDVKLEFPSPQCKEDAEWTPMRREMQEILSGLFLGYPYSSAMKSLPVLQKHGIT HIICIRQNIENFIKPNFQQLFRYLVLADIADNPVENIIRFFPMTKEFIDGSLQMGKV LVHGNAGISRSAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGFVHLQYEYAIY LAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHEEEDDFGTMQVATAQNG	
	SEQ ID NO: 33	545 bp
NOV11c, CG58564-03 DNA Sequence	ACTCTCCCACCCACCCACCAGCCCGCGGGCCAGCACCATGGAGGACGTGAAGCTGGA GTTCCCTTCCCTTCCACAGTGCAAGGAAGACGCCGAGGAGTGGACCTACCCTATGAGA CGAGAGATGCAGGAAATTTTACCTGGATTGTTCTTAGGCCCATATTCTGCTATGA AAAGCAAGCTACCTGTACTACAGAAACATTGGAATGAAGTACAGAGATGCTTTTGCT TATGTTCAAGAAAGAAGATTTGTATTAATCCTAATGCTGGATTGTCCATCAACTTC AGGAATATGAAGCCATCTACCTAGCAAAATTAACAATACAGATGATGTCAACCTCCA GATAGAAAGGTCATTATCTGTTCACTCTGGTACCACAGGCAGTTTGAAGAGAACACAT GAGGAAGAGGATGATTTTGAACCATGCAAGTGGCGACTGCACAGAATGGCTGACTTG AAGAGCAACATCATAGAGTGTGAATTTCTATTGGGAAGGAGAAAATACAAGAGAAAA TTATAATGTAAATGGTAAAAAA	
	ORF Start: ATG at 39	ORF Stop: TGA at 210
	SEQ ID NO: 34	57 aa MW at 6695.7kD
NOV11c, CG58564-03 Protein Sequence	MEDVKLEFPSPQCKEDAEWTPMRREMQEILPGLFLGYPYSSAMKSLPVLQKHLE	
	SEQ ID NO: 35	663 bp
NOV11d, CG58564-04 DNA Sequence	ACTCTCCCACCCACCCACCAGCCCGCGGGCCAGCACCATGGAGGACGTGAAGCTGGA GTTCCCTTCCCTTCCACAGTGCAAGGAAGACGCCGAGGAGTGGACCTACCCTATGAGA CGAGAGATGCAGGAAATTTTACCTGGATTGTTCTTAGGCCCATATTCTGCTATGA AAAGCAAGCTACCTGTACTACAGAAACATGGAATAACCCATATAATATGCATACGACA AAATATTGAAGCAAACCTTTATTAACCAAACCTTTCAGCAGTTATTTAGACTAAGGAAT	

	TTATTGATGGGAGCTTACAAATGGGAGGAAAAGTTCTTGTGCATGGAAATGCAGGGAT CTCCAGAAGTGCAGCCTTTGTTATTGCATACATTATGGAAACATTTGGAATGAAGTAC AGAGATGCTTTTGCTTATGTTCAAGAAAGAAGATTTGTATTAACTAATGCTGGAT TTGTCCATCAACTTCAGGAATATGAAGCCATCTACCTAGCAAAATTAACAATACAGAT GATGTCACCACTCCAGATAGAAAGGTCATTATCTGTTTCATTCTGGTACCACAGGCAGT TTGAAGAGAACACATGAAGAAGAGGATGATTTTGAACCATGCAAGTGGCGACTGCAC AGAATGGCTGACTTGAAGAGCAACT		
	ORF Start: ATG at 39	ORF Stop: TGA at 399	
	SEQ ID NO: 36	120 aa	MW at 14245.6kD
NOV11d, CG58564-04 Protein Sequence	MEDVKLEFFPSLPQCKEDAEWYTPMRREMQEILPGLFLGPYSSAMKSLPVLQKHGIT HII CIRQNI EANFIKPNFQQLFRLRLNLLMGAYKWEKFLCMEMQGSPEVQPLLLHTLW KHLE		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 11B.

Table 11B. Comparison of NOV11a against NOV11b through NOV11d.		
Protein Sequence	NOV11a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV11b	1..223	222/223 (99%)
	1..223	222/223 (99%)
NOV11c	1..55	55/55 (100%)
	1..55	55/55 (100%)
NOV11d	1..81	81/81 (100%)
	1..81	81/81 (100%)

Further analysis of the NOV11a protein yielded the following properties shown in Table 11C.

Table 11C. Protein Sequence Properties NOV11a	
PSort analysis:	0.4698 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1958 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV11a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 11D.

Table 11D. Geneseq Results for NOV11a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV11a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU09017	Human dual specificity phosphatase 38692 - Homo sapiens, 223 aa. [WO200173059-A2, 04-OCT-2001]	1..223 1..223	223/223 (100%) 223/223 (100%)	e-128
AAE08552	Human phosphatase protein - Homo sapiens, 223 aa. [WO200160992-A2, 23-AUG-2001]	1..223 1..223	223/223 (100%) 223/223 (100%)	e-128
AAM41520	Human polypeptide SEQ ID NO 6451 - Homo sapiens, 236 aa. [WO200153312-A1, 26-JUL-2001]	1..223 14..236	223/223 (100%) 223/223 (100%)	e-128
AAM39734	Human polypeptide SEQ ID NO 2879 - Homo sapiens, 223 aa. [WO200153312-A1, 26-JUL-2001]	1..223 1..223	223/223 (100%) 223/223 (100%)	e-128
AAU23521	Novel human enzyme polypeptide #607 - Homo sapiens, 190 aa. [WO200155301-A2, 02-AUG-2001]	25..171 7..145	55/147 (37%) 80/147 (54%)	1e-18

In a BLAST search of public sequence databases, the NOV11a protein was found to have homology to the proteins shown in the BLASTP data in Table 11E.

Table 11E. Public BLASTP Results for NOV11a				
Protein Accession Number	Protein/Organism/Length	NOV11a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAD10219	SEQUENCE 4 FROM PATENT WO0173059 - Homo sapiens (Human), 223 aa.	1..223 1..223	223/223 (100%) 223/223 (100%)	e-127
Q9DCF8	0610039A20RIK PROTEIN - Mus musculus (Mouse), 223 aa.	1..223 1..223	215/223 (96%) 221/223 (98%)	e-124
Q60970	PROTEIN TYROSINE PHOSPHATASE-LIKE - Mus musculus (Mouse), 223 aa.	1..223 1..223	214/223 (95%) 221/223 (98%)	e-124
Q60969	PROTEIN TYROSINE PHOSPHATASE-LIKE - Mus musculus (Mouse), 205 aa.	1..168 1..168	163/168 (97%) 167/168 (99%)	2e-93
Q99850	TYROSINE PHOSPHATASE-LIKE	116..181 1..66	66/66 (100%) 66/66 (100%)	3e-31

	Homo sapiens (Human), 66 aa (fragment).			
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PFam analysis predicts that the NOV11a protein contains the domains shown in the Table 11F.

Table 11F. Domain Analysis of NOV11a			
Pfam Domain	NOV11a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DSPc: domain 1 of 1	28..173	64/172 (37%) 127/172 (74%)	2.2e-63
Y_phosphatase: domain 1 of 1	35..179	35/279 (13%) 93/279 (33%)	1.7

Example 12.

The NOV12 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 12A.

Table 12A. NOV12 Sequence Analysis		
	SEQ ID NO: 37	3696 bp
NOV12a, CG57819-01 DNA Sequence	GTGTA AAAA TACTGTCCATTTAATGTTTCTGGGACTTTAGGTAAGAATATGAAAAC CAACCAACCTTGAGCAGGATGAACCGGAGGAATTGGAGGACAGTTCTTTGACTTC GCGAAGATCACATGTTGGTGAAGGAGCTTTCTTGAAGCAACAGGATGAGATCAAAAG GCTGAGGACCACCTTGCTGCGGTTGACCGCTGCTGGCCGGGACCTGCGGGTCGCGGAG GAGGCGGCGCGCTCTCGGAGACCGCAAGCGCGGCGAGAAAGCGGGATGGCGGCGAGC GCCTCTCCATGCACCGAGCGCCCCAGATGCACCGACTGCAAGGGCATTTCACATGCGT CGGCCCTGCCAGCCCCCGCGCGCCAGCCTCGCGTCCAAGTGGGACACAGACAGCTC CACACAGCCGGTGACCGGTGCGGAGAAACCAAGAGGGTAGGGACAGGCTGAGCT ACACAGCCCCCTCCATCGTTAAGGAGCATGCGACAAATGAAAACAGAGGTGAAGTAGC CAGTAAACCCAGTGAACCTGGCCACATCATGGCCAGCAATACCATGCAAGTGAAGAG CCACCAAGTCTCCTGAGAAAATGTGGCTAAAGATGAAAATTTGAACAGAGAAGCT CATTGGAGTGTGCTCAGAAGGCTGAGAGCTTCGGGCTTCCATTAAAGAGAAGGTAGA GCTGATTGACTTAAGAAGCTTTACATGAAAGAAATGCTTCATTGGTTATGACAAAA GCACAAATTAACAGAAGTTCAAGAGGTGAGTTGCCATCTTTTGACCAGAAATCAGGGAA TCCTGAGTGCAGCCCATGAGGCCCTCTCAAGCAAGTGAATGAGTCAAGGACAGCT GAAGGAAGAAAGCAAGAGGCTGTGAGCTTGAAGAGCCAACTGGGAAGATGTGTATC TTGCAGATGACTCTGAAGGAGTTTCAGGAGAGAGTTGAAGATTTGAAAAAGAACGAA AATTGCTGAATGACAATTATGACAAACTCTTAGAAAGCAGTGACAGCTCCAGTCAGCC CCACTGGAGCAACGAGCTCATAGCGGAACAGCTACAGCAGCAAGTCTCTCAGCTGCAG GATCAGCTGGATGCTGAGCTGGAGGACAAGAGAAAAGTTTACTTGAGCTGTCCAGGG AGAAAGCCCAAAATGAGGATCTGAAGCTTGAAGTCACCAACATAGTTCAAGACATAA ACAGGAAGTAGAGTCTCTCAAAATGCAGCCACAATTTCCCAACCTCTGCAGAGGCAA TCTGAACCAAGCACTCAGCCAGCTGATTGCAAGAGAACTCAGATCCAGCCAAAGTG AACCAAAAACCAAGAGAAAAGAACTGTCCAGGTGCTAAATGAGTTGCAAGTATC ACACGAGAGACCATTTGAACTAGAAAAGACCGGGACATGCTTATTCTGCAGCGC AAAATCAACGTGTGTTATCAGGAGGAACTGGAGGCAATGATGACAAAAGCTGACAATG ATAATAGAGATCAAAAGAAAAGCTGGAGAGGTTGACTCGACTACTAGACCTCAAGAA TAACCGTATCAAGCAGCTGGAAGAACAGCTCAAAGATGTTGCTTATGGCACCAGCCG TTGTCGTTATGTTTGAAGAACTGCCAGCCCATGGAGATGAGGATAAAGTGGATATTT CTCTGTCATCAGGGTGAGAATCTTTTGAAGTGCACATCCACAGGCTTCTTGAC ATCTGCCGCCCTAGCTCAGGCTGGAGATACCAACCTACCACTTTCTGCACCTATTCC TTCTATGACTTTGAAACCACTGTACCCCATTTATCTGTGGGGCCACAGCCCCCTCTATG ACTTCACCTCCCAGTATGTGATGGAGACAGATTGCTTTTCTTACACTACCTTCAAGA GGCTTCAGCCCGGCTTGACATACACAGGCCATGGCCAGTGAACACAGCACTTCTGCT GCAGGATGGAATTTGCTTTGACAGGGTGCTAGAGACTGTGGAGAAAGTCCATGGCTTGG CCACACTGATTGGTGTGTTGGAGAAGAGTTCCGGGTTCTAGAGTACTGGATGAGGCT	

	GCGTTTCCCATAAAACCCAGCCTACAGGCGTGCAATAAACGAAAGAAAGCCAGGTC TACCTGTCAACCGATGTGCTTGGAGGCGGAAAGGCCAGGAAGAGGAGTGAGATCGG AGTCTTGGGAACCTCAGAACGAGCTGTGGATTGAAATCACCAGTGCTGTGGCCTCCG GAGTCGATGGCTGGGAACCTCAACCCAGTCCATATGCTGTGTACCGCTTCTTACCTTT TCTGACCATGACACTGCCATCATTCCAGCCAGTAACAACCCCTACTTTAGAGACCAGG CTCGATTCCAGTGCTTGTGACCTCTGACCTGGACCATTATCTGAGACGGGAGGCCCTT GTCTATACATGTTTTGATGATGAAGACTTAGAGCCTGGCTCGTATCTTGGCCGAGCC CGAGTGCCCTTACTGCCTCTTGCAAAAATGAATCTATCAAAGGTGATTTAACTCA CTGACCCCTGCAGAGAAACCCACGGATCTATTCAAGTGCACTGATTGGAAGTTTCC CTACATACCCCTGAGAGCTTCTGAAACCAGAAGCTCAGACTAAGGGGAAGGATACC AAGGACAGTTCAAAGATCTCATCTGAAGAGGAAAAGGCTTCATTTCTTCCAGGATC AGATGGCATCTCCTGAGGTTCCCATTTGAAGCTGGCCAGTATCGATCTAAGAGAAAAAC TCCTCATGGGGGAGAAAGAAAGGAGAAGGAGCACCAGGTTGTGAGCTACTCAAGAAGA AAACATGGCAAAAGAATAGGTGTTCAAGGAAAGAATAGAATGGAGTATCTTAGCCTTA ACATCTTAAATGGAAATACACTGAAGCAGGTGAATTACACTGAGTGGAAGTTCTCAGA GACTAACAGCTTCATAGGTGATGGCTTTAAAAATCAGCAGGAGGAAGAGGAAATGACA TTATCCCATTCAGCACTGAAACAGAGGAACCTCTACATCTGTAAATGACAAGAATA CCTCTGAACAAGGTTCTGAAGTCAGTGAAGCACAACCTACCGACAGTGATGATGTCAT AGTGCCACCCATGTCTCAGAAATATCTAAGGCAGATTACAGAGAAGATGTGCATTGAA ATTGTCTCCCTGGCCTTCTACCCAGAGGCAGAAGTGATGTCTGATGAGAACATAAAAC AGGTGTATGTGGAGTACAAATTCTACGACCTACCCTTGTCCGAGCAGAGACTCCAGT GTCCCTAAGGAAGCCTAGGGCAGGAGAAGAAATCCACTTTCACTTTAGCAAGGTAATA GACCTGGACCCACAGGAGCAGCAAGGCCGAAGGCGGTTTCTGTTCCGACATGCTGAATG GACAAGATCCTGATCAAGGACAGTTAAAGTTTACAGTGGTAAGTGATCCTCTGGATGA AGAAAAGAAAGAATGTGAAGAAGTGGGATATGCATATCTTCAACTGTGGCAGATCCTG GAGTCAGGAAGAGATATTCTAGAGCAAGAGCTAGACGTTGTTAGCCCTGAAGATCTGG CTACCCCAATAGGAAGGCTGAAGGTTTCCCTTCAAGCAGCTGCTGCTCCATGCTAT TTACAAGGAGATGACTGAAGATTGTTTTCATGAAGGAACAA		
	ORF Start: ATG at 23		ORF Stop: TGA at 3686
	SEQ ID NO: 38	1221 aa	MW at 139825.2kD
NOV12a, CG57819-01 Protein Sequence	MFSGLGKNMKTQPPLSRMNRRELEDSFFRLREDHMLVKELSWKQDDEIKRLRTLLR LTAAGRDLRVAEEAAPLSETARRGQKAGWRQRLSMHQRPMHRLQGHFHCVPASPRR AQPRVQVGHRLHTAGAPVPEKPKRGRDRLSYTA PPSFKEHATNENRGEVASKPSELA HIMASNTMQVEEPPKSPKMWPKDENFEQRSSLECAQKAAELRASIKEKVELIRLKKL LHERNASLVMTKAQLTEVQEVSCHLLTQNQGI LSAHEALQKVNELRAELKEESKKA VSLKSQLEDVSILOMTLKEFQERVEDLEKERKLLNDNYDKLLESSDSSSQPHWSNELI AEQLQQQVSQLQDQLDAELEDKRVLLLSREKAQNE DLKLEVTNIIQKHQEVVELLQ NAATISQPPDRQSEPATHPAVLQENTQIQPSEPKNQEEKKLSQVLNELQVSHAETTL LEKTRDMLILQRKINVCYQEELEAMMTKADNDNRDHKEKLERLRLD LKNNRIKQLE EQLKDVAYGTRPLSLCLETLPAHGDEDKVDISLLHQGENLFELHIHQAF L TSAALQA GDTQPTTFCTYSFYDFETHCTPLSVGPQPLYDFTSQYVME TDSLFLHYLQEASARLDI HQAMASEHSTLAAGWICFDRVLETVEKVHGLATLIGAGGEFGVLEYWMLRFRFIPKS LQACNKRKKAQVYLSTDLVGRKAQEEVRSSESWEPQNELWIEITKCCGLRSRWLGTQ PSPYAVYRFFTFSDHDTAII PASNNPYFRDQARFPVLVTSDDLHYLRREALSIHV FDD EDLEPGSYLGRARVPLLP LAKNESIKGDFNLTPAEKPNGSIQVQLDWKFPYIPPEF LKPEAQTKGKDTKDSSKISSSEEEKASFPSQDMASPEVPIEAGQYRSKRKP PPHGGERK EKEHQVVSYSRRKHGKRIGVQGNRMEYLSLNI LINGNTLKQVNYTEWKFSETNSFIGD GFKNQHEEEEMTLSHSALKQKEPLHPVNDKESSEQGEVSEAQT TDSDDVIVPMSQK YPKADSEKMCIEIVSLAFYPEAEVMSDENIKQVYVEYKFYDLPLSETETPVSLRKPR GEEIHFFHSKVIDLD PQEQGRRRFLDMLNGQDPDQGLKFTTVSDPLDEEKECEE VGYAYLQLWQILESGRDILEQELDVVSPEDLATPIGR LKVS LQAAAVLHAIYKEMTED LFS		

Further analysis of the NOV12a protein yielded the following properties shown in Table 12B.

Table 12B. Protein Sequence Properties NOV12a	
PSort analysis:	0.9600 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
	No Known Signal Sequence Predicted

analysis:

A search of the NOV12a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 12C.

Table 12C. Geneseq Results for NOV12a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV12a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM78558	Human protein SEQ ID NO 1220 - Homo sapiens, 1179 aa. [WO200157190-A2, 09-AUG-2001]	63..1219 47..1177	400/1193 (33%) 640/1193 (53%)	e-172
AAM79542	Human protein SEQ ID NO 3188 - Homo sapiens, 1160 aa. [WO200157190-A2, 09-AUG-2001]	63..1219 28..1158	400/1193 (33%) 640/1193 (53%)	e-172
AAM41414	Human polypeptide SEQ ID NO 6345 - Homo sapiens, 1160 aa. [WO200153312-A1, 26-JUL-2001]	63..1219 28..1158	400/1193 (33%) 640/1193 (53%)	e-172
AAM39628	Human polypeptide SEQ ID NO 2773 - Homo sapiens, 1128 aa. [WO200153312-A1, 26-JUL-2001]	118..1219 47..1126	390/1138 (34%) 623/1138 (54%)	e-171
AAG75661	Human colon cancer antigen protein SEQ ID NO:6425 - Homo sapiens, 118 aa. [WO200122920-A2, 05-APR-2001]	445..523 33..111	40/79 (50%) 56/79 (70%)	1e-13

In a BLAST search of public sequence databases, the NOV12a protein was found to have homology to the proteins shown in the BLASTP data in Table 12D.

Table 12D. Public BLASTP Results for NOV12a				
Protein Accession Number	Protein/Organism/Length	NOV12a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96KN7	RPGR-INTERACTING PROTEIN 1 - Homo sapiens (Human), 1286 aa.	7..1221 29..1286	1203/1258 (95%) 1207/1258 (95%)	0.0
Q96QA8	RPGR-INTERACTING PROTEIN 1 - Homo sapiens (Human), 1286 aa.	7..1221 29..1286	1203/1258 (95%) 1207/1258 (95%)	0.0
Q9GLM3	RPGR-INTERACTING PROTEIN-1 - Bos taurus (Bovine), 1221 aa.	1..1221 1..1221	922/1234 (74%) 1031/1234 (82%)	0.0
Q9NR40	RPGR-INTERACTING PROTEIN - Homo sapiens (Human), 902 aa.	331..1221 1..902	883/902 (97%) 888/902 (97%)	0.0
Q9HBK6	RPGR-INTERACTING PROTEIN-1 - Homo sapiens (Human), 762 aa.	471..1221 1..762	742/763 (97%) 746/763 (97%)	0.0

PFam analysis predicts that the NOV12a protein contains the domains shown in the Table 12E.

Table 12E. Domain Analysis of NOV12a			
Pfam Domain	NOV12a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PFEMP: domain 1 of 1	293..413	23/176 (13%) 82/176 (47%)	7.9
C2: domain 1 of 1	736..825	14/101 (14%) 54/101 (53%)	1.4

Example 13.

The NOV13 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 13A.

Table 13A. NOV13 Sequence Analysis			
	SEQ ID NO: 39	678 bp	
NOV13a, CG57789-01 DNA Sequence	TGGGGCGGGAGGCATGGTCTCCACCTACCGGGTGGCCGTGCTGGGGCGCGAGGTGTG GGCAAGAGTGCCATCGTGGCCAGTTCTTGTACAACGAGTTCAGCGAGGTCTGCGTCC CCACCACCGCCCCGCCCTTTACCTGCCTGCTGTCGTCATGAACGGCCACGTGCACGA CCTCCAGATCCTCGACTTTCACCCATCAGCGCCTTCCCTGTCAATACGCTCCAGGAG TGGGCAGACACCTGCTGCAGGGGACTCCGGAGTGTCCACGCCTACATCCTGGTCTACG ACATCTGCTGCTTTGACAGCTTTGAGTACGTCAAGACCATCCGCCAGCAGATCCTGGA GACGAGGGTGATCGGAACCTCAGAGACGCCCATCATCATCGTGGGCAACAAGCGGGAC CTGCAGCGCGGACGCGTGATCCCGCGCTGGAACGTGTCGCACCTGGTACGCAAGACCT GGAAGTGGCGCTACGTGGAATGCTCGGCCAAGTACAAC TGGCACATCTGCTGCTCTT CAGCGAGCTGCTCAAGAGCGTGGCTGCGCCCGTTGCAAGCAGTGCACGCTGCCCTG CGCTTCCAGGGCGCGCTGCGCCGCAACCGCTGCGCCATCATGTGACGCTGCGCGCCC CTCGGGCTGCACCGGCACTGGCCGAGCGGAGGGCGGGGCC		
	ORF Start: ATG at 14	ORF Stop: TGA at 623	
	SEQ ID NO: 40	203 aa	MW at 23229.0kD
NOV13a, CG57789-01 Protein Sequence	MVSTYRVAVLGARGVGKSAIVRQFLYNEFSEVCVPTTARRLYLPAVVMNGHVHDLQIL DFPPIISAFPVNTLQEWADTCCRGLRSVHAYILVYDICCDFSFEYVKTIHQIILETRVI GTSETPIIIVGNKRD LQRGRVIPRWNVSHLVKRTWKCGYVECSAKYNWHILLFSELL KSVGCARCKHVHAALRFQGALRRNRCAIM		
	SEQ ID NO: 41	682 bp	
NOV13b, CG57789-02 DNA Sequence	TGGGAGGCATGGTCTCCACCTACCGGGTGGCCGTGCTGGGGCGCGAGGTGTGGGCAA GAGTGCCATCGTGGCCAGTTCTTGTACAACGAGTTCAGCGAGGTCTGCGTCCCCACC ACCGCCCGCGCCTTTACCTGCCTGCTGTCGTCATGAACGGCCACGTGCACGACCTCC AGATCCTCGACTTTCACCCATCAGCGCCTTCCCTGTCAATACGCTCCAGGAGTGGGC AGACACCTGCTGCAGGGGACTCCGGAGTGTCCACGCCTACATCCTGGTCTACGACATC TGCTGCTTTGACAGCTTTGAGTACGTCAAGACCATCCGCCAGCAGATCCTGGAGACGA GGGTGATCGGAACCTCAGAGACGCCCATCATCATCGTGGGCAACAAGCGGGACCTGCA GCGCGGACGCGTGATCCCGCGCTGGAACGTGTCGCACCTGGTACGCAAGACCTGGAAG TGCGGCTACGTGGAATGCTCGGCCAAGTACAAC TGGCACATCCTGCTGCTCTTCAGCG AGCTGCTCAAGAGCGTGGCTGCGCCCGTTGCAAGCAGTGCACGCTGCCCTGCGCTT CCAGGGCGCGCTGCGCCGCAACCGCTGCGCCATCATGTGACGCTGCGCGCCCTCGG GCTGCACCGGCACTGGCCGAGCGGAGGGCACTGGCCGAGCGGAG		
	ORF Start: ATG at 9	ORF Stop: TGA at 618	
	SEQ ID NO: 42	203 aa	MW at 23229.0kD
NOV13b, CG57789-02 Protein Sequence	MVSTYRVAVLGARGVGKSAIVRQFLYNEFSEVCVPTTARRLYLPAVVMNGHVHDLQIL DFPPIISAFPVNTLQEWADTCCRGLRSVHAYILVYDICCDFSFEYVKTIHQIILETRVI GTSETPIIIVGNKRD LQRGRVIPRWNVSHLVKRTWKCGYVECSAKYNWHILLFSELL KSVGCARCKHVHAALRFQGALRRNRCAIM		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 13B.

Table 13B. Comparison of NOV13a against NOV13b.		
Protein Sequence	NOV13a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV13b	1..203	203/203 (100%)
	1..203	203/203 (100%)

Further analysis of the NOV13a protein yielded the following properties shown in Table 13C.

Table 13C. Protein Sequence Properties NOV13a	
PSort analysis:	0.6500 probability located in plasma membrane; 0.5064 probability located in mitochondrial matrix space; 0.3844 probability located in microbody (peroxisome); 0.2556 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV13a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 13D.

Table 13D. Geneseq Results for NOV13a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV13a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB42840	Human ORFX ORF2604 polypeptide sequence SEQ ID NO:5208 - Homo sapiens, 136 aa. [WO200058473-A2, 05-OCT-2000]	1..136 1..136	136/136 (100%) 136/136 (100%)	2e-75
AAM41682	Human polypeptide SEQ ID NO 6613 - Homo sapiens, 206 aa. [WO200153312-A1, 26-JUL-2001]	5..174 15..173	66/171 (38%) 89/171 (51%)	4e-18
AAM39896	Human polypeptide SEQ ID NO 3041 - Homo sapiens, 199 aa. [WO200153312-A1, 26-JUL-2001]	5..174 8..166	66/171 (38%) 89/171 (51%)	4e-18
AAY99656	Human GTPase associated protein-7 - Homo sapiens, 281 aa. [WO200031263-A2, 02-JUN-2000]	5..173 25..191	59/179 (32%) 87/179 (47%)	3e-14
AAR05075	RAP1A Gene product incorporating at least one peptide associated with ras oncogene - Synthetic, 184 aa. [WO9000179-A, 11-JAN-1990]	5..177 4..165	57/175 (32%) 90/175 (50%)	5e-14

In a BLAST search of public sequence databases, the NOV13a protein was found to have homology to the proteins shown in the BLASTP data in Table 13E.

Table 13E. Public BLASTP Results for NOV13a				
Protein Accession Number	Protein/Organism/Length	NOV13a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96S79	RAS-LIKE PROTEIN/VTSS58635 - Homo sapiens (Human), 203 aa.	1..203 1..203	203/203 (100%) 203/203 (100%)	e-118
Q92737	Ras-like protein RRP22 (RAS-related protein on chromosome 22) - Homo sapiens (Human), 203 aa.	1..203 1..203	105/204 (51%) 134/204 (65%)	3e-50
Q95KD9	HYPOTHETICAL 22.5 KDA PROTEIN - Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), 199 aa.	5..174 8..166	66/171 (38%) 89/171 (51%)	1e-17
Q96HU8	SIMILAR TO CG8500 GENE PRODUCT - Homo sapiens (Human), 199 aa.	5..174 8..166	66/171 (38%) 89/171 (51%)	1e-17
Q9NF75	EG:BACR37P7.8 PROTEIN - Drosophila melanogaster (Fruit fly), 306 aa.	5..174 48..210	61/174 (35%) 88/174 (50%)	4e-16

PFam analysis predicts that the NOV13a protein contains the domains shown in the Table 13F.

Table 13F. Domain Analysis of NOV13a			
Pfam Domain	NOV13a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Semialdehyde_dh: domain 1 of 1	4..14	4/11 (36%) 11/11 (100%)	0.75
ras: domain 1 of 1	6..203	56/224 (25%) 125/224 (56%)	1.2e-12

Example 14.

The NOV14 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 14A.

Table 14A. NOV14 Sequence Analysis

	SEQ ID NO: 43	1790 bp
NOV14a, CG57758-01 DNA Sequence	<p>TCTCCCTCCCGCGGATGGCCTCGGCGCTGAGCTATGTCTCCAAGTTCAAGTCCCTTCG TGATCTTGTTTCGTACCCCGCTCCTGCTGCTGCCACTCGTCATTCTGATGCCGCCAA GGTCAGTTGTGCTACGTATCATCTCATGGCCATTACTGGTGACAGAAATCATC CCTCTGGCTGTACCTCTCTCATGCTGTCTTGTCTTTCCCACTCTTCCAGATTCTGG ACTCCAGGCAGGTGTGTCCAGTACATGAAGGACACCAACATGCTGTTCTGGGCGG CCTCATCGTGGCCGTGGCTGTGGAGCGCTGGAACCTGCACAAGAGGATCGCCCTGCGC ACGCTCCTCTGGGTGGGGCCAAAGCCTGCACGGCTGATGCTGGGCTTCATGGGCGTCA CAGCCCTCCTGTCCATGTGGATCAGTAACACGGCAACACGGCCATGATGGTGCCCAT CGTGGAGGCCATATTGCAGCAGATGGAAGCCACAAGCGCAGCCACGAGGCCGCGCTG GAGCTGGTGGACAAGGGCAAGGCCAAGGAGCTGCCAGGAGTCAAGTGATTTTTGAAG GCCCACTCTGGGGCAGCAGGAAGACCAAGAGCGGAAGAGGTTGTGTAAGGCCATGAC CCTGTGCATCTGTACGCGGCCAGCATCGGGGGCACCGCCACCTGACCGGGACGGGA CCCAACGTGTGCTCCTGGGCCAGATGAACGAGTTGTTTCTGCAGCAAGGACCTCG TGAACTTTGCTTCTGGTTTGCAATTTGCCTTTCCCAACATGCTGGTGATGCTGCTGTT CGCCTGGCTGTGGCTCCAGTTTGTGTTACATGTTCTCCAGTTTAAAAAGTCTGGGGC TGCGGGCTAGAGAGCAAGAAAAACGAGAAGGCTGCCCTCAAGGTGCTGCAGGAGGAGT ACCGGAAGCTGGGGCCCTTGTCCTTCGCGGAGATCAACGTGCTGATCTGCTTCTCTCT GCTGGTCATCTGTGTTCTCCGAGACCCCGGCTTCATGCCCGGCTGGCTGACTGTT GCCTGGGTGGAGGGTGAGACAAAGTATGTCTCCGATGCCACTGTGGCCATCTTTGTGG CCACCTGCTATTCTATTGTGCTTACAGAAAGCCCAAGTTTAACTTCCGCAGCCAGAC TGAGGAAGTAAAGTCTCTGTTCTGATCGCCCCCTCCCTGCTGGATGGGAAGGTA ACCCAGGAGAAAGTGCCCTGGGGCATCGTGTCTACTAGGGGGCGGATTGCTCTGG CTAAAGGATCCGAGGCCTCGGGGCTGTCCGTGTGGATGGGGAAGCAGATGGAGCCCTT GCACGAGTGCCTCCGGCAGCCATCACCTTGATCTGTCTGCTGCTGCTGCTGCTGCTT ACTGAGTGACAAGCAACGTGGCCACCACCTGTTCTGCCCCATCTTTGCTCTCA TGTCTCGCTCCATCGGCCTCAATCCGCTGTACATCATGTGCCCTGTACCCTGAGTGC CTCCTTTGCCTTCATGTTGCCTGTGGCCACCCCTCCAAATGCCATCGTGTACCAT GGGCACTCAAGTGTGCTGACATGGTGAAAAACAGGAGTCATAAAGAAATTTGGAG TCTTCTGTGTGTTTTTGGCTGTCAACACCTGGGGACGGGCCATATTTGACTTGGATCA TTTCCTGACTGGGCTAATGTGACACATATTGAGACTTAGGAAGGCCACAAGACCAC ACACACAGCCCTTACCCTCCTCAGGACTACCGAACCTTCTGGCACACCTT</p>	
	ORF Start: ATG at 16	ORF Stop: TAG at 1720
	SEQ ID NO: 44	568 aa MW at 62592.9kD
NOV14a, CG57758-01 Protein Sequence	<p>MASALSYVSKFSFVILFVTPLLLLPLVILMPAKVSCAYVILMAIYWCTEVIPLAVT SLMPVLLFPLFQILDNRQVQVYMKDNTNMLFLGGLIVAVAVERNLHKRIALRTLLWV GAKPARLMLGFMVGTALLSMWISNTATTAMMVPIVEAILQOMEATSAATEAGLELVDK GKAKELPGSQVIFEGPTLGGQEDQERKRLCKAMTLCICYAASIGGTATLTGTGPNVVL LGQMNELFPDSKDLVNFASFAPFNMLVMLLFAWLWLQFVYMFSSFKSWGCGLES KKNEKAALKVLQEEYRKLGPLSFAEINVLICFFLLVILWFSRDPGFMGPWLTVAWVEG ETKYVSDATVAIFVATLLFIVPSQKPKFNFRSQTEEGKSPVLIAPPLLDWKVTQEKV PWGIVLLGGGFALAKGSEASGLSVWMGKQMEPLHAVPPAAITLLSLLVAVFTECTS NVATTTLFLPIFASMSRSIGLNPLYIMLPCTLSASFAMFLPVATPNAIVFTYGHKLKV ADMVKTGVIMNIGVFCVFLAVNTWGRAIFDLDFPDWANTVTHIET</p>	
	SEQ ID NO: 45	1899 bp
NOV14b, CG57758-02 DNA Sequence	<p>CGTCTCGCCCGCCAGTCTCCCTCCCGCGCGATGGCCTCGGCGCTGAGCTATGTCTCCA AGTTCAAGTCCTTCGTGATCTGTTTCGTACCCCGCTCCTGCTGCTGCCACTCGTCAT TCTGATGCCCGCAAGGTCAAGTGTGCTGCTACGTATCATCTCATGGCCATTAC TGGTGACACAGAAGTCATCCCTCTGGCTGTACCTCTCTCATGCTGTCTGCTTTTCC CACTCTTCCAGATTCTGGAATCCAGGCAGGTGTGTGTCCAGTACATGAAGGACACCAA CATGCTGTTCTGGGGCGCCTCATCGTGGCCGTGGCTGTGGAGCGTGGAACTGCAC AAGAGGATCGCCCTGCGCACGCTCCTCTGGGTGGGGGCCAAGCCTGCACGGCTGATGC TGGGCTTCATGGGCGTCACAGCCCTCCTGTCCATGTGGATCAGTAACACGGCAACCA GCCATGATGGTGCCCATCGTGGAGGCCATATGCAGCAGATGGAAGCCACAAGCGCA GCCACCGAGGCGCGCTGGAGGGACAAGGTACCACAATAACAACCTGAATGCACCTGG AGGATGATACAGTGAAAGCAGTACTAGGAGGAAAGTGTGTAGCTATAATAAGCACTTA CGTCAAAAAAGTAGAAAACTTCAATAAACAATCTAATGACACTCTTAAAAAACTA GAAAAGCAAGAGCAACAGGACCTAGGCGCTGGCATCAGGCGCTCAGGACTCTGCCAGT GCCAGGAAGACCAAGAGCGGAAGAGGTTGTGTAAGGCCATGACCTGTGCATCTGCTA CGCGGCCAGCATCGGGGGCACCGCCACCCTGACCGGGACGGGACCAACGTGTGTCTC CTGGGCCAGATGAACGAGTTGTTTCTGACAGCAAGGACCTCGTGAACCTTGTCTCTCT GGTTTGCAATTGCTTTTCCCAACATGCTGGTGATGCTGCTGTTCCGCTGGCTGGGCT CCAGTTTGTGTTACATGTTCTCCAGTTTAAAAAGTCTGGGGCTCGGGCTAGAGAGC AAGAAAAACGAGAAGGCTGCCCTCAAGGTGCTGCAGGAGGAGTACCGGAAGCTGGGGC CCTTGTCTTTCGCGGAGATCAACGTGCTGATCTGCTTCTTCTGCTGGTTCATCTGTG GTTCTCCGAGAGCCCGGCTTCATGCCCGGCTGGCTGACTGTTCTGGGTGGAGGCT GAGACAAAGTCAGTCTCCGATGCCACTGTGGCCATCTTGTGGCCACCTGTCTATTCA TTGTGCTTTCACAGAAGCCCAAGTTTAACTTCCGAGCCAGACTGAGGAAGGTAAGTC TCCTGTTCTGATCGCCCGCCCTCCCTGCTGGATTGGAAGGTAACCGAGGAAGTG CCCTGGGGCATCGTGTGCTACTAGGGGGCGGATTGCTCTGGCTAAAGATCCGAGG</p>	

	CCTCGGGGCTGTCCGTGTGGATGGGGAAGCAGATGGAGCCCTTGACAGCAGTGCCCC GGCAGCCATCACCTTGATCTTGTCTTGCTCGTTGCCGTGTTCACTGAGTGCAACAAGC AACGTGGCCACCACCACCTTGTTCTGCCCCATCTTGCCCTCCATGTCTCGCTCCATCG GCCTCAATCCGCTGTACATCATGCTGCCCTGTACCCTGAGTGCCCTCCTTTGCCCTCAT GTTGCCTGTGGCCACCCCTCCAAATGCCATCGTGTTCACTATGGGCACCTCAAGGTT GCTGACATGGTAAAAACAGGAGTCATAATGAACATAATTGGAGTCTTCTGTGTGTTTT TGGCTGTCAACACCTGGGGACGGGCCATATTTGACTTGGATCATTTCCCTGACTGGGC TAATGTGACACATATTGAGACTTAGGAAGAGCCACAAGACCAC		
	ORF Start: ATG at 31	ORF Stop: TAG at 1879	
	SEQ ID NO: 46	616 aa	MW at 67816.9kD
NOV14b, CG57758-02 Protein Sequence	MASALSYVSKFKSFVILFVTPLLLLPLVILMPAKVSCCAYVILMAIYWCTEVIPLAV TSLMPVLLFPFLFQILDSRQVCVQYMKDTNMLFLGGLIVAVAVERNLHKRIALRTLLW VGAKPARLMLGFMGVTTALLSMWISNTATTAMMVPIVEAILQQMEATSAATEAGLEGQG TTINNLNALEDDTVKAVLGGKCVAIISTYVKKVEKLQINNLMTPKKLEKQEQQDLGP GIRPQDSAQCQEDQERKRLCKAMTLCICYAASIGGTATLTGTGPNVLLGQMNELFPD SKDLVNFASFAPFAPNMLVMLLFAWLWLQFVYMFSSFKKSWGCGLESKKNEKAALKV LQEEYRKLGLPLSFAEINVLCFFLLVILWFSRDPGFMPGWLTVAWVEGETKSVSDATV AIFVATLLFIVPSQKPKFNFRSQTEEGKSPVLIAPPPLLDWKVTQEKVPWGIIVLLGG GFALAKGSEASGLSVMMGKQMEPLHAVPPAAITLILSLLVAVFTECTSNVATTTFLFP IFASMSRSIGLNPLYIMLPCTLSASFAMLPVATPPNAIVFTYGHKLKQVDMVKTVGIM NIIGVFCVFLAVNTWGRAIFDLDFPDWANVTHIET		
	SEQ ID NO: 47	1899 bp	
NOV14c, CG57758-03 DNA Sequence	CGTCTCGCCCGCCAGTCTCCCTCCCGCGGATGGCCTCGGCGCTGAGCTATGTCTCCA AGTTCAAGTCTCTCGTGATCTTGTTCGTACCCCGCTCCTGCTGCTGCCACTCGTCAT TCTGATGCCCGCCAAAGTCAAGTTGCTGTGCCTACGTCAATCATCTCATGGCCATTAC TGGTGACAGAAAGTCATCCCTCTGGCTGTCACTCTCTCATGCCTGTCTTGCTTTTCC CACTCTTCCAGATTCTGGACTCCAGGCAGGTGTGTGTCCAGTACATGAAGGACACCAA CATGCTGTTCTCTGGCGGCCCTCATCGTGGCCGTGGCTGTGGAGCGCTGGAACCTGCAC AAGAGGATCGCCCTGCGCACGCTCCTCTGGGTGGGGGCCAAGCCTGCACGGCTGATGC TGGGCTTCATGGGCGTCAAGCCCTCCTGTCCATGTGGATCAGTAACACGGCAACCAC GGCCATGATGGTGCCCATCGTGGAGGCCATATTGCAGCAGATGGAAGCCACAAGCGCA GCCACCGAGGCCGCGCTGGAGGGACAAGGTACCAACAATAACAACCTGAATGCACCTGG AGGATGATACAGTGAAGCAGTACTAGGAGGAAAGTGTGTAGCTATAATAAGCACTTA CGTCAAAAAGTAGAAAAAATTCAAATAAACAACTCTAATGACACCTCTTAAAAAATA GAAAAGCAAGAGCAACAGGACCTAGGGCTGGCATCAGGCCTCAGGACTCTGCCAGT GCCAGGAAGACCAAGAGCGGAAGAGGTTGTGTGAAGGCCATGACCTGTGTCATCTGCTA CGCGGCCAGCATCGGGGGCACCGCCACCTGACCGGGACGGGACCAACGTGGTGCTC CTGGGCCAGATGAACGAGTTGTTTCTGACAGCAAGGACCTCGTGAACCTTGTCTTCT GGTTTGCAATTGCTTTCCCAACATGCTGGTGATGCTGCTGTTGCTGCTGCTGTGGCT CCAGTTTGTGTTACATGTTCTCCAGTTTAAAAAGTCCCTGGGGCTGCGGGCTAGAGAGC AAGAAAAACGAGAAGGCTGCCCTCAAGGTGCTGCAGGAGGAGTACCGGAAGCTGGGGC CCTTGCTCTTCGCGGAGATCAACGTGCTGATCTGCTTCTTCTGCTGGTTCATCTGTG GTTCTCCCGAGACCCCGGCTTCATGCCCGGCTGGCTGACTGTTGCTGGGTGGAGGGT GAGACAAAGTCAGTCTCCGATGCCACTGTGGCCATCTTTGTGGCCACCCCTGCTATTCA TTGTGCTTTCACAGAAAGCCCAAGTTTAACTTCCGACGCCAGACTGAGGAAGGTAAAGT TCCTGTTCTGATCGCCCCCTCCCTGCTGGATTGGAAGGTAAACCAGGAGAAAGTG CCCTGGGGCATCGTGTGCTACTAGGGGGCGGATTGCTCTGGCTAAAGGATCCGAGG CCTCGGGCTGTCCGTGTGGATGGGGAAGCAGATGGAGCCCTTGACGCAGTGCCCCC GGCAGCCATCACCTTGATCTTGTCTTGTCTCGTTGCCGTGTTCACTGAGTGACAAAGC AACGTGGCCACCACCCTTGTTCCTGCCCATCTTTGCTCCATGTCTCGCTCCATCG GCCTCAATCCGCTGTACATCATGCTGCCCTGTACCCTGAGTGCCCTCCTTTGCCCTCAT GTTGCTGTGGCCACCCCTCCAAATGCCATCGTGTTACCTATGGGCACCTCAAGGTT GCTGACATGGTAAAAACAGGAGTCATAATGAACATAATTGGAGTCTTCTGTGTGTTTT TGGCTGTCAACACCTGGGGACGGGCCATATTTGACTTGGATCATTTCCCTGACTGGGC TAATGTGACACATATTGAGACTTAGGAAGAGCCACAAGACCAC		
	ORF Start: ATG at 31	ORF Stop: TAG at 1879	
	SEQ ID NO: 48	616 aa	MW at 67816.9kD
NOV14c, CG57758-03 Protein Sequence	MASALSYVSKFKSFVILFVTPLLLLPLVILMPAKVSCCAYVILMAIYWCTEVIPLAV TSLMPVLLFPFLFQILDSRQVCVQYMKDTNMLFLGGLIVAVAVERNLHKRIALRTLLW VGAKPARLMLGFMGVTTALLSMWISNTATTAMMVPIVEAILQQMEATSAATEAGLEGQG TTINNLNALEDDTVKAVLGGKCVAIISTYVKKVEKLQINNLMTPKKLEKQEQQDLGP GIRPQDSAQCQEDQERKRLCKAMTLCICYAASIGGTATLTGTGPNVLLGQMNELFPD SKDLVNFASFAPFAPNMLVMLLFAWLWLQFVYMFSSFKKSWGCGLESKKNEKAALKV LQEEYRKLGLPLSFAEINVLCFFLLVILWFSRDPGFMPGWLTVAWVEGETKSVSDATV AIFVATLLFIVPSQKPKFNFRSQTEEGKSPVLIAPPPLLDWKVTQEKVPWGIIVLLGG GFALAKGSEASGLSVMMGKQMEPLHAVPPAAITLILSLLVAVFTECTSNVATTTFLFP IFASMSRSIGLNPLYIMLPCTLSASFAMLPVATPPNAIVFTYGHKLKQVDMVKTVGIM NIIGVFCVFLAVNTWGRAIFDLDFPDWANVTHIET		
	SEQ ID NO: 49	1606 bp	

NOV14d, CG57758-04 DNA Sequence	<p>GATGGCCTCGGCGCTGAGCTATGTCTCCAAGTTCAAGTCCTTCGTGATCTTGTTCGTC ACCCCGCTCCTGCTGCTGCCACTCGTCATTCTGATGCCCGCCAAGTTTGTCAAGTGTG CCTACGTCATCATCTCATGGCCATTTACTGGTGACAGAAATCATCCCTCTGGCTGT CACCTCTCTCATGCTGTCTTGTCTTTCCCACTCTTCCAGATTCTGGACTCCAGGCAG GTGTGTGTCCAGTACATGAAGGACACCAACATGCTGTTCTGGGCGGCCTCATCGTGG CCGTGGCTGTGGAGCGCTGGAACCTGCACAAGAGGATCGCCCTGCGCAGCTCCTCTG GGTGGGGGCCAAGCCTGCACGGCTGATGCTGGGCTTCATGGGCGTCACAGCCCTCCTG TCCATGTGGATCAGTAACACGGCAACACGGCCATGATGGTGCCCATCGTGGAGGCCA TATTGCAGCAGATGGAAGCCACAAGCGCAGCCACCGAGGCCGCTGGAGCTGGTGA CAAGGGCAAGGCCAAGGAGCTGCCAGGAGTCAAGTGATTTTGAAGGCCCCACTCTG GGGCAGCAGGAAGACCAAGAGCGGAAGAGGTTGTGTAAGGCCATGACCTGTGCATCT GCTACGCGGCCAGCATCGGGGGCACCGCCACCTGACCGGACGGGACCCAAACGTGGT GCTCTGGGCGCAGATGAACGAGTTGTTTCTTGACAGCAAGGACCTCGTGAACCTTTGCT TCCTGGTTTGCATTGCTTTCCCAACATGCTGGTGATGCTGCTGCTGCTGCTGCTGCT GGCTCCAGTTTGTGTTACATGAGATTCAATTTTAAAAAGTCTGGGGCTGCGGGCTAGA GAGCAAGAAAAACGAGAAGGCTGCCCTCAAGGTGCTGAGGAGGAGTACCGGAAGTTG GGGCCCTTGTCTTCCGAGAGATCAACGTGCTGATCTGCTTCTTCTGCTGGTCACTCC TGTGGTTCTCCCGAGACCCCGGCTTCATGCCCGGCTGGCTGACTGTTGCTGGGTGGA GGGTGAGACAAAGTATGTCTCCGATGCCACTGTGGCCATCTTGTGGCCACCTGCTA TTCATTGTGCTTTCACAGAAGCCCAAGTTTAACTTCCGACGCCAGATGAGGAAGAAA GGAAAACTCCATTTTATCCCCCTCCCTGCTGGATTGGAAGGTAACCCAGGAGAAAT GCCCTGGGGCATCGTGTGCTACTAGGGGGCGGATTGCTCTGGCTAAAGGATCCGAG GCCTCGGGGCTGTCCGTGTGGATGGGGAAGCAGATGGAGCCCTTGACCGCAGTGCCTC CGGCAGCCATCACCTTGATCTTGTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT CAACGTGGCCACCCACCTTGTCTCTGCCATCTTGGCTCCATGCTGCTGCTGCTGCTGCT GTCATAATGAACATAATTGGAGTCTTCTGTGTGTTTTTGGCTGTCAACACCTGGGAC GGGCCATATTTGACTTGGATCATTTCCCTGACTGGGCTAATGTGACACATATTGAGAC TTAGGAAGGCCACAAGACCACACATAGCCCTTACCCT</p>
	<div>ORF Start: ATG at 2</div> <div>ORF Stop: TAG at 1568</div>
	<div>SEQ ID NO: 50</div> <div>522 aa</div> <div>MW at 58109.6kD</div>
NOV14d, CG57758-04 Protein Sequence	<p>MASALSYVSKFKSFVILFVTPLLLLPLVILMPAKFVRCAAYVILMAIYWCTEVIPLAV TSLMPVLLFLPLFQILDSRQVCVQYMKDNTNMLFLGGLIVAVAVERNLHKRIALRLLW VGAKEPARLMLGFMGVTAALLSMWISNTATTAMMVPIVEAILQMEATSAAEAGLELVD KGKAKELPGSQVIFEGPTLGQEDQERKRLCKAMTLCICYAASIGGTATLTGTGPNV LLGQMNELFPDSKDLVNFASFVAFAPNMLVMLLFAWLWLQFVYMRFNFKKSWGGLE SKKNEKAALKVLQEEYRKLGLPLSFAEINVLCFFLLVILWFSRDPGFMGPWLTVAVWE GETKYVSDATVAIFVATLLFIVPSQKPKFNFRSQTEERKTFPFYPLLDWKVTKQEV PWGIVLLGGGFALAKGSEASLSVWVGKQMEPLHAVPPAAITLILSLLVAVFTECTS NVATTTFLFPIFASVMKTVIMNIIGVFCVFLAVNTWGRAIFDLDFPDWAVNTHIET</p>
	<div>SEQ ID NO: 51</div> <div>1781 bp</div>
NOV14e, CG57758-05 DNA Sequence	<p>GATGGCCTCGGCGCTGAGCTATGTCTCCAAGTTCAAGTCCTTCGTGATCTTGTTCGTC ACCCCGCTCCTGCTGCTGCCACTCGTCATTCTGATGCCCGCCAAGTTTGTCAAGTGTG CCTACGTCATCATCTCATGGCCATTTACTGGTGACAGAAATCATCCCTCTGGCTGT CACCTCTCTCATGCTGTCTTGTCTTTCCCACTCTTCCAGATTCTGGACTCCAGGCAG GTGTGTGTCCAGTACATGAAGGACACCAACATGCTGTTCTGGGCGGCCTCATCGTGG CCGTGGCTGTGGAGCGCTGGAACCTGCACAAGAGGATCGCCCTGCGCAGCCTCCTCTG GGTGGGGGCCAAGCCTGCACGGCTGATGCTGGGCTTCATGGGCGTCACAGCCCTCCTG TCCATGTGGATCAGTAACACGGCAACACGGCCATGATGGTGCCCATCGTGGAGGCCA TATTGCAGCAGATGGAAGCCACAAGCGCAGCCACCGAGGCCGCTGGAGCTGGTGA CAAGGGCAAGGCCAAGGAGCTGCCAGGAGTCAAGTGATTTTGAAGGCCCCACTCTG GGGCAGCAGGAAGACCAAGAGCGGAAGAGGTTGTGTAAGGCCATGACCTGTGCATCT GCTACGCGGCCAGCATCGGGGGCACCGCCACCTGACCGGACGGGACCCAAACGTGGT GCTCTGGGCGCAGATGAACGAGTTGTTTCTTGACAGCAAGGACCTCGTGAACCTTGTCT TCCTGGTTTGCATTGCTTTCCCAACATGCTGGTGATGCTGCTGCTGCTGCTGCTGCTG GGCTCCAGTTTGTGTTACATGAGATTCAATTTTAAAAAGTCTGGGGCTGCGGGCTAGA GAGCAAGAAAAACGAGAAGGCTGCCCTCAAGGTGCTGACGAGGAGTACCGGAAGTTG GGGCCCTTGTCTTCCGAGAGCTCCGCTTCATGCCCGGCTGGCTGATGCTGCTGGTGA GGGTGAGACAAAGTATGTCTCCGATGCCACTGTGGCCATCTTGTGGCCACCTGCTA TTCATTGTGCTTTCACAGAAGCCCAAGTTTAACTTCCGACGCCAGATGAGGAAGAAA GGAAAACTCCATTTTATCCCCCTCCCTGCTGGATTGGAAGGTAACCCAGGAGAAAT GCCCTGGGGCATCGTGTGCTACTAGGGGGCGGATTGCTCTGGCTAAAGGATCCGAG GCCTCGGGGCTGTCCGTGTGGATGGGGAAGCAGATGGAGCCCTTGACCGCAGTGCCTC CGGCAGCCATCACCTTGATCTTGTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT CAACGTGGCCACCCACCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT AAGAGCTTCTGTGTTCTGTACGGTGATGTTGCAGTGTGCTGCTTTCGCGAGTCTGCTC CATCGGCTCAATCCGTGTACATCATGCTGCCCTGTACCTGAGTGCCTCTTGTGCT TTCATGTTGCTGTGGCCACCCCTCCAAATGCCATCGTGTTCACCTATGGGCACTCA AGGTGCTGACATGGTGAAACAGGAGTCAATAAGAACATAATTGGAGTCTTCTGTGT GTTTTTGGCTGTCAACCTGGGGACGGCCATATTGACTTGGATCATTTCCCTGAC TGGGCTAATGTGACACATATTGAGACTTAGGAAGAGCCACA</p>
	<div>ORF Start: ATG at 2</div> <div>ORF Stop: TGA at 1550</div>

	SEQ ID NO: 52	516 aa	MW at 57173.5kD
NOV14e, CG57758-05 Protein Sequence	MASALSYVSKPKSFVILFVTPLLLPLVILMPAKFVRCAVYIILMAIYWCTEVIPLAV TSLMPVLLFPLFQILDSRQVCVQYMKDTNMLFLGGGLIVAVAVERNLHKRIALRTLW VGAKPARMLMGFMGVTALLSMWISNTATTAMMVPIVEAILQQMEATSAATEAGLELVD KGKAKELPGSQVIFEGPTLGQEDQERKRLCKAMTLCICYAASIGGTATLTGTGPNVV LLGQMNELFPDSKDLVNFASWFAPFPNMLVMLLFAWLWLQFVYMRFNFKKSWGCGLE SKKNEKAALKVLQEEYRKLGPLSFAEINVLCFFLLVILWFSRDPGFMPGWLTVAWVE GETKYVSDATVAIFVATLLFIVPSQKPKFNFRSQTEERKTPFYPPPLLDWKVTQEKV PWGIVLLGGGFALAKGSEASGLSVWMGKQMEPLHAVPPAAITLILSLLVAVFTECTS NVATTTFLPIFASMNHVPKSFVCVLYGDVAVLSFRSLAPSASIRCTSCCPVP		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 14B.

Table 14B. Comparison of NOV14a against NOV14b through NOV14e.		
Protein Sequence	NOV14a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV14b	1..568	519/616 (84%)
	1..616	524/616 (84%)
NOV14c	1..568	519/616 (84%)
	1..616	524/616 (84%)
NOV14d	1..568	483/570 (84%)
	1..522	485/570 (84%)
NOV14e	1..480	440/482 (91%)
	1..480	443/482 (91%)

Further analysis of the NOV14a protein yielded the following properties shown in Table 14C.

Table 14C. Protein Sequence Properties NOV14a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 38 and 39

A search of the NOV14a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 14D.

Table 14D. Geneseq Results for NOV14a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV14a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB23625	Human secreted protein SEQ ID NO: 50 - Homo sapiens, 627 aa. [WO200049134-A1, 24-AUG-2000]	10..566 9..623	256/623 (41%) 386/623 (61%)	e-137
AAB36158	Novel human transporter protein SEQ ID NO: 2 - Homo sapiens, 627 aa. [WO200065055-A2, 02-NOV-2000]	10..566 9..623	256/623 (41%) 386/623 (61%)	e-137
AAB42213	Human ORFX ORF1977 polypeptide sequence SEQ ID NO:3954 - Homo sapiens, 627 aa. [WO200058473-A2, 05-OCT-2000]	10..566 9..623	256/623 (41%) 386/623 (61%)	e-136
AAB36164	Novel human transporter protein SEQ ID NO: 14 - Homo sapiens, 626 aa. [WO200065055-A2, 02-NOV-2000]	10..566 9..622	252/623 (40%) 382/623 (60%)	e-136
AAB36159	Novel human transporter protein SEQ ID NO: 4 - Homo sapiens, 627 aa. [WO200065055-A2, 02-NOV-2000]	10..566 9..623	256/623 (41%) 385/623 (61%)	e-136

In a BLAST search of public sequence databases, the NOV14a protein was found to have homology to the proteins shown in the BLASTP data in Table 14E.

Table 14E. Public BLASTP Results for NOV14a				
Protein Accession Number	Protein/Organism/Length	NOV14a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O57661	INTESTINAL SODIUM/LITHIUM-DEPENDENT DICARBOXYLATE TRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) - <i>Xenopus laevis</i> (African clawed frog), 622 aa.	1..564 1..619	336/619 (54%) 444/619 (71%)	0.0
Q9ES88	NA/DICARBOXYLATE COTRANSPORTER (SOLUTE CARRIER FAMILY 13 (SODIUM-DEPENDENT DICARBOXYLATE TRANSPORTER), MEMBER 2) - <i>Mus musculus</i> (Mouse), 586 aa.	1..561 1..567	311/572 (54%) 421/572 (73%)	e-179
O35055				e-179

	COTRANSPORTER 1 (NA(+)/DICARBOXYLATE COTRANSPORTER 1) (KIDNEY DICARBOXYLATE TRANSPORTER) (SDCT1) (ORGANIC ANION TRANSPORTER 1) (OAT1) - Rattus norvegicus (Rat), 587 aa.	1..568	419/572 (72%)	
Q13183	Renal sodium/dicarboxylate cotransporter (Na(+)/dicarboxylate cotransporter) - Homo sapiens (Human), 592 aa.	1..561 1..572	318/581 (54%) 428/581 (72%)	e-179
Q28615	Renal sodium/dicarboxylate cotransporter (Na(+)/dicarboxylate cotransporter) - Oryctolagus cuniculus (Rabbit), 593 aa.	1..562 1..576	300/586 (51%) 418/586 (71%)	e-172

PFam analysis predicts that the NOV14a protein contains the domains shown in the Table 14F.

Table 14F. Domain Analysis of NOV14a			
Pfam Domain	NOV14a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Na_sulph_symp: domain 1 of 1	6..554	163/604 (27%) 424/604 (70%)	8.3e-140

Example 15.

The NOV15 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 15A.

Table 15A. NOV15 Sequence Analysis		
	SEQ ID NO: 53	1547 bp
NOV15a, CG57732-01 DNA Sequence	AACCCCTTGACTGAAGCAATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGG GCAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTGACTCACTTGGAGGAGGCAGATG GTGGCCAGAGCCTACTAGAAACGGTGTGGACCCCCACCACGGGCCAGAGCTGCCTC TGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCCTAGCCTCTCAGCCAGG AAGCTTTCCCTACAGGAGCGGCCAGCAGGAAGCTATCTGGAGGCGCAGGCTGGGCCTT ATGCCACGGGGCTGCCAGCCACATCTCCCCCGGGCCTGGCGGAGGCCACCATCGA GTCCACCCACGTGGCCATCTCAGATGCAGAGGACTGCGTGCAAGCTGAACAGTACAAG CTGCAGAGTGAGATTGGCAAGGGTGCTACGGTGTGGTGAGGCTGGCCTACAACGAAA GTGAAGACAGACACTATGCAATGAAGTCCCTTCCAAAAGAAGTTACTGAAGCAGTA TGGCTTTCCACGTCGCCTCCCCGAGAGGGTCCAGGCTGCCAGGGAGGACCAGCC AAGCAGCTGTGCCCCCTGGAGCGGGTGTAACAGGAGATTGCCATCCTGAAGAAGCTGG ACCACGTGAATGTGGTCAAAGTATCGAGGTAAGTGGATGACCCAGCTGAGGACAACCT CTATTTGCCCGCATCTTCTCCATAGGCCCGTATGGAAGTGCCCTGTACAAGCCC TTCTCGGAGGAGCAAGCTCGCCTCTACCTGCGGGACGTATCTGGGCCTCGAGTACG TGCATGCGCAGAAAGATCGTCCACAGGACATCAAGCCATCAACCTGCTCCTGGGGGA TGATGGGCACGTGAAGATCGCCGACTTTGGCGTCAGCAACAGTTTGAGGGGAACGAC GCTCAGCTGTCCAGCACGGCGGGAACCCAGCATTCATGGCCCCGAGGCCATTTCG ATTCGGGCCAGAGCTTCAGTGGGAAGTTGGATGTATGGCCACTGGCGTCAGGTTGTA CTGCTTTGTCTATGGGAAGTGCCATTTCATCGACATTTCATCCTGGCCCTCCACAGG	

	AAGATCAAGAATGAGCCCGTGGTGTTCCTGAGGAGCCAGAAATCAGCGAGGAGCTCA AGGACCTGATCCTGAAGATGTTAGACAAGAATCCCGAGACGAGAATGGGGTGCCAGA CATCAAGTTGCACCCCTTGGGTGACCAAGAACGGGGAGGAGCCCTTCCTTCGGAGGAG GAGCACTGCAGCGTGGTGGAGGTGACAGAGGAGGAGGTTAAGAACTCAGTCAGGCTCA TCCCCAGCTGGACACCGTGATCCTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGG GAACCCGTTTGAGCCCCAAGCACGGAGGGAAGAGCGATCCATGTCTGCTCCAGGAAAC CTACTGGTGAAAGAAGGGTTTGGTGAAGGGGGCAAGAGCCACAGCTCCCCGGCGTCC AGGAAGACGAGGCTGCATCCTGAGCCCTGCATGCACCC		
	ORF Start: ATG at 20		ORF Stop: TGA at 1529
	SEQ ID NO: 54	503 aa	MW at 55606.7kD
NOV15a, CG57732-01 Protein Sequence	MEGGPAVCCQDPRAELVERVAAIDVTHLEADGGPEPTRNGVDPPIRARAASVPIGST SRLLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPAWRRTIESHHVAI SDAEDCVQLNQYKLQSEIGKAYGVVRLAYNESEDRHYAMKVLSSKKLLKQYGFPRRP PPRGSAQAQGGPAKQLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLPRIL LHRPVMVEVPCDKPFSSEQARLYLRDVI LGLEYVHCQKIVHRDIKPSNLLLGDDGHVKI ADFGVSNQFEGNDAQLSSTAGT PAFMAPEAISDSGQSFSGKLDVWATGVTLVYCFVYGK CPFIDDFILALHRKIKNEPVVFPPEPEISEELKDILKMLDKNPETRIGVDPDIKLHPW VTKNGEELPSEEEHCSVVEVTEEEVKNSVRLIPSWTTVILVKSMLRKRSPGNPFEPQ ARREERSMSAPGNLLVKEGFGEGGKSPELPGVQDEAAS		
	SEQ ID NO: 55	1611 bp	
NOV15b, CG57732-02 DNA Sequence	GCGCCCAAGTTCCCAACAAGGCTACGCAGAAGAACCCTTGACTGAAGCAATGGAGG GGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGCAGAGCTGGTAGAACGGGTGGCAGC CATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCAGAGCCTACTAGAAACGGT GTGGACCCCCACCACGGGCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGAC TGCTCCCAGCCCCGGCCTAGCCTCTCAGCCAGGAAGCTTTCCTACAGGAGCGGCCAGC AGGAAGCTATCTGGAGGCGCAGGCTGGGCCTTATGCCACGGGGCTGCCAGCCACATC TCCCCCGGGCCTGGCGGAGGCCACCATCGAGTCCCACCACGTTGGCCATCTCAGATG CAGAGGACTGCGTGCAGCTGAACCAAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGC CTACGGTGTGGTGAGGCTGGCCTACAACGAAAGTGAAGACAGACACTATGCAATGAAA GTCCCTTTCAAAAAGAAGTTACTGAAGCAGTATGGCTTTCACGTGCCCTCCCCCGA GAGGGTCCCAGGCTGCCAGGGAGGACCAGCCAAGCAGCTGCTGCCCTTGAGCGGGT GTACCAGAGATTGCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACTGATC GAGGTCTCTGGATGATGACCCAGCTGAGGACAACCTCTATTGGTGTGTTGACCTCTGAGAA AGGGGCCCGTCATGGAAGTGCCCTGTGACAAGTCCTTCTCGGAGGAGCAAGCTCGCCT GTACCTGCGGGACGTCATCCTGGGCCTCGAGTACTTGCAGTGCACAGAAGATCGTCCAC AGGGACATCAAGCCATCCAACCTGCTCCTGGGGGATGATGGGCAGCTGAAGATCGCCG ACTTTGGCGTCAGCAACCAAGTTTGAAGGGAACGACGCTCAGCTGTCCAGCACGGCGGG AACCCAGCATTATGGCCCCGAGGCCATTTCTGATTCCGGCCAGAGCTTCAGTGGG AAGCGTGTGGATGTATGGGCCACTGGCGTCACGCTGTACTGCTTTGTCTATGGGAAGT GCCCCCTTCATCGACGATTTTCATCCTGGCCCTCCACAGGAAGATCAAGAATGAGCCGT GGTGTTCCTGAGGGGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATG TTAGACAAGAATCCCGAGACGAGAATTGGGGTGCCAGACATCAAGTTGCACCCCTTGGG TGACCAAGAACGGGGAGGAGCCCTTCTTTCGGAGGAGGAGCACTGCGAGCGTGGTGA GGTGACAGGAGGAGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGCTGGACACGGTG ATCCTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAACCCGTTTGAGCCCCAAG CACGGAGGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAGAAGGGTT TGGTGAAGGGGGCAAGAGCCAGAGCTCCCCGGCGTCCAGGAAGACGAGGCTGCATCC TGAGCCCTGCATGCACCCAGGGCCACCCGGCAGCACACTCATCC		
	ORF Start: ATG at 52		ORF Stop: TGA at 1567
	SEQ ID NO: 56	505 aa	MW at 55652.7kD
NOV15b, CG57732-02 Protein Sequence	MEGGPAVCCQDPRAELVERVAAIDVTHLEADGGPEPTRNGVDPPIRARAASVPIGST SRLLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPAWRRTIESHHVAI SDAEDCVQLNQYKLQSEIGKAYGVVRLAYNESEDRHYAMKVLSSKKLLKQYGFPRRP PPRGSAQAQGGPAKQLPLERVYQEIAILKKLDHVNVVKLIEVLDDPAEDNLYLVFDL LRKGPVMEVPCDKSFSEEQARLYLRDVI LGLEYLHCQKIVHRDIKPSNLLLGDDGHVK IADFGVSNQFEGNDAQLSSTAGT PAFMAPEAISDSGQSFSGKALDVWATGVTLVYCFVY GKCPFIDDFILALHRKIKNEPVVFPPEPEISEELKDILKMLDKNPETRIGVDPDIKLH PWVTKNGEELPSEEEHCSVVEVTEEEVKNSVRLIPSWTTVILVKSMLRKRSPGNPFEP PQARREERSMSAPGNLLVKEGFGEGGKSPELPGVQDEAAS		
	SEQ ID NO: 57	1725 bp	
NOV15c, CG57732-03 DNA Sequence	GCGCCCAAGTTCCCAACAAGGCTACGCAGAAGAACCCTTGACTGAAGTAATGGAGG GGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGCAGAGCTGGTAGAACGGGTGGCAGC CATCGATGTGACTCACTTGGAGGAGGCAGATGGTGGCCAGAGCCTACTAGAAACGGT GTGGACCCCCACCACGGGCAGAGCTGCCTCTGTGATCCCTGGCAGTACTTCAAGAC TGCTCCCAGCCCGGCTAGCCTCTCAGCCAGGAAGCTTTCCTACAGGAGCGGCCAGC AGGAAGCTATCTGGAGGCGCAGGCTGGGCCTTATGCCACGGGGCTGCCAGCCACATC TCCCCCGGGCCTGGCGGAGGCCACCATCGAGTCCCACCACGTTGGCCATCTCAGATG CAGAGGACTGCGTGCAGCTGAACCAAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGC CTACGGTGTGGTGAGGCTGGCCTACAACGAAAGTGAAGACAGACACTATGCAATGAAA		

	GTCCTTTCCAAAAAGAAGTTACTGAAGCAGTATGGCTTTCCACGTCGCCCTCCCCGA GAGGGTCCCAGGCTGCCAGGGAGGACCAGCCAAGCAGCTGCTGCCCTGGAGCGGGT GTACCAGGAGATTGCCATCCTGAAGAAGCTGGACCACGTGAATGTGGTCAAACCTGATC GAGGTCCTGGATGACCCGGCTGAGGACAACTCTATTGGCCCTCAGAACACGAGCCC AGAATATCCAGTTAGATTCAACAAATATCGCCAAGTCCCACTCCCTGCTTCCCTCTGA GCAGCAAGACAGTGGATCCACGTGGGCTGCGCGCTCAGTGTTTGACCTCCTGAGAAAG GGGCGCTCATGGAAGTCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCT ACCTGCGGGACGTATCCTGGGCTCGAGTACTTGCACTGCCAGAAGATCGTCCACAG GGACATCAAGCCATCCAACCTGCTCCTGGGGATGATGGGCACGTGAAGATCGCCGAC TTTGGCGTCAGCAACCACTTTGAGGGGAACGACGCTCAGCTGTCAGCACGGCGGGAA CCCCAGCATTATGCCCCCGAGGCCATTTCTGATTCCGGCCAGAGCTTCAGTGGGAA GGCCTTGGATGTATGGGCCACTGGCGTCAGTGTGTACTGCTTTGTCTATGGGAAGTGC CCGTTTCATCGACGATTTATCCTGGCCCTCCACAGGAAGACCAAGAATGAGCCGTGG TGTTTCTGAGGGGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCTGAAGATGTT AGACAAGAATCCCAGACGAGAATTGGGGTGCCAGACATCAAGTTGCACCCCTTGGGTG ACCAAGAACGGGGAGGAGCCCTTCTTCCGAGGAGGAGCACTGCAGCGTGGTGGAGG TGACAGAGGAGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGCTGGACCAAGCTGAT CCTGGTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGGAACCCGTTTGAGCCCCAAGCA CGGAGGGAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAAGAAGGGTTTG GTGAAGGGGGCAAGAGCCAGAGCTCCCGGCGTCCAGGAAGACGAGGCTGCATCCTG AGCCCTGCATGCACCCAGGGCCACCGGCAGCACATCATCC		
	ORF Start: ATG at 52		ORF Stop: TGA at 1681
	SEQ ID NO: 58	543 aa	MW at 59729.0kD
NOV15c, CG57732-03 Protein Sequence	MEGGFAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPFPPARAASVIPGST SRLLPARPSLSARKLSLQERPAGSYLEAQAGPYATGPASHISPAWRRTTIESHHVAI SDAEDCVQLNQYKLQSEIGKAYGVVRLAYNESEDHYAMKVLKSKLLKQYGFPRRP PPRGSAAGGGPAKQLPLERVYQEIAILKKLDHVNVLKLEVLDDPAEDNLYLALQN QAQNIQLDSTNIAKSHLLPSEQQDSGSTWAARSVFDLLRKGPMVEVPCDKPFSEEA RLYLRLDVLGLLEYLHCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQFEGNDAQLSST AGTPAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALHRKTKNE PVVFPPEGPEISEELKDLILKMLDKNPETRIGVPDIKLHPWVTNKGEPLPSEEEHCSV VEVTEEEVKNSVRLIPSWTTVILVKSMLRKRSFGNPFEPQARREERSMSAPGNLLVKE GFGEGGKSPELPGVQDEEAAS		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 15B.

Table 15B. Comparison of NOV15a against NOV15b through NOV15c.		
Protein Sequence	NOV15a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV15b	1..503	495/505 (98%)
	1..505	497/505 (98%)
NOV15c	1..503	492/543 (90%)
	1..543	495/543 (90%)

Further analysis of the NOV15a protein yielded the following properties shown in Table 15C.

Table 15C. Protein Sequence Properties NOV15a	
PSort analysis:	0.7600 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV15a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 15D.

Table 15D. Geneseq Results for NOV15a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV15a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU03510	Human protein kinase #10 - Homo sapiens, 513 aa. [WO200138503-A2, 31-MAY-2001]	1..503 1..513	496/513 (96%) 498/513 (96%)	0.0
AAE04361	Human kinase (PKIN)-2 - Homo sapiens, 513 aa. [WO200146397-A2, 28-JUN-2001]	1..503 1..513	496/513 (96%) 498/513 (96%)	0.0
AAY44239	Human cell signalling protein-2 - Homo sapiens, 540 aa. [WO9958558-A2, 18-NOV-1999]	64..500 90..538	289/450 (64%) 367/450 (81%)	e-165
AAM40450	Human polypeptide SEQ ID NO 5381 - Homo sapiens, 680 aa. [WO200153312-A1, 26-JUL-2001]	64..482 128..558	283/432 (65%) 356/432 (81%)	e-162
AAM40449	Human polypeptide SEQ ID NO 5380 - Homo sapiens, 680 aa. [WO200153312-A1, 26-JUL-2001]	64..482 128..558	283/432 (65%) 356/432 (81%)	e-162

In a BLAST search of public sequence databases, the NOV15a protein was found to have homology to the proteins shown in the BLASTP data in Table 15E.

Table 15E. Public BLASTP Results for NOV15a				
Protein Accession Number	Protein/Organism/Length	NOV15a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BQH3	HYPOTHETICAL 55.7 KDA PROTEIN - Homo sapiens (Human), 505 aa.	1..503 1..505	497/505 (98%) 499/505 (98%)	0.0
P97756				0.0

	PROTEIN KINASE IV KINASE ISOFORM - Rattus norvegicus (Rat), 505 aa.	1..505	478/505 (94%)	
AAH17529	SIMILAR TO CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE KINASE 1, ALPHA - Mus musculus (Mouse), 505 aa.	1..503 1..505	464/505 (91%) 478/505 (93%)	0.0
Q64572	CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE KINASE (EC 2.7.1.37) - Rattus norvegicus (Rat), 505 aa.	1..503 1..505	463/505 (91%) 476/505 (93%)	0.0
Q9R054	CALCIUM/CALMODULIN DEPENDENT PROTEIN KINASE KINASE ALPHA - Mus musculus (Mouse), 505 aa.	1..503 1..505	454/505 (89%) 471/505 (92%)	0.0

PFam analysis predicts that the NOV15a protein contains the domains shown in the Table 15F.

Table 15F. Domain Analysis of NOV15a			
Pfam Domain	NOV15a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Pkinase: domain 1 of 2	128..228	28/101 (28%) 81/101 (80%)	8.4e-16
Pkinase: domain 2 of 2	245..407	70/201 (35%) 129/201 (64%)	1.7e-52

Example 16.

The NOV16 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 16A.

Table 16A. NOV16 Sequence Analysis		
	SEQ ID NO: 59	688 bp
NOV16a, CG57709-01 DNA Sequence	GACGCGGACCCGCCATGGCGCGGAAGAAGGTGCGTCCGCGGCTGATCGCGGAGCTGGC CCGCGCGTGCGCGCCCTGCGGGAGCAACTGAACAGGCCGCGCGACTCCCAGCTCTAC GCGGTGGACTACGAGACCTTGACGCGGCCGTTCTCTGGACGCGCGCTGCCGCTCCGGG CCTGGGCCGACGTGCGCCGAGAGCCGCTCTTGACGCTGCTCGGCCGCTCCCGCT CTTCGGCTTGGGCCGCTGGTCACGCGCAAGTCCTGGCTGTGGCAGCACGACGAGCCG TGCTACTGGCGCTCACGCGGGTGCGGCCGACTACACGGCGCAGAACTTGACACAG GGAAGGCCTGGGCGATCCTGACCTCAAAGGTAAGGCTCGGGAGAGCGCGGGAGAT CGAACACGTATGTACCATGACTGGCGGCTGGTGCCCAAGCAGGAGGAGGCGCTTC ACCGCGTTCACGCGCGCGGGAAGACAGCCTGGCTCCGTGCGGTACCCGCTCTCC TCCGGGCCATGATTATCGCAGAACGACAGAAAAATGGAGACACAAGCAGGAGGCC CATGCTGAATGTGACAGGATACGATGGAACCTGGGATTACCTGCAAAACAGGAA GACAAAGGAAGGCCAAGGGCACCCCGTCTAGAATGCCAGAACGCGG	

	ORF Start: ATG at 15	ORF Stop: TAG at 669
	SEQ ID NO: 60	218 aa MW at 25647.2kD
NOV16a, CG57709-01 Protein Sequence	MARKKKVRPRLIAELARRVRALREQLNRPDSQLYAVDYETLTRPFSGRRLPVRAWADV RRRESRLQLLGRPLPLFGLGRVTRKSWLWQHDEPCYWRLTRVRPDYTAQNLDHGKAWG ILTFKKGKARESAREIEHVMYHDWRLVPKHEEEAFTFTAPEDSLASVPYPPLLRAMI IAERQKNGDTSTEEPMLNVQRIIRMEPWDYPKQEDKGRAKGTVP	

Further analysis of the NOV16a protein yielded the following properties shown in Table 16B.

Table 16B. Protein Sequence Properties NOV16a	
PSort analysis:	0.9081 probability located in mitochondrial matrix space; 0.6000 probability located in mitochondrial inner membrane; 0.6000 probability located in mitochondrial intermembrane space; 0.6000 probability located in mitochondrial outer membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV16a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 16C.

Table 16C. Geneseq Results for NOV16a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV16a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG81356	Human AFP protein sequence SEQ ID NO:230 - Homo sapiens, 218 aa. [WO200129221-A2, 26-APR-2001]	1..218 1..218	212/218 (97%) 212/218 (97%)	e-125
AAU30525	Novel human secreted protein #1016 - Homo sapiens, 85 aa. [WO200179449-A2, 25-OCT-2001]	135..218 1..84	84/84 (100%) 84/84 (100%)	3e-45
AAU30526	Novel human secreted protein #1017 - Homo sapiens, 62 aa. [WO200179449-A2, 25-OCT-2001]	187..217 12..42	31/31 (100%) 31/31 (100%)	4e-12

In a BLAST search of public sequence databases, the NOV16a protein was found to have homology to the proteins shown in the BLASTP data in Table 16D.

Table 16D. Public BLASTP Results for NOV16a

Protein Accession Number	Protein/Organism/Length	NOV16a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BVI7	HYPOTHETICAL 25.7 KDA PROTEIN - Homo sapiens (Human), 218 aa.	1..218 1..218	214/218 (98%) 214/218 (98%)	e-125
P82930	MITOCHONDRIAL 28S RIBOSOMAL PROTEIN S34 (MRP-S34) – Homo sapiens (Human), 218 aa.	1..218 1..218	213/218 (97%) 213/218 (97%)	e-124
CAC38606	SEQUENCE 229 FROM PATENT WO0129221 - Homo sapiens (Human), 218 aa.	1..218 1..218	212/218 (97%) 212/218 (97%)	e-124
Q9JIK9	TCE2 (0610007F04RIK PROTEIN) - Mus musculus (Mouse), 218 aa.	1..218 1..218	194/218 (88%) 205/218 (93%)	e-114
Q9D957	0610007F04RIK PROTEIN - Mus musculus (Mouse), 218 aa.	1..218 1..218	193/218 (88%) 205/218 (93%)	e-114

PFam analysis predicts that the NOV16a protein contains the domains shown in the Table 16E.

Table 16E. Domain Analysis of NOV16a			
Pfam Domain	NOV16a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 17.

The NOV17 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 17A.

Table 17A. NOV17 Sequence Analysis		
	SEQ ID NO: 61	894 bp
NOV17a, CG57700-01 DNA Sequence	CTCCGTGACCATGAAGGTCAAGGTCATCCCGTGCTCGAGGACAACCTACATGTACCTG GTCATCGAGGAGCTCACGCGCGAGGCGGTGGCCGTGGACGTGGCTGTGCCCAAGAGGC TGCTGGAGATCGTGGGCGGGAGGGGGTGTCTCTGACCGCTGTGCTGACCACCCACCA TCACTGGGACCAACGCGCGGGGAAACCCGGAGCTGGCGCGGCTTCGTCCCGGGCTGGCG GTGCTGGGCGCGGACGAGCGCATCTTCTCGCTGACGCGCAGGCTGGCGCAGGCGAGG AGCTGCAGTTCGGGGCCATCCACGTGCGTTGCCTCCTGACGCCCCGGCCACACCGCCGG CCACATGAGCTACTTCCTGTGGGAGGACGATTGCCCGACCCACCCGCTGTCTCG GGTGGCGACGCGCTGTTCGGTGGCGCGCTGCGGCTCGTGCCCTGGAGGGCAGCGCCAGC AGATGTACAGAGCCTGGCCGAGCTGGGTACCTGCCCCCGAGACGAAGGTGTTCTG CGGCCACGAGCACACGCTTAGCAACCTGGAGTTTGCCAGAAAGTGGAGCCCTGCAAC GACCACGTGAGAGCCAAGCTGTCCTGGGCTCAGAAGAGGGATGAGGATGACGTGCCCA CTGTGCCGTGCACTCTGGGCGAGGAGCGCTCTACAACCCCTTCTGCGGGTGGCGGA GGAGCCGGTGCAGATTACGGGCAAGGCGGTCCCGCCGACGTCTGGAGGCGCTA	

	TGCAAGGAGCGGGCGCGCTTCGAACAGGCGGGCGAGCCGCGGCAGCCACAGGCGCGGG CCCTCCTTGCGCTGCAGTGGGGGCTCCTGAGTGCAGCCCCACAGACTGAGCCACCCA GACCCCTCACAGGGCTGGGGCCTGC		
	ORF Start: ATG at 11	ORF Stop: TGA at 860	
	SEQ ID NO: 62	283 aa	MW at 31262.3kD
NOV17a, CG57700-01 Protein Sequence	MKVKVIPVLEDNYMYLVIEELTREAVAVDVAVPKRLLIEIVGREGVSLTAVLTTHHHWD HARGNPELARLRPGLAVLGADERIFSLTRRLAHGEELQFGAIHVRCLLT PGHTAGHMS YFLWEDDCPDPPALFSGDALS VAGCGSCLEGS AQQMYQSLAELGTLPPETKVF CGHE HTLSNLEFAQKVEPCNDHVRKLSWAQKRDEDDVPTVPSTLGEERLYNPF LRVAEPEV RKFTGKAVPADVLEALCKERARFEQAGEPRQPQARALLALQWGLLSAAPHD		
	SEQ ID NO: 63	888 bp	
NOV17b, CG57700-02 DNA Sequence	CTCCGTGACCATGAAGGTCAAGGTATCCCCGTGCTCGAGGACAACACTACATGTACCTG GTCATCGAGGAGCTCACGCGCGAGGCGGTGGCCGTGGAGCTGGCTGTGCCAAGAGGC TGCTGGAGATCGTGGGCCGGGAGGGGTGTCTCTGACCGCTGTGTGACCAACCCACCA TCACTGGGACCACGCGCGGGGAAACCCGAGCTGGCGCGGCTTCGTCCCGGGCTGGCG GTGCTGGGCGCGGACGAGCGCATCTTCTCGCTGACGCGCAGGCTGGCGCACGGCGAGG AGCTGCAGTTTCGGGGCCATCCACGTGCGTTGCCTCCTGACGCCCGGCCACACCGCCG CCACATGAGCTACTTCTGTGGGAGGACGATTGCCCGGACCCACCCGCCCTGTTCTCG GGCGACGCGCTGTGCGTGGCGGCTGCGGCTCGTGCCTGGAGGGCAGCGCCACAGAGA TGTACCAGAGCTGGCCGAGCTGGGTACCTGCCCGGAGACGAAGGTGTTCTGCGG CCACGAGCACACACTTAGCAACCTGGAGTTTGGCCAGAAAGTGGAGCCCTGCAACGAC CACGTGAGAGCCAAGCTGTCTGGGCTAAGAAGAGGGATGAGGATGACGTGCCCACTG TGCCGTGCACTCTGGGCGAGGAGCGCTCTACAACCCCTTCTGCGGGTGGCAGAGGA GCCGTGCGCAAGTTCACGGGCAAGGCGGTCCCGCGGACGTCCTGGAGGCGCTATGC AAGGAGCGGGCGCGCTTCGAACAGGCGGGCGAGCCGCGGACGCCACAGGCGCGGGCCC TCCTTGCCTGCACTGGGGGCTCCTGAGTGCAGCCCCACAGACTGAGCCACCCAGAC CCTCACAGGGCTGGGCCT		
	ORF Start: ATG at 11	ORF Stop: TGA at 857	
	SEQ ID NO: 64	282 aa	MW at 31205.3kD
NOV17b, CG57700-02 Protein Sequence	MKVKVIPVLEDNYMYLVIEELTREAVAVDVAVPKRLLIEIVGREGVSLTAVLTTHHHWD HARGNPELARLRPGLAVLGADERIFSLTRRLAHGEELQFGAIHVRCLLT PGHTAGHMS YFLWEDDCPDPPALFSGDALS VAGCGSCLEGS AQQMYQSLAELGTLPPETKVF CGHEH TLSNLEFAQKVEPCNDHVRKLSWAKKRDEDDVPTVPSTLGEERLYNPF LRVAEPEV KFTGKAVPADVLEALCKERARFEQAGEPRQPQARALLALQWGLLSAAPHD		
	SEQ ID NO: 65	882 bp	
NOV17c, CG57700-03 DNA Sequence	ACCATGAAGGTCAAGGTATCCCCGTGCTCGAGGACAACACTACATGTACCTGGTCATCG AGGAGCTCACGCGCGAGGCGGTGGCCGTGGAGCTGGCTGTGCCAAGAGGCTGTGGA GATCGTGGGCCGGGAGGGGTGTCTCTGACCGCTGTGTGACCAACCCACCATCACTGG GACCACGCGCGGGGAAACCCGAGCTGGCGCGGCTTCGTCCCGGGCTGGCGGTGCTGG GCGCGGACGAGCGCATCTTCTCGCTGACGCGCAGGCTGGCGCAGCGGAGGAGCTGCG GTTCCGGGGCCATCCACGTGCGTTGCCTCCTGACGCCCGGCCACACCGCGGCCACATG AGCTACTTCTGTGGGAGGACGATTGCCCGGACCCACCCGCCCTGTTCTCGGGCGAGC CGTGTGCGTGGCGGCTGCGGCTCGTGCCTGGAGGGCAGCGCCACGAGATGTACCA GAGCCTGGCGAGCTGGGTACCTGCCCGGAGACGAAGGTGTTCTGCGGCCACGAG CACACGCTTAGCAACCTGGAGTTTGGCCAGAAAGTGGAGCCCTGCAACGACACGATGA GAGCCAAGCTGTCTGGGCTAAGAAGAGGGATGAGGATGACGTGCCCACTGTGCCGTC GACTCTGGGCGAGGAGCGCTCTACAACCCCTTCTGCGGGTGGCAGAGGAGCGGTG CGCAAGTTCACGGGCAAGGCGGTCCCGCGGACGTCCTGGAGGCGCTATGCAAGGAGC GGGCGCGCTCCGAACAGGCGGGCGAGCCGCGGACGCCACAGGCGCGGGCCCTCCTTGC GCTGCAGTGGGGGCTCCTGAGTGCAGCCCCACAGACTGAGCCACCCAGACCCCTCACA GGGCTGGGGCCT		
	ORF Start: ATG at 4	ORF Stop: TGA at 850	
	SEQ ID NO: 66	282 aa	MW at 31173.2kD
NOV17c, CG57700-03 Protein Sequence	MKVKVIPVLEDNYMYLVIEELTREAVAVDVAVPKRLLIEIVGREGVSLTAVLTTHHHWD HARGNPELARLRPGLAVLGADERIFSLTRRLAHGEELRFGAIHVRCLLT PGHTAGHMS YFLWEDDCPDPPALFSGDALS VAGCGSCLEGS AQQMYQSLAELGTLPPETKVF CGHEH TSLNLEFAQKVEPCNDHVRKLSWAKKRDEDDVPTVPSTLGEERLYNPF LRVAEPEV KFTGKAVPADVLEALCKERARSEQAGEPRQPQARALLALQWGLLSAAPHD		
	SEQ ID NO: 67	855 bp	
NOV17d, CG57700-04 DNA Sequence	ACCATGAAGGTCAAGGTATCCCCGTGCTCGAGGACAACACTACATGTACCTGGTCATCG AGGAGCTCACGCGCGAGGCGGTGGCCGTGGAGCTGGCTGTGCCAAGAGGCTGTGGA GATCGTGGGCCGGGAGGGGTGTCTCTGACCGCTGTGTGACCAACCCACTATCACTGG GACCACGCGCGGGGAAACCCGAGCTGGCGCGGCTTCGTCCCGGGCTGGCGGTGCTGG GCGGAGCAGCGCATCTTCTCGCTGACGCGCAGGCTGGCGCACGGCGAGGAGCTGCG GTTCCGGGGCCATCCACGTGCGTTGCCTCCTGACGCCCGGCCACACCGCGGCCACATG AGCTACTTCTGTGGGAGGACGATTGCCCGGACCCACCCGCCCTGTTCTCGGGCGAGC CGTGTGCGTGGCGGCTGCGGCTCGTGCCTGGAGGGCAGCGCCACGAGATGTACCA GAGCCTGGCGAGCTGGGTACCTGCCCGGAGACGAAGGTGTTCTGCGGCCACGAG CACACGCTTAGCAACCTGGAGTTTGGCCAGAAAGTGGAGCCCTGCAACGACACGATGA GAGCCAAGCTGTCTGGGCTAAGAAGAGGGATGAGGATGACGTGCCCACTGTGCCGTC GACTCTGGGCGAGGAGCGCTCTACAACCCCTTCTGCGGGTGGCAGAGGAGCGGTG CGCAAGTTCACGGGCAAGGCGGTCCCGCGGACGTCCTGGAGGCGCTATGCAAGGAGC GGGCGCGCTCCGAACAGGCGGGCGAGCCGCGGACGCCACAGGCGCGGGCCCTCCTTGC GCTGCAGTGGGGGCTCCTGAGTGCAGCCCCACAGACTGAGCCACCCAGACCCCTCACA GGGCTGGGGCCT		

	AGCTACTTCCTGTGGGAGGACGATTGCCCGACCCACCCGCCCTGTTCTCGGGCGACG CGCTGTCGGTGGCCGCTGCGGCTCGTGCTGGAGGGCAGCGCCAGCAGATGTACCA GAGCCTGGCCGAGCTGGGTACCCTGCCCGGAGACGAAGGTGTTCTCGGGCCACGAG CACACGCTTAGCAACCTGGAGTTTGCCAGAAAGTGGAGCCCTGCAACGACCACAAGA GGGATGAGGATGACGTGCCACTGTGCCGTCGACTCTGGGCGAGGAGCGCCTCTACAA CCCTTCTCGGGTGGCAGAGGAGCCGGTGCACAAGTTACGGGCAAGGCGGTCCCC GCCGACGTCTGGAGGCGTATGCAAGGAGCGGGCGCGCTTCAACAGGCGGGCGAGC CGCGGCAGCCACAGCGCGGGCCCTCCTGCGCTGCAGTGGGGGCTCCTGAGTGCAGC CCACACGACTGAGCCACCCAGACCTCACAGGGCTGGGGCCT		
	ORF Start: ATG at 4	ORF Stop: TGA at 823	
	SEQ ID NO: 68	273 aa	MW at 30219.1kD
NOV17d, CG57700-04 Protein Sequence	MKVKVIPVLEDNYMYLVIEELTREAVAVDVAVPKRLLEIVGREGVSLTAVLTTHYHWD HARGNPELARLRPGLAVLGADERIFSLTRRLAHGEELRFGAIHVRCLLTPGHTAGHMS YFLWEDDCPPDPALFSGDALSVAGCGSCLEGSQQMYQSLAELGLTPPETKVFCHGHEH TLSNLEFAQKVEPCNDHKRDEDDVPTVPSTLGEERLYNPFRLVAEEPVRKFTGKAVPA DVLEALCKERARFEQAGEPRQPQARALLALQWGLLSAAPHD		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 17B.

Table 17B. Comparison of NOV17a against NOV17b through NOV17d.		
Protein Sequence	NOV17a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV17b	1..283	281/283 (99%)
	1..282	282/283 (99%)
NOV17c	1..283	279/283 (98%)
	1..282	281/283 (98%)
NOV17d	1..283	271/283 (95%)
	1..273	273/283 (95%)

Further analysis of the NOV17a protein yielded the following properties shown in Table 17C.

Table 17C. Protein Sequence Properties NOV17a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1682 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV17a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 17D.

Table 17D. Geneseq Results for NOV17a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV17a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW80783	Human bisphosphonate binding protein, DP1 (hDP1) - Homo sapiens, 260 aa. [WO9836064-A1, 20-AUG-1998]	1..256 1..256	128/257 (49%) 184/257 (70%)	6e-72
AAG10987	Arabidopsis thaliana protein fragment SEQ ID NO: 9531 - Arabidopsis thaliana, 258 aa. [EP1033405-A2, 06-SEP-2000]	1..245 1..246	107/248 (43%) 160/248 (64%)	5e-53
AAG10986	Arabidopsis thaliana protein fragment SEQ ID NO: 9530 - Arabidopsis thaliana, 268 aa. [EP1033405-A2, 06-SEP-2000]	1..245 11..256	107/248 (43%) 160/248 (64%)	5e-53
AAM78721	Human protein SEQ ID NO 1383 - Homo sapiens, 385 aa. [WO200157190-A2, 09-AUG-2001]	1..226 119..344	100/227 (44%) 135/227 (59%)	6e-45
AAY71110	Human Hydrolase protein-8 (HYDRL-8) - Homo sapiens, 361 aa. [WO200028045-A2, 18-MAY-2000]	1..226 95..320	100/227 (44%) 135/227 (59%)	6e-45

In a BLAST search of public sequence databases, the NOV17a protein was found to have homology to the proteins shown in the BLASTP data in Table 17E.

Table 17E. Public BLASTP Results for NOV17a				
Protein Accession Number	Protein/Organism/Length	NOV17a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BT45	SIMILAR TO RIKEN CDNA 1500017E18 GENE - Homo sapiens (Human), 282 aa.	1..283 1..282	280/283 (98%) 282/283 (98%)	e-163
Q9DB32	1500017E18RIK PROTEIN - Mus musculus (Mouse), 283 aa.	1..278 1..278	231/279 (82%) 251/279 (89%)	e-133
Q96S11	SIMILAR TO HAGH - Homo sapiens (Human), 218 aa.	1..228 1..218	217/228 (95%) 218/228 (95%)	e-123
Q96NR5	CDNA FLJ30279 FIS, CLONE BRACE2002772, MODERATELY SIMILAR TO HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6) - Homo sapiens (Human), 202 aa.	1..133 1..133	132/133 (99%) 133/133 (99%)	3e-73
O35952	Hydroxyacylglutathione hydrolase (EC 3.1.2.6) (Glyoxalase II) (Glx II) (Round spermatid protein RSP29) - Rattus norvegicus (Rat), 260 aa.	1..256 1..256	128/257 (49%) 184/257 (70%)	1e-71

PFam analysis predicts that the NOV17a protein contains the domains shown in the Table 17F.

Table 17F. Domain Analysis of NOV17a			
Pfam Domain	NOV17a Match Region	Identities/ Similarities for the Matched Region	Expect Value
lactamase_B: domain 1 of 1	7..173	55/221 (25%) 129/221 (58%)	5.8e-32

Example 18.

The NOV18 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 18A.

Table 18A. NOV18 Sequence Analysis

	SEQ ID NO: 69	2109 bp
NOV18a, CG58553-01 DNA Sequence	GGGTCCGGCGGGCATCGGCAAGACCATGGCGGCCAAAAATATCTGTACGACTGGGCG GCGGGCAAGCTGTACAGGGCCAGGTGGACTTCGCCTTCTTCATGCCTCGCGCGAGC TGCTGGAGAGGCGCGGCACGCGCAGCTGGCTGACCTGATCTGGACAGTGCCCCGA CCGCGGCGCGCGGTGCGCGCAGATGCTGGCCAGCCGAGCGGCTGCTCTTCATCCTG GACGGCGCGGACGAGCTGCCGGCGCTGGGGGGCCCCGAGGCGCGCCCTGCACAGACC CCTTCGAGGCGCGAGCGGCGCGCGGTGCTAGGCGGGCTGCTGAGTAAGCGCTGCT GCCACGCGCCTCTCTGCTGGTGACACGCGCGCCGCGCCCCCGGAGGCTGCAGGGC CGCTGTGTTCCCGCAGTGCGCGGAGGTGCGCGGCTTCTCCGACAAAGGACAAGAAGA AGTATTTCTACAAGTTCTTCCGGATGAGAGGAGGGCCGAGCGCGCTACCGCTTCGT GAAGGAGAACGAGACGCTGTTCCGCTGTGCTTCGTGCCCTTCGTGTGCTGGATCGTG TGACCGGTGCTGCGCGCAGCAGCTGGAGCTCGGTCCGGACCTGTCGCGCAGCTCCAAGA CCACCACGTGAGTGACCTGCTTTTCATCACCAGCGTTCTGAGCTCCGCTGAGC CGACGGGCCCCGGTTGCAGGGCGACCTGCGCAATCTGTGCGCCTGGCCCGCAGGGG GTCCTCGGACGCGAGGGCGAGTTTGCCGAGAAGGAACTGGAGCAACTGGAGCTTCGTG GCTCCAAAGTGACAGCTGTTTCTCAGCAAAAAGGAGCTGCCGGCGTGTGGAGAG AGAGGTACCTACAGTTCATCGACAGAGCTTCAGGAGTCTTCGCGGCACTGTCC TACCTGCTGGAGGACGGCGGGGTGCCAGGACCGCGCTGGCGGCGTGGGACACTCC TGCGTGGGGACGCCAGCGCACAGCCACTTGGTGCTCACCACGCGCTTCTCTTCGG ACTGCTGAGCGCGGAGCGGATGCGCGACATCGAGCGCACTTCGGCTGCATGGTTTCA GAGCGTGTGAAGCAGGAGGCCCTGCGGTGGGTGCAGGGACAGGGACAGGGCTGCCCG GAGTGGCACCAGAGGTGACCGAGGGGGCCAAAGGGCTCGAGGACACCGAGAGGCAGA GGAGGAGGAGGAGGAGAGGAGGCCAACTACCCACTGGAGTTGCTGACTGCTGTAC GAGACGCGAGGAGGACGCGTTTGTGCGCAAGCCCTGGGCGGTTCCCGAGCTGGCG TGCAGCGAGTGCCTTCTGCCGATGACGCTGGCTGTTCTGAGCTACTGCGTGAAGTG CTGCCCTGCTGCACAGGCACTGCGGCTGATCAGCTGCAGATTGGTTGCTGCGCAGGAG AAGAAGAAGAAGAGCTTGGGAAGCGGCTCCAGGCCAGCCTGGGCGACCAAAAACAC TGCCAGCCTCCCTTCTTCATCCACTCTTTCAGGCAATGACTGACCCACTGTGCCATCT GAGCAGCCTCAGCTGTCCCACTGCAAACTCCCTGACGCGGTCTGCCGAGACCTTCT GAGGCCCTGAGGGCAGCCCCGCACTGACGAGCTGGGCTCTCCCAACAGGCTCA GTGAGGCAGGATGCTGCTGCTGAGTGAGGCGCTAGCCTGGCCGAGCTCAGGCTGCA GACGGTCAGGGTACAGTGCCTGACCCCCAGCGAGGGCTCCAGTACCTGGTGGGTATG CTTCGCGAGAGCCCTGCCCTGACCACTGATCTCAGCGGCTGCCAAGTCCCGGCC CCATGTTGACCTACCTGTGTGAGTCTGTCAGCACCAGGGATGCGGCTGCAGACCT CAGTCTGGCCTCTGTGGAGCTGAGCGAGCAGTCACTACAGGAGCTTCAGGCTGTGAAG AGAGCAAAGCGGATCTGGTCATCACACCCAGCGCTGGACGGCCACCACAACCTC CCAAGGAATCATCTCGACCTTCTGAGGCTCTGGTGGCCAGAGCAGGGTGAAGACCC TAGTCAAAGTCCCTGTGGAGA	
	ORF Start: ATG at 26	ORF Stop: TGA at 2054
	SEQ ID NO: 70	676 aa MW at 74650.3kD
NOV18a, CG58553-01 Protein Sequence	MAAKNIIYDWAAGKLYQGQVDFAFMPCGELLERPGTRSLADLILDQCPDRGAPVPQM LAQPQRLFLFDGADLPALGGPEAAPCTDPFEAASGARVLGGLLSKALLPTALLLV TRAAAPGRLQGRLCSPQCAEVRGFSKDKKKYFYKFFRDERRAERAYRFVKENETLFA LCFVFPVCWIVCTVLRQQLGRDLRSKTTTSVYLLFITSVLSSAPVADGPRLOQD LRNLCRLAREGLGRRRAQFAEKELEQLELRGSKVQTLFLSKKELPGVLETEVTYQFID QSFQESFAALSYLEDDGVPRTAAGGVGTLRQDAQPHSHLVLTTRFLFGLLSAERM DIERHFGCMVSERVQKEALRWVQGGQGGCPGVAPEVTEGAKGLEDTEEPPEEEEGE NYPLELLYCLYETQEDAFVRQALGRFPPELALQVRVFCRMDVAVLSYCVRCPPAAQAL LISRLVAAQEKKKSLGKRLQASLGTQKLPASLLHPLFQAMTDPLCHLSSLTLSHC KLPDAVCRDLSEALRAAPALTELGLLHNRLSEAGLRMLSEGLAWPQCRVQTVRVQLPD PQRGLQYLVGMLRQSPALTTLDLSGQLPAPMVTYLCVAVLQHQCGQLQTLASVELS EQSLQELQAVKRAKPDLVITHPALDGHPPPKELISTF	

Further analysis of the NOV18a protein yielded the following properties shown in Table 18B.

Table 18B. Protein Sequence Properties NOV18a	
Psort analysis:	0.7400 probability located in nucleus; 0.6000 probability located in endoplasmic reticulum (membrane); 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV18a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 18C.

Table 18C. Geneseq Results for NOV18a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV18a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE04546	Human G-protein coupled receptor-2 (GCREC-2) protein - Homo sapiens, 891 aa. [WO200142288-A2, 14-JUN-2001]	1..676 210..891	671/682 (98%) 671/682 (98%)	0.0
AAU00023	Human activated T-lymphocyte associated sequence 2, ATLAS-2 - Homo sapiens, 1851 aa. [WO200114564-A2, 01-MAR-2001]	1..633 210..904	605/695 (87%) 610/695 (87%)	0.0
ABB11735	Human vasopressin receptor homologue, SEQ ID NO:2105 - Homo sapiens, 597 aa. [WO200157188-A2, 09-AUG-2001]	1..490 106..595	485/490 (98%) 485/490 (98%)	0.0
AAR33389	AII/AVPv2 receptor - Synthetic, 481 aa. [WO9305073-A, 18-MAR-1993]	193..670 1..480	322/481 (66%) 371/481 (76%)	e-174
AAM89960	Human immune/haematopoietic antigen SEQ ID NO:17553 - Homo sapiens, 329 aa. [WO200157182-A2, 09-AUG-2001]	1..274 9..282	265/274 (96%) 266/274 (96%)	e-151

In a BLAST search of public sequence databases, the NOV18a protein was found to have homology to the proteins shown in the BLASTP data in Table 18D.

Table 18D. Public BLASTP Results for NOV18a				
Protein Accession Number	Protein/Organism/Length	NOV18a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC34689	SEQUENCE 3 FROM PATENT WO0114564 - Homo sapiens (Human), 1851 aa.	1..633 210..904	605/695 (87%) 610/695 (87%)	0.0
Q91WS2	HYPOTHETICAL 62.5 KDA PROTEIN - Mus musculus (Mouse), 556 aa (fragment).	107..659 1..554	390/557 (70%) 450/557 (80%)	0.0
Q63035	VASOPRESSIN RECEPTOR - Rattus norvegicus (Rat), 483 aa.	193..670 1..482	324/483 (67%) 372/483 (76%)	e-173
AAL12498	CRYOPYRIN - Homo sapiens (Human), 920 aa.	3..657 234..914	232/709 (32%) 355/709 (49%)	5e-94
AAL12497	CRYOPYRIN - Homo sapiens (Human), 1034 aa.	3..648 234..848	223/658 (33%) 344/658 (51%)	6e-93

PFam analysis predicts that the NOV18a protein contains the domains shown in the Table 18E.

Table 18E. Domain Analysis of NOV18a			
Pfam Domain	NOV18a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 19.

The NOV19 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 19A.

Table 19A. NOV19 Sequence Analysis		
	SEQ ID NO: 71	2686 bp
NOV19a, CG58626-01 DNA Sequence	<p>CCGGCGGCGTCTCCACAGCATGAATTACCGGGCGCGGGTCCCCACGGAGCCCCGAG CATAACGGCCGAGGCGGCGGCGGCGGCGCTGGGAGCTGGGCTCAGACGCGAGGCCAG CGTTCGGCGGCGGCGTCTGCTGCTTCGAGCACCTGCCCGGGGACCCGAGCAGCGG CGACGTGCCCTTGGCCCTGCTGCGCGGGGAACCCGGGCTGCATTGGCGCCGGGCACC GACGACCACAACCACCACTCGCGCTGGACCCCTGCCTCAGTGACGAGAACTATGACT TCAGCTCCGCCGAGTCGGGCTCCTCGCTGCGCTACTACAGCGAGGGTGAGAGCGGCGG CGGCGGCAGCTCCTTGTGCTGCACCCGCGCAGCAGCCTCCGCTGGTCCCGACGAAC TCGGGGGGCGGCGCGCAGGAGGGTCCCCGGGGAAGGAAACGTACCCGGCTTG GCGGCCCGGCGGCGGCAACCGCTATGAGGTAGTGACGGAGCTGGGCCCGGAGGAGT ACGCTGGTTCTACAAGGAGGACAAGAAGACCTGGAAGCCCTTCATCGGCTACGACTCG CTCCGCATCGAGCTCGCTTCGGACCCCTGCTGACACACGGGTGCCGGGCCCCAGG GCGGGGACCGGGACGGCGACCATGTGTGCTCCCCACGGGCCAGCCTCCAGTTCCGG AGAAGATGACGATGAGGACCGCGCTGCGGCTTCTGCCAGAGTACGACGGGGCAGGAG CCGGAGATGGTGAGCTGTGAACATCGAGCCTGTGTGCGTGGGGCGGCGCTCTACG</p>	

	AGGTGGATGTGACCCAAGGAGAGTGTACCCGGTGTACTGGAACCGTGCTGATAAAAT ACCAGTAATGCGTGGACAGTGGTTTATTGACGGCACTTGGCAGCCTCTAGAAGAGGAA GAAAGTAATTTAATTGAGCAAGAACATCTCAATTGTTTTAGGGGCCAGCAGATGCAGG AAAATTTTCGATATTGAAGTGTCAAAATCCATAGATGGAAAAGATGCTGTTTCATAGTTT CAAGTTGAGTCGAAACCATGTGGACTGGCACAGTGTGGATGAAGTATATCTTTATAGT GATGCAACAACATCTAAAATTGCAAGAACAGTTACCCAAAACCTGGGATTTCTAAAG CATCAAGTAGTGGTACCAGACTTCATAGAGGTTATGTAGAAGAAGCCACATTAGAAGA CAAGCCATCACAGACTACCCATATTTGATTTGTTGTGCATGGCATTGGGCAGAAAATG GACCAAGGAAGAATTATCAAAAATACAGCTATGATGAGAGAAGCTGCAAGAAAAATAG AAGAAAGGCATTTTCCAACCATGCAACACATGTTGAATTTCTGCCCTGTTGAGTGGCG GTCAAACTTACTCTTGATGGAGACACTGTTGATTCCATTACTCCTGACAAAGTACGA GGTTTAAGGGATATGCTGAACAGCAGTGCATGGACATAATGATTATACCTAGTCCAC TTTATAGAGATGAACCTAGTTAAAGGCCCTCAGCAAGAGCTGAATCGATTGTATTCCCT TTTCTGTTCTCGAATCCAGACTTTGAAGAAAAGGGGTAAGTCTCAATAGTATCA CATTCCCTTGGGATGTGTAATTACTTATGACATAATGACTGGCTGGAAATCCAGTTCGGC TGTATGAACAGTGTCTGCAAAAGGAAGAAGAGTTGCCGTGATGAACGATGGATGAGCTA TGAAGAACGACATCTTCTTGATGAACCTATATAAATAAAGACGCTGAGGAAATA GAAGAACGGCTTCACGGATTGAAAGCATCATCTATGACACAAACACCTGCCTTAAAT TTAAGGTAGAGAAATTTCTCTGTATGGGATCCCATTAGCAGTTTTCTTGGCGTTGCG TGGCATCCGCCCAGGAAATCTGGAAGTCAAGACCATATTTTGCCTAGAGAGATTTGT AACCGGTTACTAAATATTTTTCCTACAGATCCAGTGGCTTATAGATTGAACCAT TAATACTGAACACTACAGCAACATTTACCTGTCCAGATCCACTGGTACAATACTTC AAATCCTTTACCTTATGAACATATGAAGCCAAGCTTTCTCAACCCAGCTAAAGAACCT ACCTCAGTTTCAGAGAATGAAGGCATTTCAACCATACCAAGCCCTGTGACCTCACCAG TTTTGTCCCGCCGACACTATGGAGAATCTATAACAAATATAGGCAAGCAAGCATATT AGGTGCTGCTAGCATTGGAAAGGACTTGGAGGAATGTTGTTCTCAGATTGGAACGT TCATCTACAACACAGTCACTGAAACATCAAAAGACTCAATGGAAGATGAGAAGAAGC CAGTTGCCTCACCTTCTGCTACCACCGTAGGGACACAGACCTTCCACATAGCAGTTT TGGCTTCTCGATTCTGCAGTGGAGTTGGATCACAGGATTGATTTTGAACCTCAGAGAA GGCCTTGTGGAGAGCCGCTATTGGTCAGCTGTACGTCGCATACTGCCTATTGGTCAT CCTTGGATGTTGCCCTTTTCTTTTAACTTCATGTATAAATGAGCAGCATGATGA TGCAAAACCCAATTTAGATCCAACTCTGAACTCTCTTGAAGGACATGAATGGCCTAA CTGATTTTTTTTTTCC
	ORF Start: ATG at 20 ORF Stop: TGA at 2636
	SEQ ID NO: 72 872 aa MW at 97063.4kD
NOV19a, CG58626-01 Protein Sequence	MNYPGRGSPRSPHNHNRGGGGAWELGSDARPAFGGGVCCFEHLPGGDPDDGVLPLAL LRGEPGLHLAPGTDDHNNHLALDPCLSDENYDFSSAESGSSLRYYSEGESGGGSSLS LHPPQPPPLVPTNSGGGATGGSPGERKRTRLGGPAARHRYEVVTELGPPEVRWFYKE DKKTWKPFIFYDSLRIELAFRTLQTTGARPOGGDRDGDHVCSPGFPASSSGEDDDED RACGFCQSTTGHEPEMVELVNIIEPVCVRGGLYEVDVTQGECPVYWNRADKIPVMRGQ WFIDGTWQPLEEEESNLIEQHLNCFRQQMQENFDIEVSKSIDGDAVHSFKLSRNH VDWHSVDEVYLYSDATTSKIARTVTQKLGFASKASSGTRLHRGYVEEATLEDKPSQTT HIVFVHIGIQKMDQGRIIKNTAMMREAARKIEERHFSNHATHVEFLPVEWRSKLTLD GDTVDSITPDKVRGLRDLNLSAMDIMYYTSPLYRDELVKGLQQLNRLYSLFCSRNP DFEEKGGKVSIVSHSLGCVITYDIMGWNPVRLYEQLLQKEELPDERWMSYEERHLL DELYITKRRLKEIEERLHGLKASSMTQTPALKFKVENFFCMGSPYAVFLALRGIRPGN TGSQDHILPREICNRLNIFHPTDPVAYRLEPLILKHYSNISPVQIHWYNTSNLPYE HMKPSFLNPAKEPTSVSENEGISTIPSPVTSPLVSRRHYESITNIGKASILGAASIG KGLGGMFLSRFGRSSTTQSSETSKDSMEDEKKPVASPSATTVGTQTLPHSSSGFLDSA VELDHRIDFELREGLVESRYWSAVTSHTAYWSSLDVALFLFTFMKHEHDDAKPNLD PI

Further analysis of the NOV19a protein yielded the following properties shown in Table 19B.

Table 19B. Protein Sequence Properties NOV19a	
PSort analysis:	0.4555 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV19a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 19C.

Table 19C. Geneseq Results for NOV19a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV19a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG64151	Arabidopsis thaliana gravitropism protein - Arabidopsis thaliana, 933 aa. [JP2001120279-A, 08-MAY-2001]	257..547 156..454	104/316 (32%) 156/316 (48%)	1e-38
AAM41595	Human polypeptide SEQ ID NO 6526 - Homo sapiens, 677 aa. [WO200153312-A1, 26-JUL-2001]	261..548 52..328	94/301 (31%) 138/301 (45%)	6e-25
AAB92643	Human protein sequence SEQ ID NO:10972 - Homo sapiens, 1000 aa. [EP1074617-A2, 07-FEB-2001]	119..608 226..664	132/524 (25%) 204/524 (38%)	2e-24
AAM39809	Human polypeptide SEQ ID NO 2954 - Homo sapiens, 615 aa. [WO200153312-A1, 26-JUL-2001]	274..548 3..266	90/288 (31%) 131/288 (45%)	4e-23
AAB93825	Human protein sequence SEQ ID NO:13636 - Homo sapiens, 694 aa. [EP1074617-A2, 07-FEB-2001]	404..608 227..449	76/229 (33%) 113/229 (49%)	6e-23

In a BLAST search of public sequence databases, the NOV19a protein was found to have homology to the proteins shown in the BLASTP data in Table 19D.

Table 19D. Public BLASTP Results for NOV19a				
Protein Accession Number	Protein/Organism/Length	NOV19a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O46606	PHOSPHATIDIC ACID-PREFERRING PHOSPHOLIPASE A1 - Bos taurus (Bovine), 875 aa.	1..872 1..875	802/876 (91%) 829/876 (94%)	0.0
Q9C0F8	KIAA1705 PROTEIN - Homo sapiens (Human), 498 aa (fragment).	378..872 4..498	493/495 (99%) 494/495 (99%)	0.0
Q96LL2	CDNA FLJ25408 FIS, CLONE TST02965, HIGHLY SIMILAR TO BOS TAURUS PHOSPHATIDIC ACID-PREFERRING PHOSPHOLIPASE A1 MRNA - Homo sapiens (Human), 454 aa.	419..872 1..454	453/454 (99%) 454/454 (99%)	0.0
AAH18552	HYPOTHETICAL 27.3 KDA PROTEIN - Mus musculus (Mouse), 249 aa (fragment).	624..869 1..246	224/246 (91%) 236/246 (95%)	e-130
AAL32232	HYPOTHETICAL 85.1 KDA PROTEIN - Caenorhabditis elegans, 753 aa.	122..867 11..750	255/794 (32%) 374/794 (46%)	6e-91

PFam analysis predicts that the NOV19a protein contains the domains shown in the Table 19E.

Table 19E. Domain Analysis of NOV19a			
Pfam Domain	NOV19a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DUF203: domain 1 of 1	252..458	42/219 (19%) 105/219 (48%)	7.5
DDHD: domain 1 of 1	611..858	96/266 (36%) 236/266 (89%)	3.3e-116

Example 20.

The NOV20 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 20A.

Table 20A. NOV20 Sequence Analysis

	SEQ ID NO: 73	773 bp
NOV20a, CG57597-01 DNA Sequence	GGTAAGGACACAAGATGCCAAATAGGGTAAGGAATGGTCCAGAAACCTGTGAACCTCTG CATTGCAGGCATGCACCACCACTCCTGGCTAATTTTTTGTATTTTGTAGTCCATCGAA TCCGGCTCAAACCTTTTATTTCTCTTATGTAAAAGCTGTGTACTTTCAGAAAAACATGT ACAGTTATCCCTGGCAGTCCCGGGTGGGGTCTGCGCGGCCCTGGAGGCCTGGCCGGC CTTGCAGATCGCTGTGAGAATGGCTTCGGGGGTGTGCACAGCCAGGAGAAGGCCAAG TGGCTGGGGGTGCAGTGGAGGATTACTTCATGCGCAATGCTGACTTGGAGCTAGATG AGGTGGAAGACTTCCTTGGAGAGCTGTTGACCAACGAGTTTGATACAGTTGTGGAAGA CGGGAGTCTGCCCCAGGTGAGCCAGCAACTGCAGACCATGTTCCACCACTTCCAGAGG GGTGATGGGGCTGCTCTGAGGGAGATGGCCTCCTGCATCACTCAGAGAAAATGCAAGG TCACAGCCACTGCACCTTAAGACAGCTAGAGAGACTGATGAGGATGAAGATGATGTGGA CAGTGTGGAAGAGATGGAGGTACAGCTACGAATGATGGGGCTGCTACAGATGGGGTC TGCCCCCAGCCTGAACCTCTGATCCAGACGCTCAGACTATTAAGGAAGAGGATATAG TGGAAGATGCTGGACCATGTCCGGAGAAAAAATGAGTGGGGATGATTGGAATGG CTTTGGGCCCTTATTGCT	
	ORF Start: ATG at 15	ORF Stop: TGA at 732
	SEQ ID NO: 74	239 aa MW at 26579.5kD
NOV20a, CG57597-01 Protein Sequence	MPNRVRNGPETCELCIAGMHHSWLIFCIFSAIESGSNLLFLCKSCVLQKNMYSYPW QCRGGVCAALEAWPALQIAVENGFVHSGEAKWLGGAVEDYFMRNADLELDEVEDF LGELLTNEFDTVVEDGSLPQVSQQLQTMFHHFQRGDGAALREMACTQRKCKVTATA LKTARETDEDEDDVDSVEEMVTATNDGAATDGVCPQPEPSPDPAQTIKEEDIVEDGW TIVRRKK	

Further analysis of the NOV20a protein yielded the following properties shown in Table 20B.

Table 20B. Protein Sequence Properties NOV20a	
PSort analysis:	0.3000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV20a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 20C.

Table 20C. Geneseq Results for NOV20a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV20a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG81374	Human AFP protein sequence SEQ ID NO:266 - Homo sapiens, 191 aa. [WO200129221-A2, 26-APR-2001]	61..239 13..191	178/179 (99%) 178/179 (99%)	e-101
AAG57770	Arabidopsis thaliana protein fragment SEQ ID NO: 74486 - Arabidopsis	63..239 18..178	56/182 (30%) 94/182 (50%)	1e-13

	SEP-2000]			
AAG57771	Arabidopsis thaliana protein fragment SEQ ID NO: 74487 - Arabidopsis thaliana, 156 aa. [EP1033405-A2, 06- SEP-2000]	74..239 1..150	52/171 (30%) 89/171 (51%)	2e-11

In a BLAST search of public sequence databases, the NOV20a protein was found to have homology to the proteins shown in the BLASTP data in Table 20D.

Table 20D. Public BLASTP Results for NOV20a				
Protein Accession Number	Protein/Organism/Length	NOV20a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q969E8	UNKNOWN (PROTEIN FOR MGC:20451) (PROTEIN FOR IMAGE:3953868) - Homo sapiens (Human), 191 aa.	61..239 13..191	178/179 (99%) 178/179 (99%)	e-101
Q9NAD8	Y51H4A.15 PROTEIN - Caenorhabditis elegans, 225 aa.	1..239 1..225	66/239 (27%) 122/239 (50%)	5e-23
Q06672	HIGHLY ACIDIC C-TERMINUS - Saccharomyces cerevisiae (Baker's yeast), 249 aa.	63..238 79..244	46/177 (25%) 82/177 (45%)	5e-11
Q9VBI0	CG14543 PROTEIN - Drosophila melanogaster (Fruit fly), 195 aa.	71..238 24..195	49/174 (28%) 81/174 (46%)	2e-10
Q9UUA9	HYPOTHETICAL HIGHLY ACIDIC C-TERMINUS PROTEIN - Schizosaccharomyces pombe (Fission yeast), 179 aa.	70..239 22..178	42/172 (24%) 83/172 (47%)	2e-06

Pfam analysis predicts that the NOV20a protein contains the domains shown in the Table 20E.

Table 20E. Domain Analysis of NOV20a			
Pfam Domain	NOV20a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 21.

The NOV21 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 21A.

Table 21A. NOV21 Sequence Analysis		
	SEQ ID NO: 75	7741 bp
NOV21a, CG57804-01 DNA Sequence	<p>TTGTCCTCTTTGTGTTTTCCAGACATTCTAAGTGAGACTGTCCACATCATCTAGGAAAA TGGTGGCCCTGTCTTAAAGATTGTGTGCCCACTGCAACGTGGTGAAGACCATGCA GTTTGAACCATCTACAGCTGTGTACGATGCGTGTGAGTCACTCGGGAACGGGTGCCT GAGGCACAACTGGGCAAGCTTCTGACTATGGACTCTTCTTTCCGGATGAAGACCCGA GGAAAGGGATTGGCTGGAAGCGGGCAGAACACTGGATTACTACATGTTGCGGAATGG GGATATTTTGAATATAAAAAGAAACAGAGACCTCAGAAAATCCGGATGCTGGATGGA TCTGTGAAGACAGTGTGGTGGATGATCCAGACTGTGGGGGAGCTCCTGGTCACTA TTTGTAGCAGAATAGGAATAACAAATTATGAAGAATACTCCTTAATCCAAGAACTAT TGAAGAAAAGAAAGAGGAAGGAACGGGCACACTCAAAAAGACAGGACACTGTTACGA GATGAGAGGAAAATGGAGAAGTTGAAGGCCAAGCTGCACACAGATGATGACCTAAATT GGCTGGATCACAGCCGAACATTAGAGAACAGGAGTAGATGAAAACGAAACGTTGCT GCTTAGACGGAAGTTCTTTTACTCTGATCAGAATGTAGATTCGAGAGACCCCGTGCAG CTGAACTTGCTTTATGTTTCAAGGCACGGGATGACATCCTGAATGGCTCTCACCTGTCT CCTTCGAGAAAGCTTGTGAGTTTGGTGGATTTCAAGCCCAGATACAAATTGGACCTCA TGTGGAACATAAACACAACTGGATTTTGTAGATCTGAAGGAATTCCTGCCCAAGAA TATATCAAGCAGAGAGGAGCTGAAAAGAGGATCTTTCAGGAGCATAAGAACTCGGAG AGATGAGTGAATAGAAGCCAAGGTCAAGTACGTCAAACCTCGCAGGTCCCTCCGCAC ATATGGCGTGTCTTCTTCTCGGTGAAGGAGAAGATGAAGGCCAAGAACAGCTGGTG CCTCGCTGTCTGGGATCACAAAGACTCGGTGATGCGCGTGGATGAGAAGACCAAGG AAGTGTGAGAGAGTGGCCCTCACACCGTCAAGCGCTGGGACGCTCACCAAGAG CTTCACACTGGATTTTGGGGAGTATCAGGAAAGCTACTATTAGTACAAACCCAGAG GGAGAGCAGATATCCAGCTGATTGAGGCTACATTGACATCATCTGAAAAGGGAA CATACGTGACATCTGTGGGGTCTCCTCATTGCACCTCCACATGGCTGGTGTCTCTCAG TGACCAACCACTTTTCCCGCAGGTCCACCATCTTGACAGCAGCAGTTCAACCGGACC GGGAAGGCAGAGCACGGCTCAGTGGCGCTGCCGGCCGTGATGCCCTCGGGCTCCAGCG GGCTGAGACCTTCAACGTTGGCAGCATGCCCTCGCCACAGCAGCAGGTGATGGTTGG GCAGATGACCCAGGCGCACATGCCGCCACTGACCTCAGCCAGCAGGCTCATGGGG ACCATCAACACAAGCATGCACGCCCTCCAGCAGGCCAGGATGATCTCAGTGAAGCTCG ACTCGCTGCCACCTCTCGGCCAGGATATGGCATCTAGGGTATGGGTTGAGAACAAGT CGACGAATCCAAACACGAAATCCATTCTCAAGTTGATGCTATCACGGCCGGAACGGCT TCAGTTGTTAAGCTCAGAGCTGGTGACCCCTGCAGACACTGACTCAGCATGTTGCGGAT GTGCGATCACCACTATTCTTCCAACTGACCGAGATGTCCAAGGGTGTGAAGCTATT GGCCGCCCTCATGGATGATGAGGTGGGCAGCGGGAGGACTTGCTCAGAGCTGCCAGG ACCCTCGCTGGGGCGGTGTGAGCTGCTGAAAGCTGTGACAGCTGCTGCTGCTGAGAGC CTCGACAGACAGTTTGTGACTGCTGTCGAGCATCGGACAAGCCAGTGGGGATCTTCT GAGACAGATTGGAGAGAATGAGACTGATGAGCGATTCCAGGATGTTTTAATGAGTTTG GCCAAAGCTGTTGCCAATGCAGCTGCCATGTTGGTACTAAAGGCAAGAATGTTGCC AAGTGGCGGAGACACTGTCTACAGAACAGGGTAATTGCTGCTGCCACCCAGGTGTGC CCTCTCACCTCCAGCTTGTGGCATGTGCCAAGGTTGTGAGCCCCACTATTAGCTCC CCTGTGTGCCAGGAGCAGCTGATTGAAGCAGGGAAGCTGGTGGACCGCTCGGTGGAGA ACTGTGTGCGGTGCTGCCAGGCGGCCACTACCGATAGTGAAGCTCCTGAAGCAGGTGAG CGCAGCGGCCAGCTGGTTCAGCCAGGCCCTCCATGATCTCCTGAGCATGTGCGGCAG TTTGGCAGCGGAGCGAGCCCATCGGCCGCTACGACCAGGCTACTGACACCATCATGT GTGTACCGAGAGCATCTTCAAGCTCATGGGTGACGCTGGTGAATGGTGGCGCAGGC GCGGGTTCTGGCCCAAGCCACATCAGACCTCGTCAATGCCATGAGGTGAGTGCAGAA GCCGAAATGCAGATGGAGAATTCAAAGAAGCTCCTGGCAGCAGCAAACTCTTAGCTG ACTCCACTGCTCGCATGGTGAAGCTGCAAAGGGGGTGCAGGCCAACCCAGAGAATGA GGACCAGCAGCAAAGGCTGAGAGAAGCTGCAGAAGGCCTCCGGGTAGCAACCAACGCA GCTGCCCAAGATGCTATTAAGAAAAAATGTCAACCGACTGGAGGTTGCAGCCAAAGC AGGCCGAGCGGAGCCACACAGACCATCGCCGCTCCAGAAATGCAGCTGTTTCCAA CAAGAACCCTGCGGCCAGCAGCAGCTGGTCCAGAGTTGCAAGGCAGTGGCTGATCAC ATCCCTCAGCTGGTCCAGGAGTGAAGGGGAGCCAAGCTCAAGCTGAAGACCTGAGTG CCCAGCTGGCTCTCATCTCCAGCCAGAACTTCTCCAGCTGGAAAGCAAGATGAGT GTCTCTGCAAGCCGAGTGCACCCGCTGAGTGACAGGCGCAGCCATGCAGCTG AGCCAGTGTGCCAAGACCTGGCCACAGCTTGGCGGAGCTGCGTACCGCTCGCAGA AGGCCATGAAGCTTGTGGTCCGATGGAATCGATTGAGCTCTGGAAGCAAGTGCAGAC GCTTAAGAATGAAGTGCAGGATGCCAAGATGGCAGCCGTGGAGAGCCAGCTGAAGCCA CTTCAGGGGAACGCTGGAATAATGTGCTCAGGACCTGGGAAGCAGATCCAGGGCGG TGGGCTCCTCCATGGCAGCTGTGACCTGTGCTGCTCAAGGCAACGAACACTACAC AGGGTGGCTGCTAGAGAGACGGCCCAAGCTCTGAAAACACTGGCCAGCGGCGCT GGAGTGGCTGCATCGACAACCGACCCCGCGGCCCGCCATGCCATGTTAGATTCTGCTC GAGACGTGATGGAGGGCTCCGCCATGCTCATTCAAGAGGCCAAGCAGGCCCTGATTGC ACCTGGAGATGAGAGCGTCAACAAAGACTGGCTCAGGTGGCTAAAGCCGTCTCACAC TCCTTGAATAACTGCGTAATTGCTCCTGGGCAGAAAGATGTGGACGTGGCCCTGA</p>	

	<p>AGAGCATCGGGGAGTCCAGCAAGAAGCTGCTTGTGGATTTCGCTACCTCCAAGCACGAA GCCTTTCCAGGAAGCCAGAGTGAAGTGAACAGGCAGCAGCTGATCTGAACCACTCT GCTGGGGAAGTGGTCCATGCCACCCGGGGCCAGAGTGGAGAGTGGCTGCAGCCTCTG GAAAGTTCAGTGATGATTTTGGTGAATTCCTCGATGCTGGCATTGAGATGGCTGGCCA AGCTCAGACAAAAGAAGACCAGATCCAAGTGATAGGGAACCTCAAGAATATCTCGATG GCATCCAGCAAGCTGCTGTAGCTGCCAAGTCTCTCTGTAGATCCAGGAGCTCCCA ATGCGAAAAATCTCTGGCTGCAGCTGCAAGAGCTGTGACAGAGAGCATCAATCAACT CATCACTCTGTGTACCCAAACAGCTCCGGGCCAGAAAGAGTGCAGTAATGCCCTGCGG GAGCTCGAGACTGTGAAGGGGATGTTGGACAATCTTAATGAACCTGTTGACCTCT CTTACTTTGACTGCATTGAGAGTGTGATGGAAAACTCCAAGTTCTGGGTGAATCGAT GGCAGGGATTTCACAGAATGCCAAGACCGGAGACCTCCCTGCCTTTGGGGGAATGTGTG GGGATTGCATCCAAGGCTCTCTGTGGGCTGACAGAGGCTGCAGCCCAAGGCTGCATACT TGGTTGGCATCTCTGATCCAAACAGCCAGGCAGGCCACAGGGCCCTGGTGAGCCCAT CCAGTTTGGCAGGGCTAACCAAGGCCATCCAGATGGCATGCCAGAATTTGGTGGACCT GGCAGCAGCCCATCAGAGTCTGTGACCCGCCACAATTGTTGCCAAGCACACGTCAG CCTTGTGCAATGCCCTGCCGATCGCTCATCCAAGACGGCCAAACCAAGTAGCCAAAGAG GCACCTCGTCCAGCTCAGCCAAAGGAAGTGCACCAAGCACTGCCAAGCTGGTGAAGACC ATCAAGGCCCTGGATGGGATTCTCTGAAGACAACCGCAATAAGTGTGCGATCGCCA CCGACCCCTTGATTGAAGCTGTGGAGAACCTGACAGCGTTGCGCTCAACCCCTGAGTT TGTCAGCATTCCTGCCAGATCAGCTCCGAGGGTTCACAGGCACAGGAACCAATCCTG GTCTCAGCCAGAGACCATGTGGAGAGTTCATCGTACCTCATTCGACTGCAGCTCTC TGGCCATCAACCCCAAAGACCCACCCACCTGGTCTGTACTGGCTGGACATTCCTATAC AGTGTCCGACTCCATCAAGAGTCTCATCACTTCTATCAGGACCAAGGCCCTGGACAG AGGGAGTGTGATTACTCCATCGATGGCATCAACCGGTGCATCCGGGACATTCGAGCAGG CCTCGCTGGCCGCGTCCAGCCAGAGCTGGCCACGAGGACGACATCTGTGTGGAGGC CCTGCAGGAGCAGCTGACTTCGGTGGTCCAGGAAATCGGACACCTTATCGATCCCATC GCCACAGCGGCTCGGGGAGAAGCAGCTCAGCTGGGACATAAGGTGACACAATGGCAA GCTATTTTGAGCCCTTGATCTTAGCCGCAAGTTGGTGTGGCTCCGAGATTCCTGATCA TCAGCAGCAGATGACGGTGTGGACCAGACCAAGACTCTCGCAGAGTCTGCTTTCAG ATGTTGTATGACGCCAAAGAAGGTGGCGGAAACCCCAAGGCACACACACCCATGACG CCATCAGAGGCGCCCGCAGTTGATGAAGGAAGCCGTGGATGACATCATGGTGACGCT GAACGAAGCTGCCAGTGAAGTGGGCTGGTTGGGGCATGGTGGAGCCATTCGAGCAA GCCATGAGCAAGCTGGATGAAGCACTCTCCAGAACCAAGGGAAACATTGTGCACT ATCAGACGACTGTGGTTAAATACTCCAAAGCCATTGCGGTGACAGCTCAGGAAATGAT GACTAAGTCGGTTACTAACCCGAGGAGTTGGGAGGACTGGCTTCAAAATGACCACT GACTATGGGCACCTGGCTTCCAGGGCCAGATGGCAGCAGCCACGGCGGAACCAAGG AGATCGGATTCCAGATTGCACTCGTGTGACAGACCTGGGCCACGGCTGTATCTTCTCT GGTGACAGAGGCGGGGCCCTCCAGGTCTGCCCCACAGACAGCTACACCAAGAGGGAG CTGATCGAATGCGCCGTCGCGTCCAGGAAAGGTCTCTTGGTGTCTCTGGCTCTCC AGGCCGGGAACAAAGGAACCCAGGCATGCATTACAGCCGCCACCGCTGTGTCTGGGAT CATTGCGGACCTGGACACCACCATTATGTTTGCACAGCGGGGACGCTGAATGCAGAG AACAGTGAGACCTTCGACAGCCACAGGAGAACATTCCTAAGACGGCCAAAGGCCCTTGG TAGAAGACACGAACTACTTGTGTGAGGAGCTGCGTCCACTCTGACAGAGCTGGCCCA GGCGGCCAGTCTCAGCAGCCACCATCACCCAGCTCGCAGAAGTGGTCAAGCTGGGG GCAGCCAGCTGGGCTCCGACGACCCCGAGACCCAGGTGGATTGATCAATGCCATCA AAGATGTGGCCAAGGCCCTTTCTGATCTCATCAGTGCTACCAAGGAGCTGCCAGCAA GCCAGTGGACGACCTTCCATGTACAGCTCAAGGGGGTGCAGAGGTGGTGGTGAAC AATGTACCTCGCTCTCAAGACTGTAAAGGCAGTGGAGGATGAGGCCACCCGGGGCA CCAGGGCGCTTGAGGCCACAAATGAATGCATAAAGCAGGAGCTTACGGTGTTCAGCT AAAAGACGTACTGAAAAGACATCATCACTGAAGAATCCATAAGGATGACGAAAGGC ATCACCATGGCAACAGCCAAAGCCGTGGCAGCTGGGAACTCATGTAGACAGGAGGACG TGATTGCTACTGCAACCTGAGCCGGAAGCCGTGTGAGATATGTTGACGGCTTGCAC GCAAGCATCTTCCACCCGATGTGAGTGACGAGGTGAGAACCAGAGCCTTGCCTTTC GGGACGGAGTGACACCTTGGCTACTTGGACCTCCTGGAGCAGCTTGTGATCTTCTC AGAAACCAACCCAGAAATCAAGCAGCAGCTGGCCGCTTTCTCAAGCGAGTGCAGCG CGCTGTGACAGAGCTCATCCAGGCGGCGGAAGCCATGAAAGGAACAGAGTGGGTGGAT CCAGAAGACCAACTGTATTGCAGAAACAGAGTTACTGGGGGCTGCAGCATCCATCG AAGCTGCTGTCTGAAGAAGTTAGAGCAACTGAAGCCAAAGAGCAAAACCAAAACCAAGCGGA TGAGACCTGGACTTTGAGGAACAGATCTTGAAGCTGCTAAATCCATTGCTGCTGCC ACAAGCGCCCTGGTCAAATCGGCCTCAGCAGCCAGAGGGAGCTGGTGGCCCAAGGAA AGGTGGGCTCCATCCCTGCCAATGCTGCAGACGACGACAGTGGTGCAGGGGTGAT TTCTGCTGCCCGGATGGTGGCGGCTGCGACAGCAGTCTCTGTGAGCGGCGCAATGCC TCCGTTCCAGGACACGCCAGCGAGGAGAAGCTCATCTCATCTGCCAAGCAGGTGCGCG CTTCCACGGCTCAGCTGCTGGTGGCTGCAAGGTGAAGGCCAGCCAGGATTTCAGAGGC CATGAGGCGGCTACAGGCGGCGAGGAAATGCTGTGAAAAGAGCCTCAGACAACTTTGTC CGTGCAGCCAGAGGAGCTTTTGGCAAAGCTGATGACGACGATGTTGTAGTGGAAA CCAAGTTTGTGGGGGGCATTGCTCAGATCATCGCCGCCAGGAAGAAATGCTAAAGAA AGAGCGAGAACTGGAAGAAGCAAGGAAAAAAGTGGCCAAATCCGCCAGCAGCAGTAT AAGTTTTCACCCACGAGCTGAGGGAAGATGAGGGCTAAAGGTGCGAGCCAGATGGC GAGCCCCAGGGGATGGCCCTGGCTGAA</p>
	<div>ORF Start: ATG at 58</div> <div>ORF Stop: TAA at 7693</div>
	<div>SEQ ID NO: 76</div> <div>2545 aa</div> <div>MW at 271692.8kD</div>
NOV21a,	MVALSLKICVRHCVVKTQFEPSTAVYDACRVIRERVPEAQTGQASDYGLFLSDEDPR RKGIWLEAGRTLQYMLRNGDILEYKKQRPQKIRMLDGSVKTVMVDDSKTVGELLVT

CG57804-01 Protein Sequence	<p>ICSRIGITNYEESLIQETIEEKKEEGTGLKKDRITLLRDERKMEKLKAKLHTDDDLN WLDHSRTFREQGVDENETLLRRKFFVSDQNVDSRDPVQLNLLYVQARDIILNGSHVP SFEKACEFGGFGQAQIQFGPHVEHKHKPGFLDLKEFLPKEYIKQRGAEKRIHQEHKNCG EMSEIEAKVKYVKLARSRLTYGVSFVLVKEKMKGKNKLVPRLLGTTKDSVMRVEKTK EVLQEWPLTTVKRWAASPKSFTLDFGEYQESYYSVQTTEGEQISQLIAGYIDIIILKKG TYVTSVGSPhCTPHGWCSLSDQTTFPGRSTILQQQFNRTGKAHGSVALPAVMRSGSS GPETFNVGSMPSPOQQVMVGMHRGHMPPLTSAQQALMGTINTSMHAVQQAQDDLSEL DSLPLPLGQDMASRVVQNKVDESKHEIHSQVDAITAGTASVVNLTAGDPADTDTYAVG CAITTISSNLTEMSKGVKLLAALMDDEVSGEDLLRAARTLAGAVSDLLKAVQPTSGE PRQTVLTAAGSIGQASGDLRLQIGENETDERFQDVLMSLAKAVANAAAMLVLKAKNVA QVAEDTVLQNRVIAAATQCALSTSOLVACAKVVSPTISSPVCQEQLIEAGKLVDRSVE NCVRACQAATTDSLELLKQVSAASVVSQALHDLQLHVRFQFASRGEPIGRYDQATDTIM CVTESIFSSMGDAGEMVRQARVLAQATSDLVNAMRSDAEAEIDMENSKKLLAAAKLLA DSTARMVEAAKGAAANPENEDQQQLREAAEGLRVATNAAQNAIKKIVNRLEVAAK QAAAAATQTIAASQNAAVSNKNPAAQQQLVQSCKAVADHIPQLVQCVRGSSQAQAEELS AQLALIISQNFQLPGSKMVSSAKAAVPTVSDQAAMQLSQCAKNLATSLAELRTASQ KAHEACGPMEIDSLNTVQTLKNELODAKMAAVESQLKPLPGETLEKCAQDILGSTSKA VGSSMAQLLTCAAQGNHEHTGVAARETAQALKTLAQAARGVAASTTDPAAAHAMLD RDVMEGSAMLIQEAQALIPGDAERQORLAQVAKAVSHSLNNVCNCLPGQKQDVVAL KSIGESSKKLLVDSLPPSTKPFQEAQSELNQAAADLNQSAQEVVHATRGSGELAAAS GKFSDDFGFLDAGIEMAGQAQTKEDQIQVIGNLKNISMASSKLLLAAKSLSDVPGAP NAKNLLAAARAVTESINQLITLCTQQAPGQKECDNALRELETVKGMLDNPNPEVSD SYFDCIESVMENSKVLGESMAGISQNAKTGDLPAFGECVGIASKALCGLTEAAQAAY LVGISDPNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAATIVAKHTS ALCNACRIASSKTANPVAKRHFVQSAKEVANSTANLVKTIKALDGFSEDNRNKCR TAPLIEAVENLTAFASNPEFVSI PAQISSEGSQAQEPILVSAKTMLESSSYLIRTARS LAINPKDPPTWSVLGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRCIRDIEQ ASLAAVSLSLATRDDISVEALQEQLTSVVQEIGHLIDPIATAARGEAAQLGHKVTQLA SYFEPLILAAVGVASKILDHQQQMTVLDQTKTLAESALQMLYAAKEGGNPKAQHTHD AITEAQLMKEAVDDIMVTLNEAASEVGLVGMVDAIAEAMSKLDEGTPPEPKGTFVD YQTTVVVKYSKAIATAQEMMTKSVTNPEELGGLASQMTSDYGHFAFGQMAAATAEPE EIGFQIRTRVQDLGHGCI FLVQKAGALQVCPTDSYTKRELI ECARAVTEKVS LVL QAGNKGTOACITAAVSGIIADLDTTIFATAGTLNAENSETFADHRENILKTAKAL VEDTKLLVSGAASPTDKLAQAQSSAATITQLAEVVKLGAAASLGSDDPETQVVLINAI KDVAKALSDLISATKGAASKPVDDPSMYQLKGAAKVMVTNVTSLKTVKAVEDEATRG TRALEATIECIKQELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAGNSCRQED VIATANLSRKAVSDMLTACKQASFPDVSDEVTRALRFGTECTLGYLDDLEHLVLVIL QKPTPEFKQLAASFSCRVAGAVTELIQAAEAMKGETWVDPEDPTVIAETELLGAAASI EAAAKKLEQLKPRAKPKQADETLDFEQILEAAKSIAAATSALVKSASAAQRELVAAQ KVGSI PANAADGQWSQGLISAARMVAAATSSLCEAANASVQGHASEEKLISAKQVA ASTAQLLVACKVKADQDSEAMRRLQAAGNAVKRASDNLVRAAQKAAFGKADDDVVVE TKFVGGIAQIIAAQEEMKKERELEEARKKLAQIRQQYKFLPTELREDEG</p>
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Further analysis of the NOV21a protein yielded the following properties shown in Table 21B.

Table 21B. Protein Sequence Properties NOV21a	
PSort analysis:	0.5964 probability located in mitochondrial matrix space; 0.3037 probability located in mitochondrial inner membrane; 0.3037 probability located in mitochondrial intermembrane space; 0.3037 probability located in mitochondrial outer membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV21a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 21C.

Table 21C. Geneseq Results for NOV21a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV21a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB41087	Human ORFX ORF851 polypeptide sequence SEQ ID NO:1702 - Homo sapiens, 2541 aa. [WO200058473-A2, 05-OCT-2000]	1..2543 1..2540	1913/2546 (75%) 2231/2546 (87%)	0.0
AAM39312	Human polypeptide SEQ ID NO 2457 - Homo sapiens, 1165 aa. [WO200153312-A1, 26-JUL-2001]	1381..2545 1..1165	1161/1165 (99%) 1163/1165 (99%)	0.0
AAM79794	Human protein SEQ ID NO 3440 - Homo sapiens, 1177 aa. [WO200157190-A2, 09-AUG-2001]	1378..2545 10..1177	1156/1168 (98%) 1160/1168 (98%)	0.0
AAM41098	Human polypeptide SEQ ID NO 6029 - Homo sapiens, 1177 aa. [WO200153312-A1, 26-JUL-2001]	1378..2545 10..1177	1156/1168 (98%) 1160/1168 (98%)	0.0
AAM41079	Human polypeptide SEQ ID NO 6010 - Homo sapiens, 1177 aa. [WO200153312-A1, 26-JUL-2001]	1378..2545 10..1177	1156/1168 (98%) 1160/1168 (98%)	0.0

In a BLAST search of public sequence databases, the NOV21a protein was found to have homology to the proteins shown in the BLASTP data in Table 21D.

Table 21D. Public BLASTP Results for NOV21a				
Protein Accession Number	Protein/Organism/Length	NOV21a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9Y490	Talin - Homo sapiens (Human), 2541 aa.	1..2543 1..2540	1910/2546 (75%) 2230/2546 (87%)	0.0
P26039	Talin - Mus musculus (Mouse), 2541 aa.	1..2543 1..2540	1907/2546 (74%) 2230/2546 (86%)	0.0
Q9UPX3	KIAA1027 PROTEIN - Homo sapiens (Human), 1695 aa (fragment).	853..2543 1..1694	1262/1694 (74%) 1483/1694 (87%)	0.0
Q9VSL8	CG6831 PROTEIN (TALIN) -	1..2532 1..2534	1197/2563 (46%) 1707/2563 (65%)	0.0

	fly), 2836 aa.			
Q9Y4G6	KIAA0320 PROTEIN - Homo sapiens (Human), 949 aa (fragment).	1597..2545 1..949	947/949 (99%) 948/949 (99%)	0.0

PFam analysis predicts that the NOV21a protein contains the domains shown in the Table 21E.

Table 21E. Domain Analysis of NOV21a			
Pfam Domain	NOV21a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ubiquitin: domain 1 of 1	64..88	8/27 (30%) 20/27 (74%)	4.3
Band_41: domain 1 of 1	123..316	67/211 (32%) 172/211 (82%)	1.3e-92
IRS: domain 1 of 1	312..404	19/109 (17%) 46/109 (42%)	1.2
I_LWEQ: domain 1 of 5	674..768	31/98 (32%) 59/98 (60%)	11
transport_prot: domain 1 of 1	667..814	24/182 (13%) 88/182 (48%)	10
I_LWEQ: domain 2 of 5	852..894	18/47 (38%) 31/47 (66%)	2.4e+02
Vinculin: domain 1 of 1	860..903	12/48 (25%) 30/48 (62%)	1.3
I_LWEQ: domain 3 of 5	925..984	21/62 (34%) 37/62 (60%)	5.9e+04
TP_methylase: domain 1 of 1	861..1036	26/226 (12%) 105/226 (46%)	8
Apolipoprotein: domain 1 of 1	981..1229	48/288 (17%) 141/288 (49%)	3.5
CAP: domain 1 of 1	917..1354	94/557 (17%) 209/557 (38%)	4.4
I_LWEQ: domain 4 of 5	1529..1545	10/17 (59%) 13/17 (76%)	56
STAT: domain 1 of 1	1660..1821	35/211 (17%) 95/211 (45%)	8.2

LEA: domain 1 of 1	1768..1834	15/76 (20%) 42/76 (55%)	7
Histone_HNS: domain 1 of 1	2232..2356	29/143 (20%) 63/143 (44%)	3.7
I_LWEQ: domain 5 of 5	2345..2536	100/202 (50%) 183/202 (91%)	2e-101

Example 22.

The NOV22 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 22A.

Table 22A. NOV22 Sequence Analysis			
	SEQ ID NO: 77	2214 bp	
NOV22a, CG57551-01 DNA Sequence	ATTCTCTCCCTGCCCTCGTGCAGCCGCTGCCATGGCCCAGACACTGCAGATGGAGATC CCGAACCTTCGGCAACAGCATCCTGGAGTGCCTCAATGAACAGCGGCTGCAGGGCCCTGT ACTGTGACGTGTCACTGGTGGTCAAGGGCCATGCCTTCAAGGCCACCGGGCCGTGCT TGCTGCCAGCAGCTCCTACTTCCGGGACCTGTTCAACAACAGCCGAGCGCGCTGGTG GAGCTGCCGGCGGCTGTGCAGCCCCAGTCTTTCAGCAGATCCTCAGCTTCTGCTACA CGGGCCGGCTGAGCATGAACGTGGGCGACCACTTCTGCTCATGTACACGGCTGGCTT CCTGCAGATCCAGGAGATCATGGAGAAGGGCACCAGATTCTTCTCAAGGTGAGCTCC CCGAGCTGCGACTCCAGGGCTGCATGCCGAGGAGGGCCCCATCGCTCGGAGCCCCAGA GCCCCGTGGCGCAGACATCGGGCTGGCCAGCCTGTAGCACCCCGCTGCCCTCGTGTG GCGGGTGAAGACGGAGCAGCAGGAGTCCGACTCCGTGCAGTGCATGCCGTGGCCAAG CGGCTGTGGGACAGTGGCCAGAAGGAGGCTGGGGCGGGCGCAATGGCAGCCGCAAGA TGGCCAAGTTCTCCACGCCGACCTGGCTGCCAACCGGCTCACCAGCCCCGCCACC CCAACAGGCTCCGGTGGTGGCAGCAGCCAGCCCGCGCTGGCTGCGGGAGCAGGGCAG CCAGCCGGTGGGGTGGCAGCAGCAGGGGGTGTGGTGAAGTGGGCCAGCAGTCCGAGC GGACCGCTCCGAGCCTCAAGCGCTACACCAGCGACAGCCCTGGCTCCTACCCACA TGAGGAGGACGAGGAGGAGGATGGTGGCGAGGAGGGCATGGATGAGCAGTACCGGAG ATCTGCAACATGTACACCATGTACAGCATGATGAACGTCCGCCAGACAGCCGAGAAGG TGGAGGCCCTCCCGGAGCAGGTAGCCCCGAGTCCCGAAATCGCATCCGGTTCGGCA AGACCTGGCGTCTCTCCCGCTGAACCTTATCAACCAGATTGGGAACCGCTGCCACCCC AAGCTCTACGACGAGGGCGACCCCTCTGAGAAGCTGGAGCTGGTGACAGGCACCAACG TGTACATCACAAGGGCGCAGCTGATGAAGTGCACGTCAGCGCAGGCACGCGGCACAA GGTCTTACTGCGGCGGCTCCTGGCTCCTTCTTTGACCGGAACACAGTGGCCCAACAGC TGCGGCACCGGCATCCGCTCTTCTACCAACGATCCCCGTGGAAGCCCTGGACAGCC GCGTGCTCCACGCTGTCAAGTACTACTGCCAGAACTTCGCCCCCACTTCAAGGAGAG CGAGATGAATGCCATCGCGCCGACATGTGCACCAACGCCCGCGCGCTCGTGCGCAAG AGCTGGATGCCAAGGTCAAGGTGCTCAAGGCTGAGGATGACGCCTACACCACCTTCA TCAGTGAACCGGCAAGATCGAGCCGACATGATGGGTGTGGAGCATGGCTTCGAGAC CGCCAGCCACGAGGGCGAGGGGGTCCCATCGCTGAAGCCCTGCAGTAACCCGCCAG CCTCCCGCGGGGCGCACACTTCCCTCCCAACACACACACACTGCCATCTTGGT CATGAGCTACTGTCTGTCTCCCTCCCGAGGACCCGCGGTGGTGCTGCATGTTCCCGGCC CTCTGCCCTCTGTCTACCCCTTTCCTCCACCGAGAGCTGGGCCGGGAGAGGACCG CAGGGCAGGTGGCGTGGTCCGTGTTGCCTTCTTTAACACACACTCGTGCAGTGGGG GAGTTCTGGCTCCCCAACCTAACCCCTAGCCGTCTCTCCACACTCACCAGGCCACC AGGGGAGGGGGCTGGCTGGGGGTCTTGGGAAGGCCCTCCCGAGGCTTAGGCCACC TCGCGGAAGCCTTCAGCCTCCGCCCTCACTGCAGCCCTTGGGACTTGAGGGGGCC CCAGGGGTCTCAGGACCCCTCCACCACCTCCAGTGTCTCCAGCTCTCCAAAAGCG CCTTCTGTCAACCTCGTCTATCCCTGCGCTGGGGGTGGGGTAGGCGAGGCCGTGG GGACTACCATTTTATAGCTGGGGAACAGGCTCCGAGAAATTGCACAACCGACCTCA GGTGGCCGGC		
	ORF Start: ATG at 32	ORF Stop: TAA at 1613	
	SEQ ID NO: 78	527 aa	MW at 57283.8kD
NOV22a, CG57551-01 Protein Sequence	MAQTLQMEIPNFGNSILECLNEQRLQGLYCDVSVVVKGHAFKAHRAVLAASSSYFRDL FNNRSRAVVVLPAAVQPSFQQLSFCYTGRLSMNVGDQFLMYTAGFLQIQEIMEKG TEFFLKVSSPSCDSQGLHAEEAPSEPPQSPVAQTSGWPACSTPLPLVSRVKTQQESD SVQCMFPAKRLWDGQKEAGGGNGSRKMAKFSTPDLAANRPHQPPPPQAPVVAQAQ PAVAAGAGQAPAGVAAAGGVVSGPSTERTSPGTSSAYTSDSPGSYHNEEDEDGGE EGMDEQYRQICNMYTMYSMNVGQTAEKVEALPEQVAPESRNRIRVRQDLASLPAELI NQIGNRCHPKLYDEGDPSEKLELVGTNVYITRAQLMNHVSAGTRHKVLLRRLASF FDRNTLANSCTGIRSSNTNDRRKPLDSRVLHAVKYCYQNFAPNFKESMNAIAADMC		

	TNARRVVRKSWMPKVKVLKAEDDAYTTTFISETGKIEPDMMGVEHGFETASHEGEAGPI AEALQ
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Further analysis of the NOV22a protein yielded the following properties shown in Table 22B.

Table 22B. Protein Sequence Properties NOV22a	
PSort analysis:	0.6000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV22a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 22C.

Table 22C. Geneseq Results for NOV22a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV22a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB41621	Human ORFX ORF1385 polypeptide sequence SEQ ID NO:2770 - Homo sapiens, 228 aa. [WO200058473-A2, 05-OCT-2000]	300..527 1..228	228/228 (100%) 228/228 (100%)	e-131
ABB17117	Human nervous system related polypeptide SEQ ID NO 5774 - Homo sapiens, 190 aa. [WO200159063-A2, 16-AUG-2001]	409..501 1..93	64/94 (68%) 73/94 (77%)	7e-29
AAG78615	Human zinc finger transcription factor BioZFTF45 - Homo sapiens, 413 aa. [CN1299825-A, 20-JUN-2001]	5..159 7..170	62/164 (37%) 92/164 (55%)	2e-25
AAY73351	HTRM clone 1484257 protein sequence - Homo sapiens, 810 aa. [WO9957144-A2, 11-NOV-1999]	7..291 1..277	83/291 (28%) 124/291 (42%)	8e-18
AAM41058	Human polypeptide SEQ ID NO 5989 - Homo sapiens, 804 aa. [WO200153312-A1, 26-JUL-2001]	7..291 2..271	84/295 (28%) 123/295 (41%)	2e-17

In a BLAST search of public sequence databases, the NOV22a protein was found to have homology to the proteins shown in the BLASTP data in Table 22D.

Table 22D. Public BLASTP Results for NOV22a				
Protein Accession Number	Protein/Organism/Length	NOV22a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96RE7	NAC1 PROTEIN - Homo sapiens (Human), 527 aa.	1..527 1..527	526/527 (99%) 526/527 (99%)	0.0
O35260	NAC-1 PROTEIN - Rattus norvegicus (Rat), 514 aa.	1..527 1..514	462/530 (87%) 475/530 (89%)	0.0
Q9CZ72	4930511N13RIK PROTEIN - Mus musculus (Mouse), 514 aa.	1..527 1..514	462/530 (87%) 476/530 (89%)	0.0
Q96BF6	SIMILAR TO RIKEN CDNA 0610020I02 GENE - Homo sapiens (Human), 587 aa.	1..501 1..478	289/522 (55%) 335/522 (63%)	e-140
AAH22103	RIKEN CDNA 0610020I02 GENE - Mus musculus (Mouse), 586 aa.	1..485 1..459	281/502 (55%) 327/502 (64%)	e-139

PFam analysis predicts that the NOV22a protein contains the domains shown in the Table 22E.

Table 22E. Domain Analysis of NOV22a			
Pfam Domain	NOV22a Match Region	Identities/ Similarities for the Matched Region	Expect Value
BTB: domain 1 of 1	14..124	40/143 (28%) 88/143 (62%)	6.2e-23

Example 23.

The NOV23 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 23A.

Table 23A. NOV23 Sequence Analysis		
	SEQ ID NO: 79	1497 bp
NOV23a, CG57411-01 DNA Sequence	ATGGCCACTGCACAGGTGGAAGTGGTGAGGGTGGTCCCCGGGCTCCAGTAGGGGAGA AGCTGGAGCTCGTCCTGTGCAACCTGCAGGCAGACGTCTGGAGTTGCTGCTGGAGTT TGTCTACAGGGGCTCCCTGGTCATCGACTCGGCCAAGCCAGACATGCTGGAGGCG GCCAGCAAGTTCCAGTTCCACACCTTCTGCAAAGTCTGCGTGTCTTTCTCGAGAAGC AGCTGACGGCCAGCAACTGCCTGGGCGTGTGGCCATGGCCGAGGCCATGCAGTGCA CGAGCTCTACCACATGGCCAAGGCCTTCGCGCTGCAGATCTTCCCCGAGGTGGCCGCC CAGGAGGAGATCCTCAGCATCTCCAAGGACGACTTCATCGCCTACGTCTCCAACGACA GCCTCAACACCAAGGCTGAGGAGCTGGTGTACGAGACAGTCATCAAGTGGATCAAGAA	

	GGACCCCGCAGACGCACACAGCTGCAGTACGCGGCTGAGCTCCTGGCCGTGGTCCGC CTCCCCTTCATCCACCCAGCTACCTGCTCAATGTGGTTGACAATGAAGAGCTGATCA AGTCATCAGAAGCCTGCCGGGACCTGGTGAACGAGGCCAAACGCTACCATATGCTGCC CCACGCCCCCGCAGGAGATGCAGACGCCCCGAACCCGGCCGGCGTCCCTGCAGGTGTG GCTGAGGTGATCGTCTTGGTTGGGGGCCGTGAGTGGTGGGGATGACCCAGCGCTCGC TGGTGGCCGTCACTGCTGGAACCCGAGAACAAAGTGGTACCCCTTGGCCTCGCT GCCCTTCTATGACCGGAGTTCTTCAGTGTAGTGAGTGCAGGGGACAACATCTACCTC TCAGGTGGGATGGAATCAGGGGTGACGCTGGCTGATGTCTGGTGTACATGTCCCTGC TTGATAACTGGAACCTCGTCTCCAGAAATGACAGTCCCCCGCTGTGGCACAATAGCCT CGTCTACGATGGGAAGATTACACCCCTCGGGGGACTTGGCGTGGCAGGCAACGTGGAC CACGTGGAGTCCCTGCAGGTGTGGCTGAGGTGATCGTCTTGGTTGGGGCCGTGAGA TGGTGGGGATGACCCAGCGCTCGCTGGTGGCCGTACCTGCTGGAACCCGAGAACAA CAAGTGGTACCCCTTGGCCTCGCTGGTGGGATGGAATCAGGGGTGACGCTGGCTGAT GTCTGGTGTACATGTCCCTGCTTGATAACTGGAACCTCGTCTCCAGAAATGACAGTCC CCCGCTGTGGCACAATAGCCTCGTCTACGATGGGAAGATTACACCCCTCGGGGGACT TGGCGTGGCAGGCAACGTGGACACGTGGAGGCCCTACGAGCCACAACCAACATGG ACCCTCCTCCCCACATGCCCTGCCCTGTGTTCAGACACGGCTCGCTCGTGATAAAGA AATATATTCAAAGCGGCTGACATCAGCAGAAAGCCACGATAAGACT		
	ORF Start: ATG at 1	ORF Stop: TGA at 1468	
	SEQ ID NO: 80	489 aa	MW at 54208.2kD
NOV23a, CG57411-01 Protein Sequence	MATAQVELVQGGPRAPVGEKLELVLSNLQADVLELLLEFVYTGSLVIDSANAKTLLEA ASKFQFHTFCVKCVSFLEKQLTASNLGLVLAEMQCSSELYHMAKAFALQIFPEVAA QEEILSISKDDFIAYVSNDSLNTKAELVYETVIKWKDPATRTQLQYAAELLAVVR LFFIHPSYLLNVVDNEELIKSSEACRDLVNEAKRYHMLPHARQEMQTPRTRPRVPAGV AEVIVLVGGRQMVGMTQRLVAVTCWNPQNNKWPPLASLPFYDREFFSVVSAGDNIYL SGGMESGVTLADVWCYMSLLDNWNLVSRMTVPRCRHNSLVYDGKIYTLGGLGVAGNV HVEVPAGVAEVIVLVGGRQMVGMTQRLVAVTCWNPQNNKWPPLASLGMESGVTLAD VWCYMSLLDNWNLVSRMTVPRCRHNSLVYDGKIYTLGGLGVAGNVHDVEAYEPTNTW TLLPHMPCPVFRHGC VIKKYIQSG		

Further analysis of the NOV23a protein yielded the following properties shown in Table 23B.

Table 23B. Protein Sequence Properties NOV23a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.2271 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space; 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV23a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 23C.

Table 23C. Geneseq Results for NOV23a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV23a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB40940	Human ORFX ORF704 polypeptide sequence SEQ ID NO:1408 - Homo sapiens, 335 aa. [WO200058473-A2, 05-OCT-2000]	19..351 4..334	317/333 (95%) 320/333 (95%)	e-180
AAM38711	Human polypeptide SEQ ID NO 1856 - Homo sapiens, 574 aa. [WO200153312-A1, 26-JUL-2001]	22..472 78..559	151/488 (30%) 222/488 (44%)	2e-61
AAB43090	Human ORFX ORF2854 polypeptide sequence SEQ ID NO:5708 - Homo sapiens, 506 aa. [WO200058473-A2, 05-OCT-2000]	22..468 9..487	150/491 (30%) 241/491 (48%)	3e-59
AAM38956	Human polypeptide SEQ ID NO 2101 - Homo sapiens, 587 aa. [WO200153312-A1, 26-JUL-2001]	22..468 90..568	149/491 (30%) 240/491 (48%)	1e-58
AAM94018	Human stomach cancer expressed polypeptide SEQ ID NO 106 - Homo sapiens, 568 aa. [WO200109317-A1, 08-FEB-2001]	25..470 76..553	148/490 (30%) 231/490 (46%)	3e-56

In a BLAST search of public sequence databases, the NOV23a protein was found to have homology to the proteins shown in the BLASTP data in Table 23D.

Table 23D. Public BLASTP Results for NOV23a				
Protein Accession Number	Protein/Organism/Length	NOV23a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96CT2	HYPOTHETICAL 76.8 KDA PROTEIN - Homo sapiens (Human), 707 aa (fragment).	19..489 203..707	390/507 (76%) 406/507 (79%)	0.0
Q96PW7	KIAA1921 PROTEIN - Homo sapiens (Human), 545 aa (fragment).	19..489 41..545	390/507 (76%) 406/507 (79%)	0.0
Q96BF0	SIMILAR TO HYPOTHETICAL PROTEIN FLJ14106 - Homo sapiens (Human), 503 aa.	19..351 172..502	329/333 (98%) 330/333 (98%)	0.0

Q9D5K3	4930429H24RIK PROTEIN - Mus musculus (Mouse), 484 aa.	33..485 1..477	165/492 (33%) 248/492 (49%)	2e-66
Q9UH77	Kelch-like protein 3 - Homo sapiens (Human), 587 aa.	22..468 90..568	150/491 (30%) 241/491 (48%)	1e-58

PFam analysis predicts that the NOV23a protein contains the domains shown in the Table 23E.

Table 23E. Domain Analysis of NOV23a			
Pfam Domain	NOV23a Match Region	Identities/ Similarities for the Matched Region	Expect Value
BTB: domain 1 of 1	4..79	24/143 (17%) 53/143 (37%)	3.7
Kelch: domain 1 of 4	223..272	9/50 (18%) 28/50 (56%)	0.94
Kelch: domain 2 of 4	275..320	11/47 (23%) 27/47 (57%)	0.016
Kelch: domain 3 of 4	322..396	14/75 (19%) 44/75 (59%)	3.3e-05
Kelch: domain 4 of 4	426..471	19/47 (40%) 35/47 (74%)	7.2e-10

Example 24.

The NOV24 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 24A.

Table 24A. NOV24 Sequence Analysis		
	SEQ ID NO: 81	4268 bp
NOV24a, CG57399-01 DNA Sequence	<p>ATGACCTGGGACACAGCTCTCTGGACCTCAGTTTTTCTGATTGGGCTCCTTCCTACCC TTGGTTTCGCTAATTGCATCCTCCAGACTTCTGGTAAAAATGTGTACTTTAAGAGGTAG ATACCCCCAGCCCCACAACCACCTCTCTGCTTGTCTCCCCTAGTCCACCAGCTCCGA CCAGCAGACATCAAAGTGGTGGCCGCCCTGGGTAATGATGAAACCTTCCAGGAAAGTG GTGCAGGGCAGCTAAGTGAGCCTGACCCAGGCAGTGGTCTTGCCACAGGCTGCTT GCCTGGGGTAAAAAAGGAAATGCAAGATGTGGTAGGTGAGAGAACGCCAGCCGTCGC CGCAGCCTCCGCCGCGAGAAAGCCCTTGTTCCCGCTGCTGGGAAGGAGAGTCTGTGCC GACAAGATATTTTCATTTCCTTGTTGGAAATTATCAAGCATTTTCCTCCCTCCCTCA GGACATCAACCTGGAGAAAGACTGGAAGCTGGTCACACTCTTCATTGGGGTCAACGAC TTGTGTCATTACTGTCCACTTGTTCAGGGCCCCGTTATAGACCTGGGTGGGATGGATA CCCTCCACTCCCTGCAGCTCCCAAGGGCTTCGTCAACGTGGTGGAGGTCTAGGAGCT GGCTAGCCTGTACCAGGGCCAAGGCGGGAATGTGCCATGCTGGCAGCTCAGGAAGCC TGGAACAGCCTCTGGCCTCCAGCAGGTACAGTGAGCAGGAGTCTTCACCGTGGTTT TCCAGCCTTTCTTCTATGAGACCACCCATCTGACCCCGACTCCAGGATTCTACCAC GCTGGCCTGGCATCTCTGGAATAGGATGATGGAGCCAGCAGGAGAGAAAGATGAGCCA TTGAGTGTAATAACACGGGAGGCAATGAAGTGTCCCTCTCAGGAGAGCCCCATCTGT TCAGCTACAGAAACAGCAACTACCTGACCAGACTGCAGAAACCCCAAGACAAGCTTGT AAGAGAAGGAGCGGAAATCAGATGTCCTGACAAAGACCCCTCCGATACGGTTCACACC TCAGTTCATAGGCTGAAGCCGGCTGACATCAACGTAATTGGAGCCCTGGGTGACTCTC TCACGGCAGGCAATGGGGCCGGTCCACACCTGGGAACGTCTTGGACGTCTTGACTCA GTACCGAGGCTGTCTGGAGCGTCGGCGGAGATGAGAACATCGGCACCGTTACCACC</p>	

	<p>CTGGCAGACATCTCCGGGAATTCAACCCCTTCCCTGAAGGGCTTCTCTGTTGGCACTG GGAAAGAAACCACTCTTAATGCTTCTTAAACCAGGCTGTGGCAGGAGGCGAGCTGA GCAGGCCAGGAGGCTGGTGGACCTGATGAAGAATGACACGAGGATACACTTTCAGGAA GACTGGAAGATAATAACCCCTGTTTATAGGCGGCAATGACCTCTGTGATTTCTGCAATG ATCTGGTACACTATTCTCCCCAGAAGTTTACAGACAACATTGGAAGGCCCTGGACAT CCTCCATGCTGAGTCTCAGGTTCTCGGGCATTGTGAACCTGGTGACGGTGTCTTGAG ATCGTCAACCTGAGGGAGCTGTACCAGGAGAAAAAGTCTACTGCCCAAGGATGATCC TCAGGTCACTGTGTCCCTGTGTCTGAAGTTTGATGATAACTCAACAGAACTTGTCTAC CCTCATCGAATTCACAAGAAGTTTTCAGGAGAAGACCCACCACTGATTGAGAGTGGG CGATATGACACAAGGGAAGATTTTACTGTGGTGTGCAGCCGCTTCTTGAACACGTTGG ACATGCCAAGACCCAGGAAGGATTGCCTGACAACTTTTCTTCGTCTCTGACTGTTT CCACTTCAGCAGCAAGTCTCACTCCCCGAGCAGCCAGTGTCTCTGGAACAATATGCTG GAGCCTGTTGGCCAGAAGACGACTCGTCATAAGTTTGAACCAAGATCAATATCATCT GTCCGTACAGGTCAGCCGTTTCTGAGGACCTACAAGAACAGCATGCAGGGTCATGG GACCTGGCTGCCATGCAGGGACAGAGCCCTTCTGCCTTGCAACCTACCTCAGTGCAT GCCCTGAGACCTGCAGACATCCAAGTTGTGGTGTCTCTGGGGGATTCTCTGACCCGCTG GCAATGGAATTGGCTCCAAACCAGACGACCTCCCGATGTCAACACAGTATCGGGG ACTGTCTACAGTGCAGGAGGGGACGGCTCCCTGGAGAATGTGACCACCTTACCTAGT TCTATCCTTCGGGAGTTTAAACAGAACTCACAGGCTACGCCGTGGGCAGGGGTGATG CCAATGACAGAATGCATTCTCAATCAAGCTGTTCCCGGAGCAAAGGCTAGGGATCT TATGAGCCAACTCCAACTCTGATGCAGAAGATGAAGATGATCATAGAGTAAATTTTC CATGAAGACTGGAAGGTCTACAGTGTCTGATCGGAGGCAGCGATTATGTGACTACT GCACAGATTGGAATCTGTATTCTGCAGCCAACTTTGTTCCACCTTCCGCAATGCCCT GGACGCTCTGCATAGAGAGGTGCCAGAGTCTGGTCAACCTCGTGACTTCTCTGAAC CCCCTATCATGCGGCAGGTGTTCTTGGGAAACCCAGACAAGTGCCAGTGCAGCAGG CCAGCGTTTGTGTAACTGCGTCTGACCCCTGCGGGAGAACTCCCAAGAGCTAGCCAG GCTGGAGGCCCTTACGCCAGCCTACAGAGCAGCATGCGCGAGCTGGTGGGGTCAGGC CGCTATGACACGACGAGGAGTCTCTGTGGTGTCTGCAGCCCTTCTTCCAGAACTCC AGCTCCCTGTCTGCAGGATGGGCTCCAGATACGTCCTTCTTTGCCCCAGAGTGCAT CCACCCAAATCAGAAATCCACTCCCAGCTGGCCAGAGCCCTTTGGACCAATATGCTT GAACCACTTGAAGCAAAACAGAGACCTGGACCTGAGAGCAGAGATGCCCATCACCT GTCCCACTCAGAAATGAGCCCTTCTGAGAACCCTCGGAATAGTAACTACAGTACCC CATCAAGCCAGCCATTGAGAACTGGGCGAGTACTTCTGTGTACAGAGTGAAGGCT TCCAATAGTGTTCACCTCTGTCCACAGCTCCGACCAGCAGACATCAAGTGGTGG CCGCCCTGGGTGACTCTCTGACTACAGCAGTGGGAGCTCGACCAAACTCCAGTGA CCTACCCACATCTTGGAGGGGACTCTCTTGGAGCATTGGAGGGGATGGGAGTGGAG ACTCACACCACACTGCCAGTATTCTGAAGAAGTTCAACCTTACCTCCTTGGCTTCT CTACCAGCAGCTGGGAGGGGACAGCAGGACTAAATGTGGCAGCGGAAGGGGCCAGAGC TAGGAGGACATGCCAGCCAGGCTGGGACCTGGTAGAGCAATGAACCAAGTACGCC ATACACTTTTCAAGAACTGGAAGATAATAACCTGTTTATAGGCGGCAATGACCTCT GTGATTTCTGCAATGATCTGGTAGGTGAATATGTTTCCAGCAGTCCAAACAGGCCCTGGA CATCCTCTCTGAGGAGCTCCCAAGGGCTTTCGTCAACGTGGTGGAGGTCTGAGGCTG GCTAGCCTGTACCAAGGCCAAGCGGGAAATGTGCCATGCTGGCAGCTCAGAACCACT GCCTTGCCTCAGACACTCGAAAGCTCCCTGGAGAAGCAAGAACTGAAGAAAGTGAA CTGGAACCTCCAGCATGGCATCTCCAGTTTCTCTACTGGCACCAATACACAGCGT GAGGACTTTGCGGTGTGGTGCAGCCTTCTTCCAAAACACTCACCCTCACTGAACA GAGGGGACACTGACCTCACCTTCTTCTCCGAGGACTGTTTCTACTTCAGACCGCGG GCATGCCGAGATGGCCATGCACTCTGGAACAACATGCTGGAACCACTGGGCGGCAAG ACTACCTCCAACAACCTTACCCACAGCCGAGCCAACTCAAGTGGCCCTCTCTGTGA GTCCTTACCTTACACCTCGGGAACAGCCGATTGCTCCAGCAGGCTGAAGAAGC CCCCGAGGTGCTCTACTGGGCTGTCCAGTGGCAGCGGGAGTCCGCCCTGTGGTGGGC ATCATCGGGACAGTGGTCTGAGGTCAGGAGAGGTGGCCGAGGGAAGATCTCTCAA TGAGCCTGCGCACTGTGGCCCTTAGGCCCGGG</p>
	<p>ORF Start: ATG at 1 ORF Stop: TAG at 4258</p>
	<p>SEQ ID NO: 82 1419 aa MW at 158435.1kd</p>
NOV24a, CG57399-01 Protein Sequence	<p>MTWDTALWTSVFLIGLLPTLGFANCILQTSKGMCTLRGRYPQPPQPLCLSPVHQLR PADIKVVAALGNDETFOESGAGQLSEDPDPRQWSWPQACLPGVKKEMQDVVGERTPSRR RSLRRREALVPAAGKESLCRQDIFISLLEIKHFPSPQDINLEKDWKLVTFLFIGVND LCHYCPVQGPVIDLGGMDTLHSLQLPRAFNVVVEVMELASLYQQGQGCAMLAAQEA WNSLLASSRYSEQESFTVVFPFFYETTPSDPRLQDSTTLAWHLWNRMMEPAGEKDEP LSVKHGRPMKPSQESPYLFSYRNSNYLTRLQKPKDQLVREGAERCPDKDPSTVPT SVHRLKPADINVIGALGDSLTAAGNAGSTPGNVLDVLTQYRGLSWVGGDENIGTVTT LADILREFNPSLKGFSVGTGKETSPNAFLNQAVAGGRAEQARRLDLMDNDTRLHFQE DWKIIITFIGGNDLDFCNDLVHYSQNFNTDNIGKALDILHAESYPRAFVNLVTVLE IVNLRRELYQEKVKYCPMILRSLCPVLKFDNDSTELATLIEFNKKFQEKTHQLIESG RYDTREDFTVVQPFENVDMPKTQGLPDNSFFAPDCFFHSSKSHSRAASALWNNML EPVGQKTRHKFENKINITCPSQVQPLRTYKNSMQGHGTWLPDRDRAPSALHPTSVH ALRPADIQVVAALGDSLTAAGNIGSKPDDLDPVTTQYRGLSYAGGDSLENVTLP SILREFNRNLTGYAVGTGDANDTNAFLNQAVPGAKARDLMSQVQTLQMCKDDHRVNF HEDWKVITVLIGGSDLCDYCTDSNLYSAANFVHHLRNLVDLHREVPVRLVNLVDFLN PTIMRQVFLGNPDKCPVQASVLCNCVLTRENSQELARLEAFSRAQSSMRELTVGS RYDTQEDFSVVLQPFQNIQLPVLQDGLPDTFFAPDCIHPNKFHSLARALWTNML EPLGSKTETDLRAEMPITCPTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCTEWKA SNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSDLPTSWRGLSWSIGDGNLE</p>

	THTTLPSTLKKFNPYLLGFSTSTWEGTAGLNVAEAGARRRDMPAQAWDLVERMKNSP IHFQEDWKIITLFIGGNDLDFCNDLVGEYVQHIQQALDILSEELPRAFPVNVVEVMEL ASLYQGGGKCAMLAAQNNCTCLRHSQSSLEKQELKKVNNWLQHGISSFSYWHQYTOR EDFAVVVQPFQNTLTPLNRGDTDLTFFSEDCFHFSRDRGHAEMAIALWNNMLEPVGRK TTSNNFTHSRALKCPSPVSPYLYTLRNSRLLPDQAEAEVLYWAVPVAAGVGLVVG IIGTVVWRRCRRGRREDPPMSLRVAL		
	SEQ ID NO: 83	1624 bp	
NOV24b, CG57399-02 DNA Sequence	GCCGGCTGACATCAATGTAATTGGAGCCCTGGGTGACTCTCTCACGGCAGGCAATGGG GCCGGGTCCACACCTGGGAACGCTCTTGGACGCTTTGACTCAGTACCGAGGCTGTCTCT GGAGCGTCGGCGGAGATGAGAACATCGGCACCGTTACCACCTGGCGAACATCCTCCG GGAATTCACACCTTCCCTGAAGGGCTTCTCTGTTGGCACTGGGAAAGAAACAGTCTCT AATGCCTTCTTAAACAGGCTGTGGCAGGAGGCCGAGCTGAGGATCTACCTGTCCAGG CCAGGAGGCTGGTGGACCTGATGAAGAATGACACGAGGATACACTTTCAGGAAGACTG GAAGATAATAACCTGTTTATAGGCGGCAATGACCTCTGTGATTTCTGCAATGATCTG GTCCACTATTCTCCCAGAACTTCACAGACAACATTGGAAGGCCCTGGACATCTCTCC ATGCTGAGGTTCTCGGGCATTGTGAACCTGGTGACGGTGCTTGAGATCGTCAACCT GAGGGAGCTGTACCAGGAGAAAAAGTCTACTGCCCAAGGATGATCCTCAGGTCTCTG TGTCCTCTGTCTCTGAAGTTTGATGATAACTCAACAGAACTTGCTACCTCATCGAAT TCAACAAGAAGTTTCAGGAGAAGACCCACCACTGATTGAGAGTGGGCGATATGACAC AAGGGAAGATTTTACTGTGGTTGTGCAGCCGTTCTTTGAAAACGTGGACATGCCAAAG ACCTCGGAAGGATTGCCTGACAACTCTTCTTCGCTCTGACTGTTTCCACTTCAGCA GCAAGTCTCACTCCCGAGCAGCCAGTGTCTCTGGAACAATATGCTGGAGCCTGTGTGG CCAGAAGACGACTCGTCATAAGTTTGAAAAACAAGATCAATATCACATGTCCGAACAG GTCCAGCCGTTTCTGAGGACCTACAAGAACAGCATGCAGGGTCATGGGACCTGGCTGC CATGCAGGGACAGAGCCCTTCTGCCTTGCAACCTACCTCAGTGCATGCCCTGAGACC TGCAGACATCCAAGTTGTGGCTGTCTGGGGGATTCTCTGACCGCTGGCAATGGAATT GGCTCCAAACAGACGACCTCCCCGATGTCAACACAGATATCGGGGACTGTGCATACA GAGAAAGTAAACAGGGTTCTTATCAGACTCCTGGGTGAGCAATCAACAGGAAATG CACCAGAAAAGCACCAAATCCCTGAATCTTCACTCCCGCTTGCATGTATACGTGTA CAGTGGTGTTCCTACGTCTCTGTTACTGTCTTTATGTGTTTATTCTGATGTTGTCTTG TAGTCACACAGCTGCCTTTACATATATGTACACATCTGCACAGAAAACCTCTGAACCC CATCGCACACTTCGAGAGGCCATAACCAAGACACAATCACAATCAGCCATGTCTTGAA AGATTAGCAATTCGACAAGAGGAAAGGGTGAGAAAGGGCATCCCGAACACGGAAGTGG AGAAGCTCAGGTGTGTTCAGGCGAGCGGTTGCGTGTAGATATTCTCAAGTTTCTTTCT CTCTAATAAAGTTCTCATTCTGTAGGCTTCAAAGTAAGTGGCGAGTAGCTCAGAAT		
	ORF Start: ATG at 311	ORF Stop: TGA at 1241	
	SEQ ID NO: 84	310 aa	MW at 35240.6kD
NOV24b, CG57399-02 Protein Sequence	MKNDTRIHFQEDWKIITLFIGGNDLDFCNDLVHYSQNFNDNIGKALDILHAEVPR FVNLVTVLEIVNLRELYQEKKVYCPRLMLRSLCPCVLKFDNSTELATLIEFNKFFQE KTHQLIESGRYDTRDFTVVVQPFENVMPKPTSEGLPDNSFFAPDFHFSKSHSRA ASALWNNMLEPVGQKTRHKFENKINITCPNQVQPFRLTYKNSMQHGTWLPDRDRAP SALHPTSVHALRPADIQVVAALGDSLTAGNGIGSKPDDLDPVTTQYRGLSYRESKPGF LSDSWVSKSNRKCTRKAPNP		
	SEQ ID NO: 85	4425 bp	
NOV24c, CG57399-03 DNA Sequence	CTGGAGCATTCTGGCATGGGGCTGCGGCCAGGCATTTTCTCTCTGGAGCTGCTGCTGC TTCTGGGGCAAGGTACCCCTCAGATCCATACCTCTCTAGAAAGAGTACATTGGAAGG GCAGCTATGGCCAGAGACAGTTCACTCTCTGAAGCCTTCTGATATTAAATTTGTGGCA GCCATTGGCAATCTGGAATTTGTGCCAGACCCAGGGACGGGCGATCTGGAGAAGCAAG ACGAAAGGCCACAGCAGGTGTGATGGGAGTGATGACAGTCTCTTTCAGACATCATCAG ATATTTCACTCTTCTGTTCCAATGCCCTGTGTGCCACACTGGAAGAGAGTCTATACCC CAGCATGGTGTCTGAGGACTTGTGGATTGAGGCTCAAGAACTGGTGAGAAACATGAAAG AGAACCAACTTGACTTTCAATTTGACTGGAAGCTCATCAATGTGTTCTTTCAGTAATGC AAGCCAGTGTTTACCTGTGCCCCCTCTGTCTCAACAGAAATGGGCTTGCGGCGGGCGGTG GATGAGCTGATGGGGGTGCTGGACTACCTGCAGCAGGAGGTGCCAGAGCATTTGTAA ACCTGGTGGACCTCTCTGAGGTGTCAGAGGTCTCTCGTCAGTATCACGGCACTTGGCT CAGCCCTGCACAGAGCCCTGTAATTGCTCAGAGGAGACCAACCGGCTGGCCAAAGGTG GTGATGCAGTGGTCTTATCAGGAAGCCTGGAACAGCCTCCTGGCCTCCAGCAGGTACA GTGAGCAGGAGTCTTCAACCGTGGTTTTCCAGCCTTCTTCTATGAGAACACCCCATC TGACCCCGACTCCAGGATTCTACCACGCTGGCCTGGCATCTCTGGAATAGGATGATG GAGCCAGCAGGAGAGAAAGATGAGCCATTGAGTGTAAACACGGGAGGCCAATGAAAT GTCCCTCTCAGGAGAGCCCCATCTGTCTCAGCTACAGAAACAGCAACTACCTGACCAG ACTGCAGAAACCCCAAGACAAGCTTGAGGTAAGAGAGGAGCGGAAATCAGATGTCTCT GACAAAGACCCCTCCGATACGGTTCCCACTCAGTTCATAGGCTGAAGCCGGCTGACA TCAACGTAATTGGAGCCCTGGGTGACTCTCTCACGGCAGGCAATGGGGCGGGTCCAC ACCTGGGAACGTCTTGGACGCTCTGACTCAGTACCGAGGCTGTCTCTGGAGCGTGGGC GGAGATGAGAACATCGGCACCGTTACCACCTTGGCGGACATCTCCGGGAATTCAACC CTTCCCTGAAGGGCTTCTCTGTTGGCACTGGGAAAGAAACAGTCTTAATGCCTTCTT AAACCAGGCTGTGGCAGGAGGCCGAGCTGAGCAGGCCAGGAGGCTGGTGGACCTGATG AAGAATGACACGAGGATACACTTTCAGGAAGACTGGAAGATAATAACCTGTTTATAG CGGCAATGACCTCTGTGATTTCTGCAATGATCTGGTACACTATTCTCCCGAACTT CACAGACAACATTGGAAGGCCCTGGACATCTCCATGCTGAGGTTCTCTGGGCATTT		

170

YTQREDFAVVVQPPFQNTLTPLNRGDTDLTFFSEDCFHFSRGRHAEMAIALWNNMLEP VGRKTTSSNFTHSRAKLKCPSPESPYLYTLRNSRLLPDQAEAEPEVLYWAVPVAAGVG LVVGIIGTVVWRRCRRGGRRDPPMSLRTVAL

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 24B.

Table 24B. Comparison of NOV24a against NOV24b through NOV24c.		
Protein Sequence	NOV24a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV24b	454..748	283/295 (95%)
	1..293	285/295 (95%)
NOV24c	27..1419	1211/1426 (84%)
	23..1423	1261/1426 (87%)

Further analysis of the NOV24a protein yielded the following properties shown in Table 24C.

Table 24C. Protein Sequence Properties NOV24a	
PSort analysis:	0.6850 probability located in endoplasmic reticulum (membrane); 0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.1080 probability located in nucleus
SignalP analysis:	Likely cleavage site between residues 24 and 25

A search of the NOV24a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 24D.

Table 24D. Geneseq Results for NOV24a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV24a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW30751	Rat phospholipase-B/lipase - Rattus rattus, 1450 aa. [JP09248190-A, 22-SEP-1997]	50..1403 60..1447	911/1404 (64%) 1077/1404 (75%)	0.0
ABB11053	Human phospholipase B homologue,	985..1203 45..267	205/224 (91%) 213/224 (94%)	e-117

	267 aa. [WO200157188-A2, 09-AUG-2001]			
AAM25824	Human protein sequence SEQ ID NO:1339 - Homo sapiens, 267 aa. [WO200153455-A2, 26-JUL-2001]	985..1203 45..267	205/224 (91%) 213/224 (94%)	e-117
AAM95420	Human reproductive system related antigen SEQ ID NO: 4078 - Homo sapiens, 148 aa. [WO200155320-A2, 02-AUG-2001]	979..1106 4..133	110/130 (84%) 117/130 (89%)	3e-56
ABB11237	Human phospholipase homologue, SEQ ID NO:1607 - Homo sapiens, 132 aa. [WO200157188-A2, 09-AUG-2001]	393..478 43..132	84/90 (93%) 86/90 (95%)	3e-40

In a BLAST search of public sequence databases, the NOV24a protein was found to have homology to the proteins shown in the BLASTP data in Table 24E.

Table 24E. Public BLASTP Results for NOV24a				
Protein Accession Number	Protein/Organism/Length	NOV24a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q05017	Phospholipase ADRAB-B precursor (EC 3.1.-.-) - Oryctolagus cuniculus (Rabbit), 1458 aa.	6..1416 2..1456	1042/1466 (71%) 1179/1466 (80%)	0.0
O70320	PHOSPHOLIPASE B - Cavia porcellus (Guinea pig), 1463 aa.	7..1414 3..1458	965/1474 (65%) 1135/1474 (76%)	0.0
O54728	PHOSPHOLIPASE B - Rattus norvegicus (Rat), 1450 aa.	50..1403 60..1447	911/1404 (64%) 1077/1404 (75%)	0.0
Q96DP9	CDNA FLJ30866 FIS, CLONE FEBRA2004110, HIGHLY SIMILAR TO PHOSPHOLIPASE ADRAB-B PRECURSOR (EC 3.1.-.-) - Homo sapiens (Human), 270 aa.	454..714 1..259	257/261 (98%) 258/261 (98%)	e-151
Q9N2Z4	HYPOTHETICAL 41.4 KDA PROTEIN - Caenorhabditis elegans, 377 aa.	343..673 37..369	130/343 (37%) 202/343 (57%)	1e-59

PFam analysis predicts that the NOV24a protein contains the domains shown in the Table 24F.

Table 24F. Domain Analysis of NOV24a

Pfam Domain	NOV24a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Lipase_GDSL: domain 1 of 3	360..484	54/147 (37%) 116/147 (79%)	4.8e-42
Lipase_GDSL: domain 2 of 3	705..834	57/147 (39%) 116/147 (79%)	4.5e-44
SecA_protein: domain 1 of 1	834..851	10/20 (50%) 17/20 (85%)	4.9
Vitellogenin_N: domain 1 of 1	1107..1124	8/18 (44%) 17/18 (94%)	3.8
Lipase_GDSL: domain 3 of 3	1062..1185	48/147 (33%) 114/147 (78%)	6.3e-37

Example 25.

The NOV25 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 25A.

Table 25A. NOV25 Sequence Analysis

	SEQ ID NO: 87	1348 bp
NOV25a, CG59311-01 DNA Sequence	CTGGGTCGCCCCCTGTTCTACCCAGATTGGGATGGCAGCGAGCTGATCCTGGAGCCCG CGGGCCGCTGCTGCTGGGACGAGCCGCTGCGCATCGCAGTGGCGGCCCTGGCCCCGGA GCAGCCAGTCACGCTGCGCAGCTCCCTGCGCGACGAAGAGGGCGCGCTCTTCCGGGCC CACGCGCGCTACCGTGCCGACGCGCCGCGACGAGCTGGACCTGGAGCGCGCGCCCGCGC TGGGAGGCAGCTTCGCGGGGCTCCAGCCCATGGGGCTGCTGTGGGCGTGGAGCCCGA GAAAGCCTTGGTGCGGCTGGTGAAGCGCGACGTGCGGACGCCCTTCGCGTGGAGCTG GAAGTGCTGGACGCCACGACACCGAGCCCGGGCGGCTGCTGTGCTGGCGCAGAACAA AGCGGACCTTCTCGGGCGGGGGTGGCGCGGAGCCGGTGCGCGCGGGCCCGTGCG CGCCGCGCTCTTCTGCGCCGGATAGGGGGCCCTTCTGGGATCATGTGATCTGTTT GGGAGCAGCAGGGGCCCTTGTGAATACAGGGCCAGCCTCTGGCGGACATGGTTTG CTGTGCTTGCCCTGGCTTATTTAGATTGTAAGACCTCCCGAAGATCTGAATGATGT ACATCTGGAGTACTTTGAAGAAGCCGTGGACTTTATGCTGCAGCATCCAAAGGTGAAA GGTCTAGTATTGCGCTTCTTGGATTTTCAAAGGAGGTGACCTGTGTCTCTCAATGG CTTCTTTCTGAAGGGCATCACAGCCACTGTACTTATCAATGCCTGTGTAGCCAACAC AGTAGCTCCTCTACATTACAAGGATATGATTATTCCTAACTTGTGATGATCTAGGA AAAGTAAAAATCACTAAGTCAGGATTCTCACTTTTATGGACACTTGGAGCAATCCAC TGGAGGAACACAATCACCAGTCTTGTTCATTGGAAGGCGCAGGTGCCCTTCTT GTTTATTGTTGGCATGGATGATCAAAGCTGGAAGAGTGAATTCTATGCTCAGATAGCC TCTGAAAGGCTACAAGCTCATGGAAAGAAAGACCCAGATAATCTGTTACCCAGAAA CTGGTCACTGTATTGACCCACCTTATTTCTCTCTCTAGAGCTTCTGTGACGCTGT TTTGGGTGAGGCAATATTCTATGGAGGTGAGCCAAAGGCTCACTCAAAGGCACAGGTA GATGCTGCGCAGCAAAATCAAACCTTTCTTCATAAAATCTCAATGGTAAAAAATCTG TCAAGCACAGCAAAATATAACATTGTAGCCACAGACCAGATACCATTAATAAAAAATCC TATTCATACAACCT	
	ORF Start: ATG at 31	ORF Stop: TAA at 1294
	SEQ ID NO: 88	421 aa MW at 46815.4kD
NOV25a, CG59311-01 Protein Sequence	MAATLILEPAGRCWDEPLRIAVRGLAPEQPVTLRSLRDEEGALFRAHARYRADARD ELDLERAPALGGSFAGLQPMGLLWALEPEKALVRLVKRDVRTPFAVELEVLDGHDTEP GRLLCLAQNKRFDLRPGVRRPVRAGPVRAALFLPPDRGPFPGIIDLPSSRGLCEYR ASLLAGHGFVLAAYPRFEDLPEDLNDVHLEYFEEAVDFMLQHPKVGPSIALLGFS KGGDLCLSMASFLKGITATVLIACVANTVAPLHYKDMIIPKLVDLDGKVKITKSGFL TFMDTWSNPLEEHNHQSILVPLEKAQVPFLFIVGMDQSWKSEFYAQIASERLQAHGKE	

	RPQIIICYPETGHCIDPPYFPPSRASVHAVLGEAIFYGGEPAHSAKAQVDAWQQIQTF HKHLNGKKS VKHSKI		
	SEQ ID NO: 89	1021 bp	
NOV25b, CG59311-02 DNA Sequence	AGATTGGGATGGCAGCGACGCTGATCCTGGAGCCCGCGGGCCGCTGCTGCTGGGACGA GCCGCTGCGCATCGCAGTGCAGCGGCTGGCCCCGGAGCAGCCAGTCACGCTGCGCAGC TCCCTGCGCGACGAAGAGGGCGCGCTCTTCCGGGCCACGCGCGCTACCGTGCCGACG CCTCTAATCCCGGCACTTTGGGGGGCCAAAGGCAGGGGGCCCTTTCTGGGATCATTGA TCTGTTTGGGAGCAGCAGGGGCCCTTTGTGAATACAGGGCCAGCCTCCTGGCCGGACAT GGTTTTGCTGTGCTTGCCCTGGCTTATTTCAAGATTGAAGACCTCCCGAAGATCTGA ATGATGTACATCTGGAGTACTTTGAAGAAGCCGTGGACTTTATGCTGCAGCATCCAA GGTGAAAGGTCTAGTATTGCGCTTCTTGGATTTCCTCAAAGGAGGTGACCTGTGTCTC TCAATGGCTTCTTCTTGAAGGGCATCACAGCCACTGTACTTATCAATGCCTGTGTAG CCAACACAGTAGCTCCTCTACATTACAAGGATATGATTATTTCTAACTTGTGATGA TCTAGGAAAAGTAAAAATCACTAAGTCAGGATTCTCACTTTTATGGACACTTGGAGC AATCCACTGGAGGAACAATCACCAGTCTTGTGTTCCATTGGAAAAGGCGCAGGTGC CCTTCTTGTATTATTTGGCATGGATGATCAAAGCTGGAAGAGTGAATTCTATGCTCA GATAGCCTCTGAAAGGCTACAAGCTCATGGGAAAGAAAGACCCAGATAATCTGTTAC CCAGAACTGGTCACTGTATTGACCCACCTTATTTCTCTCTTAGAGCTTCTGTGC ACGCTGTTTTGGGTGAGGCAATATTCTATGGAGGTGAGCCAAAGGCTCACTCAAAGGC ACAGGTAGATGCTGGCAGCAAATTCAAACCTTCTTCCATAAACATCTCAATGGTAAA AAATCTGTCAAGCACAGCAAATATAACATTGTAG		
	ORF Start: ATG at 9	ORF Stop: TAA at 1011	
	SEQ ID NO: 90	334 aa	MW at 36926.0kD
NOV25b, CG59311-02 Protein Sequence	MAATLILEPAGRCWCDEPLRIAVRGLAPEQPVTLRTSLRDEEGALFRAHARYRADASN PGTLGGQGRGPPFGIIDLFGSSRGLCEYRASLLAGHGFAVLALAYFRFEDLPEDLNDV HLEYFEEAVDFMLQHPKVGPSIALLGFSKGGDLCLSMASFLKGITATVLINACVANT VAPLHYKDMIIPKLVDDLGVKITKSGFLTFMDTWSNPLEEHNHQS LVPLEKAQVPFL FIVGMDDQSWKSEFYAQIASERLQAHGKERPQIIICYPETGHCIDPPYFPPSRASVHAV LGEAIFYGGEPAHSAKAQVDAWQQIQTFHKLNGKKS VKHSKI		
	SEQ ID NO: 91	1021 bp	
NOV25c, CG59311-03 DNA Sequence	AGATTGGGATGGCAGCGACGCTGATCCTGGAGCCCGCGGGCCGCTGCTGCTGGGACGA GCCGCTGCGCATCGCAGTGCAGCGGCTGGCCCCGGAGCAGCCAGTCACGCTGCGCAGC TCCCTGCGCGACGAAGAGGGCGCGCTCTTCCGGGCCACGCGCGCTACCGTGCCGACG CCTCTAATCCCGGCACTTTGGGAGGCCAAGGCAGGGGGCCCTTTCTGGGATCATTGA TCTGTTTGGGAGCAGCAGGGGCCCTTTGTGAATACAGGGCCAGCCTCCTGGCCGGACAT GGTTTTGCTGTGCTTGCCCTGGCTTATTTCAAGATTGAAGACCTCCCGAAGATCTGA ATGATGTACATCTGGAGTACTTTGAAGAAGCCGTGGACTTTATGCTGCAGCATCCAAA GGTGAAAGTCTAGTATTGCGCTTCTTGGATTTCCTCAAAGGAGGTGACCTGTGTCTC TCAATGGCTTCTTCTTGAAGGGCATCACAGCCACTGTACTTATCAATGCCTGTGTAG CCAACACAGTAGCTCCTCTACATTACAAGGATATGATTATTTCTAACTTGTGATGA TCTAGGAAAAGTAAAAATCACTAAGTCAGGATTCTCACTTTTATGGACACTTGGAGC AATCCACTGGAGGAACAATCACCAGTCTTGTGTTCCATTGGAAAAGGCGCAGGTGC CCTTCTTGTATTATTTGGCATGGATGATCAAAGCTGGAAGAGTGAATTCTATGCTCA GATAGCCTCTGAAAGGCTACAAGCTCATGGGAAAGAAAGACCCAGATAATCTGTTAC CCAGAACTGGTCACTGTATTGACCCACCTTATTTCTCTCTTAGAGCTTCTGTGC ACGCTGTTTTGGGTGAGGCAATATTCTATGGAGGTGAGCCAAAGGCTCACTCAAAGGC ACAGGTAGATGCTGGCAGCAAATTCAAACCTTCTTCCATAAACATCTCAATGGTAAA AAATCTGTCAAGCACAGCAAATATAACATTGTAG		
	ORF Start: ATG at 9	ORF Stop: TAA at 1011	
	SEQ ID NO: 92	334 aa	MW at 36926.0kD
NOV25c, CG59311-03 Protein Sequence	MAATLILEPAGRCWCDEPLRIAVRGLAPEQPVTLRTSLRDEEGALFRAHARYRADASN PGTLGGQGRGPPFGIIDLFGSSRGLCEYRASLLAGHGFAVLALAYFRFEDLPEDLNDV HLEYFEEAVDFMLQHPKVGPSIALLGFSKGGDLCLSMASFLKGITATVLINACVANT VAPLHYKDMIIPKLVDDLGVKITKSGFLTFMDTWSNPLEEHNHQS LVPLEKAQVPFL FIVGMDDQSWKSEFYAQIASERLQAHGKERPQIIICYPETGHCIDPPYFPPSRASVHAV LGEAIFYGGEPAHSAKAQVDAWQQIQTFHKLNGKKS VKHSKI		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 25B.

Table 25B. Comparison of NOV25a against NOV25b through NOV25c.		
Protein Sequence		

	Match Residues	Similarities for the Matched Region
NOV25b	154..421 67..334	268/268 (100%) 268/268 (100%)
NOV25c	154..421 67..334	268/268 (100%) 268/268 (100%)

Further analysis of the NOV25a protein yielded the following properties shown in Table 25C.

Table 25C. Protein Sequence Properties NOV25a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3630 probability located in microbody (peroxisome); 0.1958 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV25a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 25D.

Table 25D. Geneseq Results for NOV25a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV25a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41490	Human polypeptide SEQ ID NO 6421 - Homo sapiens, 494 aa. [WO200153312-A1, 26-JUL-2001]	1..421 74..494	288/421 (68%) 347/421 (82%)	e-175
AAM39704	Human polypeptide SEQ ID NO 2849 - Homo sapiens, 483 aa. [WO200153312-A1, 26-JUL-2001]	1..421 63..483	288/421 (68%) 346/421 (81%)	e-175
AAY71112	Human Hydrolase protein-10 (HYDRL-10) - Homo sapiens, 483 aa. [WO200028045-A2, 18-MAY-2000]	1..421 63..483	288/421 (68%) 346/421 (81%)	e-175
AAB93479	Human protein sequence SEQ ID NO:12766 - Homo sapiens, 483 aa. [EP1074617-A2, 07-FEB-2001]	1..421 63..483	287/421 (68%) 346/421 (82%)	e-175
AAY07932				e-105

	encoded from gene 81 - Homo sapiens, 182 aa. [WO9918208-A1, 15-APR-1999]	1..181	181/181 (100%)	
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In a BLAST search of public sequence databases, the NOV25a protein was found to have homology to the proteins shown in the BLASTP data in Table 25E.

Table 25E. Public BLASTP Results for NOV25a				
Protein Accession Number	Protein/Organism/Length	NOV25a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P49753	Peroxisomal acyl-coenzyme A thioester hydrolase 2 (EC 3.1.2.2) (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128) - Homo sapiens (Human), 421 aa.	1..421 1..421	288/421 (68%) 347/421 (82%)	e-175
Q9QYR7	Peroxisomal acyl-coenzyme A thioester hydrolase 2 (EC 3.1.2.2) (Peroxisomal long-chain acyl-coA thioesterase 2) (PTE-Ia) - Mus musculus (Mouse), 432 aa.	1..421 12..432	264/421 (62%) 331/421 (77%)	e-157
O88267	Cytosolic acyl coenzyme A thioester hydrolase, inducible (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (Long chain acyl-CoA hydrolase) (CTE-I) (LACH2) (ACH2) - Rattus norvegicus (Rat), 419 aa.	1..421 1..419	268/421 (63%) 318/421 (74%)	e-153
Q9QYR9	Acyl coenzyme A thioester hydrolase, mitochondrial precursor (EC 3.1.2.2) (Very-long-chain acyl-CoA thioesterase) (MTE-I) - Mus musculus (Mouse), 453 aa.	3..413 44..452	264/411 (64%) 321/411 (77%)	e-153
O55137	Cytosolic acyl coenzyme A thioester hydrolase, inducible (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (Long chain acyl-CoA hydrolase) (CTE-I) - Mus musculus (Mouse), 419 aa.	1..413 1..411	262/413 (63%) 319/413 (76%)	e-153

PFam analysis predicts that the NOV25a protein contains the domains shown in the Table 25F.

Table 25F. Domain Analysis of NOV25a			
Pfam Domain	NOV25a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 26.

The NOV26 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 26A.

Table 26A. NOV26 Sequence Analysis			
	SEQ ID NO: 93	1375 bp	
NOV26a, CG59309-01 DNA Sequence	GGGACGCCGGACGCCGCTCCGGACATTCCGGCGCGCTTGCCACGATCTTGGACGGGTCTC GGGCTCGACCTTTGAATTCCTCCGCTCCGGCTCCAAGATGTGACGCAACGCTGATCCTG GAGCCCCCAGGCCGCTGCTGCTGGAACGAGCCGGTGCGCATTCGCGTGC GCGGCTGG CCCGGAGCAGCGGGTTACGTGCGCGCTCCCTGCGCGACGAGAAGGGCGCGCTCTT CCGGGCCCCACGCGCTACTGCGCCGACGCCCGCGGCGAGCTGGACCTGGAGCGCGCA CCCGGCTGGGCGGCAGCTTCGCGGGA CTGAGCCCATGGGGCTGCTCTGGGCCCTGG AACC CGAGAAGCCTTTTGGCGCTTCTGAAGCGGGACGTACAGATTCTCTTTGTCTGT GGAGTTGAGGTGCTGGACGCCACGACCCGAGCCTGGACGCGCTGTGTCGACGGCG CAGCAGGAGCGCCACTTCTCCCGCCAGGGGTGCGGCGCCAGTCCGTGCGAGCGGGCC GGGTGCGCGCCACGCTCTTCTGCCGCCAGGTGAGCCTGGACCTTCCAGGGATCAT TGACATCTTTGGTATTGGAGGGGGCTCTTGAATATCGAGCCAGCCTCCTTGCTGGC CATGGCTTTGCCACGTTGGCTCTAGCTTATTATAACTTTGAAGATCTCCCAATAACA TGGACAACATATCCTGGAGTACTTCGAAGAAGCCGTATGCTACATGCTTCAACATCC CCAGGTTAAAGGCCAGGCATTGGGCTTTTGGGCATTTCTTAGGAGCTGATATTGT CTCTCAATGGCCTCATTCTTGAAGATGTCTCAGCCACAGTTTCCATCAATGGATCTG GGATCAGTGGGAACACAGCCATCAACTATAAGCACAGTAGCATTCACCATTTGGGCTA TGACCTGAGGAGAATCAAGGTAGCTTTCTCAGGCCTCGTGGACATTGTGGATATAAG AATGCTCTCGTAGGAGGGTACAAGAACCCAGCATGATTCCAATAGAGAAGGCCAGG GGCCATCTGCTCATTTGTGGTCAGGATGACCATAACTGGAGAAGTGAAGTTGTATGC CCAAACAGTCTCTGAACGGTTACAGGCCCATGGAAGGAAAAACCCAGATCATCTGT TACCCTGGGACTGGGCATTACATCGAGCCTCCTTACTTCCCCTGTGCCAGCTTCCC TTCACAGATTACTGAACAAACATGTTATATGGGGTGGGGAGGCCAGGGCTCATTCTAA GGCCCAGGAAGATGCCTGGAAGCAAATCTAGCCTTCTTCTGCAACACCTGGGAGGT ACCCAGAAAACAGCTGTCCCTAAATTGTAATGCATTGTCT		
	ORF Start: ATG at 96	ORF Stop: TAA at 1362	
	SEQ ID NO: 94	422 aa	MW at 46455.1kD
NOV26a, CG59309-01 Protein Sequence	MSATLILEPPGRCCWNEPVRIAVRGLAPEQVRVTLRASLRDEKGFRAHARYCADARG ELDLERAPALGGSFAGLEPMGLLWALEPEKPFWRFLKRDVQIPFVVEVLGDHDEP GRLLCQAQHERHFLPPGVRQSVRAGRVRATLFLPPGEPGPPGIIIDIFGIGGGLLEY RASLLAGHGAFATLALAYNFEDLPNNMDNISLEYFEEAVCYMLQHPQVKGPGIGLLGI SLGADICLSMASFLKNVSATVISINGSGISGNTAINYKHSSIPPLGYDLRRIKVAFSGL VDIVDIRNALVGGYKNPSMPIEKAQGPILLIVGQDDHNWRSELYAQTVERLQAHGK EKPQIIICYPGTGHYIEPPYPLCPASLHRLLNKHVIWGGEPRAHSAQEDAWKQILAF FCKHLGGTQKTAVPKL		

Further analysis of the NOV26a protein yielded the following properties shown in Table 26B.

Table 26B. Protein Sequence Properties NOV26a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.2585 probability located in lysosome (lumen); 0.1940 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space

SignalP analysis:	No Known Signal Sequence Predicted
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A search of the NOV26a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 26C.

Table 26C. Geneseq Results for NOV26a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV26a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41490	Human polypeptide SEQ ID NO 6421 - Homo sapiens, 494 aa. [WO200153312-A1, 26-JUL-2001]	1..422 74..494	296/422 (70%) 341/422 (80%)	e-179
AAM39704	Human polypeptide SEQ ID NO 2849 - Homo sapiens, 483 aa. [WO200153312-A1, 26-JUL-2001]	1..422 63..483	296/422 (70%) 341/422 (80%)	e-179
AAY71112	Human Hydrolase protein-10 (HYDRL-10) - Homo sapiens, 483 aa. [WO200028045-A2, 18-MAY-2000]	1..422 63..483	296/422 (70%) 341/422 (80%)	e-179
AAB93479	Human protein sequence SEQ ID NO:12766 - Homo sapiens, 483 aa. [EP1074617-A2, 07-FEB-2001]	1..422 63..483	295/422 (69%) 340/422 (79%)	e-178
AAY07932	Human secreted protein fragment encoded from gene 81 - Homo sapiens, 182 aa. [WO9918208-A1, 15-APR-1999]	242..422 1..181	93/181 (51%) 123/181 (67%)	2e-48

In a BLAST search of public sequence databases, the NOV26a protein was found to have homology to the proteins shown in the BLASTP data in Table 26D.

Table 26D. Public BLASTP Results for NOV26a				
Protein Accession Number	Protein/Organism/Length	NOV26a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9QYR8	PEROXISOMAL LONG CHAIN ACYL-COA THIOESTERASE IB - Mus musculus (Mouse), 421 aa.	1..422 1..421	312/422 (73%) 362/422 (84%)	0.0
P49753	Peroxisomal acyl-coenzyme A thioester hydrolase 2 (EC 3.1.2.2) (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128) - Homo sapiens (Human), 421 aa.	1..422 1..421	296/422 (70%) 341/422 (80%)	e-178
Q9QYR7	Peroxisomal acyl-coenzyme A thioester hydrolase 2 (EC 3.1.2.2) (Peroxisomal long-chain acyl-coA thioesterase 2) (PTE-Ia) - Mus musculus (Mouse), 432 aa.	1..422 12..432	281/424 (66%) 333/424 (78%)	e-163
O55137	Cytosolic acyl coenzyme A thioester hydrolase, inducible (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (Long chain acyl-CoA hydrolase) (CTE-I) - Mus musculus (Mouse), 419 aa.	1..422 1..419	275/423 (65%) 330/423 (78%)	e-162
O88267	Cytosolic acyl coenzyme A thioester hydrolase, inducible (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (Long chain acyl-CoA hydrolase) (CTE-I) (LACH2) (ACH2) - Rattus norvegicus (Rat), 419 aa.	1..422 1..419	276/423 (65%) 329/423 (77%)	e-162

PFam analysis predicts that the NOV26a protein contains the domains shown in the Table 26E.

Table 26E. Domain Analysis of NOV26a			
Pfam Domain	NOV26a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DLH: domain 1 of 2	144..188	17/52 (33%) 32/52 (62%)	63
DLH: domain 2 of 2	394..411	9/18 (50%) 13/18 (72%)	2.6

Example 27.

The NOV27 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 27A.

Table 27A. NOV27 Sequence Analysis			
	SEQ ID NO: 95	1333 bp	
NOV27a, CG57364-01 DNA Sequence	<p>CCTGGCCCCAAGCTCCCCACTCTGGTGCCCCGAGCAGCCCTGTGGGCAAGCAGCCGC CGCCATGGCCGAGCACCTGGAGCTGCTGGCAGAGATGCCCATGGTGGGCAAGATGAGC ACACAGGAGCGGCTGAAGCATGCCAGAAAGCGGCGGCCAGCAGGTGAAGATGTGGG CCCAGGCTGAGAAGGAGGCCAGGGCAAGAAGGGTCTGGGGAGCGTCCCCGGAAGGA GGCAGCCAGCCAAGGGCTCCTGAAGCAGGTCTCTTCCCTCCCACTGTTGTCTTCTG GAGGCCGCTGCCCAAATGACCTGGAAGAAGTCCGCCAGTTCTTGTGGAGTGGGGTCA GCCCTGACTTGGCCAACGAGGACGGCCTGACGGCCCTGCACCCAGTGTGTCATTGATGA TTTCCGAGAGATGGTGCAGCAGCTCCTGGAGGCTGGGGCCAACATCAATGCCTGTGAC AGTGAGTGTGGAGCGCCTCTGCATGCTGCGGCCACCTGCGGCCACCTGCACCTGGTGG AGCTGCTCATCGCCAGTGGCGCCAATCTCCTGGCGGTCAACACCGACGGGAACATGCC CTATGACCTGTGTGATGATGAGCAGACGCTGGACTGCCTGGAGACTGCCATGGCCGAC CGTGGCATCACCCAGGACAGCATCGAGGCCGCCCGGGCCGTGCCAGAACTGCGCATGC TGGACGACATCCGAGCCGGCTGCAGGCCGGGGCAGACCTCCATGCCCCCTGGACCA CGGGGCCACGCTGCTGCACGTGCGAGCCGCCAACGGGTTGAGCGAGGCGGCTGCCCTG CTGTGCGAACACCGAGCCAGCCTGAGCGCTAAGGACCAAGACGGCTGGGAGCCGCTGC ACGCCGCGGCTACTGGGGCCAGGTGCCCTTGGTGGAGTGTCTGTGTGCGCACGGGGC CGACCTGAACGCAAAAGTCCCTGATGGACGAGACGCCCCCTTGATGTGTGCGGGGACGAG GAGGTGCGGGCCAAAGCTGCTGGAGTGAAGCACAAGCAGCAGCCCTCTGCGCGCCC AGAGCCGCCAGCGCTCCTTGTGCGCGCCCGCACCTCCAGCGCCGGCAGCCGCGGGAA GGTGGTGAAGCGGGATGAGCCTAACCAGCGCAGCGGCTGACGCATGTCCCAAGAGCG GCGCGCCAGCAGGTGAAGATGTGGGCCAGGCTGAGAAGGAGGGCCAGGCAAGAAG GGTCTTGGGAGCGTCCCCGGAAGGAGGCAGCCAGCCAAGGGCTCTGAAGCAGGTCC TCTTCCCTCCAGTGTGTCTTCTGGAGGCCGCTGCCGAAATGACCTGGAAGAAG</p>		
	ORF Start: ATG at 63	ORF Stop: TGA at 1194	
	SEQ ID NO: 96	377 aa	MW at 41019.9kD
NOV27a, CG57364-01 Protein Sequence	<p>MAEHLLELLAEMPMVGRMSTQERLKHAQKRRQQVKMWAQAEKEAQKKGPGERPRKEA ASQGLLKQVLFPPSVVLEAAARNDLLEVRQFLGSGVSPDLANEDGLTALHQCCIDDF REMVQQLLEAGANINACDSECTPLHAAATCGHLHLVELLIASGANLLAVNTDGNMPY DLCDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSLQAGADLHAPLDHG ATLLHVAANGFSEAAALLLEHRASLSAKDQDGWEPLHAAAYWGQVPLVELLVAHGAD LNAKSLMDETPLDVCGDEVRAKLLLELKHKHDALLRAQSRQSRLLRRRTSSAGSRGKV VRRDEPNPAQRLTHVPEARPAGEDVPGP</p>		

Further analysis of the NOV27a protein yielded the following properties shown in Table 27B.

Table 27B. Protein Sequence Properties NOV27a	
PSort analysis:	0.3000 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.1547 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV27a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 27C.

Table 27C. Geneseq Results for NOV27a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV27a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM40636	Human polypeptide SEQ ID NO 5567 - Homo sapiens, 440 aa. [WO200153312-A1, 26-JUL-2001]	89..351 1..263	262/263 (99%) 263/263 (99%)	e-151
AAM38850	Human polypeptide SEQ ID NO 1995 - Homo sapiens, 410 aa. [WO200153312-A1, 26-JUL-2001]	119..351 1..233	233/233 (100%) 233/233 (100%)	e-132
AAM78864	Human protein SEQ ID NO 1526 - Homo sapiens, 567 aa. [WO200157190-A2, 09-AUG-2001]	1..351 1..348	209/351 (59%) 265/351 (74%)	e-118
ABB11817	Human KIAA0823 protein homologue, SEQ ID NO:2187 - Homo sapiens, 536 aa. [WO200157188-A2, 09-AUG-2001]	45..354 3..318	173/316 (54%) 226/316 (70%)	3e-94
AAM79848	Human protein SEQ ID NO 3494 - Homo sapiens, 536 aa. [WO200157190-A2, 09-AUG-2001]	45..354 3..318	173/316 (54%) 226/316 (70%)	3e-94

In a BLAST search of public sequence databases, the NOV27a protein was found to have homology to the proteins shown in the BLASTP data in Table 27D.

Table 27D. Public BLASTP Results for NOV27a				
Protein Accession Number	Protein/Organism/Length	NOV27a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96I34	UNKNOWN (PROTEIN FOR MGC:14333) - Homo sapiens (Human), 528 aa.	1..351 1..351	351/351 (100%) 351/351 (100%)	0.0
Q923M0	MYOSIN PHOSPHATASE TARGETING SUBUNIT 3 MYPT3 - Mus musculus (Mouse), 524 aa (fragment).	1..351 1..351	301/351 (85%) 320/351 (90%)	e-171
AAL62093	PROTEIN PHOSPHATASE 1 REGULATORY SUBUNIT 16B - Mus musculus (Mouse), 568 aa.	1..351 1..348	210/351 (59%) 266/351 (74%)	e-118
Q95N27				e-118

	Bos taurus (Bovine), 568 aa.	1..348	266/351 (74%)	
Q96T49	CAAX BOX PROTEIN TIMAP - Homo sapiens (Human), 567 aa.	1..351 1..348	209/351 (59%) 265/351 (74%)	e-117

PFam analysis predicts that the NOV27a protein contains the domains shown in the Table 27E.

Table 27E. Domain Analysis of NOV27a			
Pfam Domain	NOV27a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ank: domain 1 of 5	70..102	8/33 (24%) 20/33 (61%)	99
ank: domain 2 of 5	103..135	16/33 (48%) 26/33 (79%)	7.1e-08
ank: domain 3 of 5	136..168	15/33 (45%) 26/33 (79%)	2.9e-07
ank: domain 4 of 5	231..263	16/33 (48%) 24/33 (73%)	2e-06
ank: domain 5 of 5	264..296	16/33 (48%) 27/33 (82%)	2.7e-08

Example 28.

The NOV28 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 28A.

Table 28A. NOV28 Sequence Analysis		
	SEQ ID NO: 97	1719 bp
NOV28a, CG59348-01 DNA Sequence	CGGGCACAGGCTCACCTCGAGTGGCACAGGAATCCAGGTAGATGACGGCGGCCGCG GCTGGTGTGTCAGGGTCGGCAGCTCCCGCGGCAGCGGCCGGCGCCCCGGGATCTGGGG GCGCACCTCAGGGTCGACGGGGGTGCTGATCGGGGACAGGCTGTACTCCGGGGTGCT CATCACCTTGGAGAAGTGCCTCCTGCGCTGACGACAAGCTCCGTTTCACGCCGTCCATG TCGAGCGGCCTCGACCCGACACAGAGACCGACCTCCGCGTGGTGGGCTGCGAGCTCA TCCAGGCGGCCGGTATCCTGCTCCGCTGCCGAGGTGGCCATGGCTACCGGGCAGGT GTTGTTCCAGCGGTTCTTTTATACCAAGTCCTTCGTGAAGCACTCCATGGAGCATGTG TCAATGGCCTGTGTCACCTGGCTTCCAAGATAGAAGAGGCCCAAGACGCATACGGG ACGTCATCAATGTGTTTCACCGCCTTCGACAGCTGAGAGACAAAAAGAAGCCCGTGCC TCTACTACTGGATCAAGATTATGTTAATTAAAGAACCAAATTATAAGGCGGAAAGA CGAGTTCTCAAGAGTTGGGTTTCTGCGTCCATGTGAAGCATCCTCATAAGATAATCG TTATGTACCTTCAGGTGTTAGAGTGTGAGCGTAACCAACACCTGGTCCAGACCTCATG GAATTACATGAACGACAGCCTTCGCACCGACGCTTTCGTGCGGTTCCAGCCAGAGAGC ATCGCCTGTGCTGCATTTATCTTGCTGCCCGGACGCTGGAGATCCCTTTGCCCAATC GTCCCCATTGGTTTCTTTGTTTGGAGCAACTGAAGAAGAAATTCAGGAATCTGCTT AAAGATCTTGACGCTTATGCTCGGAAAAAGGTTGATCTCACACACCTGGAGGTTGAA GTGGAAGAAAGAACGACGCTATCGAAGAGGCAAGGCCCAAGCCCGGGGCTGTTGC CTGGGGGCACACAGGTGCTGGATGGTACCTCGGGGTTCTCTCTGCCCCCAAGCTGGT GGAATCCCCCAAGAAAGTAAAGGGAGCAAGCCTTCCCCACTGTCTGTGAAGAACACC AAGAGGAGGCTGGAGGGCGCAAGAAAGCAAGGCGGACAGCCCCGTGAACGGCTTGC CAAAGGGGCGAGAGCTCGGAGTCGGAGCCGAGCCGTGAGCAGAGCTACTCGAGGTC CCCATCCGATCAGCGTCTCTAAGAGGAGGAAAGTGACAGCGGCTCCACATCTGGT	

	GGGTCCAAGTCGCAGAGCCGCTCCCGGAGCAGGAGTGAATCCCCACCGAGACAGGCC CCCGCAGCGCTCCCTACAAGGCTCTGAGATTCCGGGCTCCCGAAGTCCAAGGACTG CAAGTACCCCGAGAAGCCACACAAGTCTCGGAGCCGAGTCTTCCCGTTCTCGAAGC AGGTCA CGGGAGCGGGCGGATAATCCGGGAAAATACAAGAAGAAAGTCATTACTACA GAGATCAGCGACGAGAGCGCTCGAGGTCGTATGAACGCACAGGCCGTCGCTATGAGCG GGACACCCCTGGGCACAGCAGGCATCGGAGGTGACACGTGCTTCAGACCGGTCTGGGG TGCGGCGCACACCTGGGCCCGTCAGGGCTCAGCTCGGCAGCAGCTCTGAGGGCAGCT CAATGAAAAGTGAATGCACACGCCCTTGTGGCGTG		
	ORF Start: ATG at 44		ORF Stop: TGA at 1598
	SEQ ID NO: 98	518 aa	MW at 58034.5kD
NOV28a, CG59348-01 Protein Sequence	MTAAAAGAAGSAAPAAAAGAPSGSGAPSGSQVLIIGDRLYSGVLITLNCLLPDDKLR FTPSMSSGLDTEITDLRVVGCELIQAAGILLRLPQVAMATGQVLFQFFYTKSFVKH SMEHVSMACVHLASKIEEAPRRIRDVINVFHRLRQLRDKKPVPLLLDQDYVNLKNQI IKAERRVLKELGFCVHVHHPKIIVMYLQVLECEHNQHLVQTSWNMNDLSRDTDFVFR FQPESIAACACIYLAARTLEIPLPNRPHWFLFGATEEEIQEICLKILQLYARKKVDLT HLEGEVEKRKHAIEEAKAQARGLPGGTQVLDGTSGFSPAPKLVPKPKGKSKPSPL SVKNTKRRLEGAKKAKADSPVNLPGGRESRSRSRSREQSYRSRSPRSASPKRRKSDS GSTSGGSKSQRSSRSRSDSPRQAPRSAPYKGSEIRGSRKSKDCKYPQKPHKSRSS SRSSRSRERADNPGRYKKKSHYYRDRRRERSYERTGRRYERDHPGHSRHR		

Further analysis of the NOV28a protein yielded the following properties shown in Table 28B.

Table 28B. Protein Sequence Properties NOV28a	
Psort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.2400 probability located in nucleus; 0.1900 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV28a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 28C.

Table 28C. Geneseq Results for NOV28a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV28a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM94028	Human stomach cancer expressed polypeptide SEQ ID NO 126 - Homo sapiens, 298 aa. [WO200109317-A1, 08-FEB-2001]	221..518 1..298	298/298 (100%) 298/298 (100%)	e-172
AAG64403	Human paneth cell enhanced expression-like protein - Homo sapiens, 298 aa. [WO200138372-A1, 31-MAY-2001]	221..518 1..298	298/298 (100%) 298/298 (100%)	e-172

AAB94641	Human protein sequence SEQ ID NO:15526 - Homo sapiens, 298 aa. [EP1074617-A2, 07-FEB-2001]	221..518 1..298	298/298 (100%) 298/298 (100%)	e-172
AAM78533	Human protein SEQ ID NO 1195 - Homo sapiens, 526 aa. [WO200157190-A2, 09-AUG-2001]	2..518 8..526	316/526 (60%) 390/526 (74%)	e-168
AAB94371	Human protein sequence SEQ ID NO:14909 - Homo sapiens, 526 aa. [EP1074617-A2, 07-FEB-2001]	2..518 8..526	316/526 (60%) 390/526 (74%)	e-168

In a BLAST search of public sequence databases, the NOV28a protein was found to have homology to the proteins shown in the BLASTP data in Table 28D.

Table 28D. Public BLASTP Results for NOV28a				
Protein Accession Number	Protein/Organism/Length	NOV28a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96S94	HYPOTHETICAL 58.1 KDA PROTEIN - Homo sapiens (Human), 520 aa.	3..518 5..520	516/516 (100%) 516/516 (100%)	0.0
Q9JJA7	BRAIN CDNA, CLONE MNCB-5160, SIMILAR TO MUS MUSCULUS PANETH CELL ENHANCED EXPRESSION PCEE MRNA - Mus musculus (Mouse), 518 aa.	1..518 1..518	466/519 (89%) 482/519 (92%)	0.0
Q9UK58	CYCLIN L ANIA-6A - Homo sapiens (Human), 526 aa.	2..518 8..526	316/526 (60%) 390/526 (74%)	e-167
Q9R1Q2	CYCLIN ANIA-6A - Rattus norvegicus (Rat), 527 aa.	2..518 9..527	312/526 (59%) 391/526 (74%)	e-165
Q9WV44	CYCLIN ANIA-6A - Mus musculus (Mouse), 531 aa.	3..518 15..531	314/526 (59%) 385/526 (72%)	e-162

PFam analysis predicts that the NOV28a protein contains the domains shown in the Table 28E.

Table 28E. Domain Analysis of NOV28a			
Pfam Domain	NOV28a Match Region	Identities/ Similarities for the Matched Region	Expect Value

cyclin: domain 1 of 1	46..190	28/163 (17%) 86/163 (53%)	0.0022
Srg: domain 1 of 1	221..230	4/10 (40%) 10/10 (100%)	6.7
transcript_fac2: domain 1 of 1	235..253	12/19 (63%) 15/19 (79%)	0.86
cyclin_C: domain 1 of 1	196..311	22/139 (16%) 65/139 (47%)	2.6

Example 29.

The NOV29 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 29A.

Table 29A. NOV29 Sequence Analysis			
	SEQ ID NO: 99	1069 bp	
NOV29a, CG59245-01 DNA Sequence	CGGGGCTGGTCCGCAGCTGGGCCGCCATGGAGTCCACGCTGGGCGCGGGCATCGTGA TAGCCGAGGCGCTACAGAACAGCTAGCCTGGCTGGAGAACGTGTGGCTCTGGATCAC CTTTCTGGGCGATCCCAAGATCCTCTTTCTGTTCTACTTCCCGCGGGCTACTACGCC TCCCGCGGTGTGGGCATCGCGGTGCTCTGGATCAGCCTCATCACCAGATGGCTCAACC TCATCTTCAAGTGGTTTCTTTTGGAGACAGGCCCTTTTGGTGGGTCCATGAGTCTGG TTACTACAGCCAGGCTCCAGCCCAGGTTACCAAGTCCCTCTTCTTGTGAGACTGGT CCAGGTGGCAGCCCTTCTGGACACTGCATGATCACAGGAGCAGCCCTCTGGCCCATAA TGACGGCCCTGTCTTCGCAAGTGCCTGGGTAAGGGTGATGCCTAGCCTGGCTTATTG CACCTTCCTTTTGGCGGTTGGCTTGTGCGGAATCTTCATCTTAGCACATTTCCCTCAC CAGGTGCTGGCTGGCCTAATAACTGGTTGGCTGATGACTCCCCGAGTGCCTATGGAGC GGGAGCTAAGCTTCTATGGGTGACTGCACTGGCCCTCATGCTAGGCACCAGCCTCAT CTATTGGACCCCTCTTTACACTGGGCTGGATCTTTCTTGGTCCATCAGCCTAGCCTTC AAGTGGTGTGAGCGGCTGAGTGGATACAGTGGATAGCGGCCCTTTGCCTCCCTGA GCCGTGACTCAGGGGCTGCCCTGGGCTGGGCATTGCCTTGCACTCTCCCTGCTATGC CCAGGTGCGTCCGGCACAGCTGGGAAATGGCCAGAAGATAGCCTGCCTTGTGCTGGCC ATGGGGCTGCTGGGCCCCCTGGACTGGCTGGGCCACCCCTCAGATCAGCCTCTTCT ACATTTTCAATTTCTCAAGTACACCTCTGGCCATGCCTAGTCTGGCCCTCGTGCC CTGGGCAGTGACATGTTAGTGCCAGGAAGCACCGCCCATCCACTCTTCTGACTT CTTGTGTGCTCCCTTTCCTTTCCC		
	ORF Start: ATG at 28	ORF Stop: TGA at 1039	
	SEQ ID NO: 100	337 aa	MW at 37808.0kD
NOV29a, CG59245-01 Protein Sequence	MESTLGAGIVIAELQNLAWLENVWLWITFLGDPKILFLFYFPAAYYASRRVGI AVL WISLITEWLNLFKWFLEFGRPFWWVHESGYYSQAPAVHQFPSSCETGPGGSPSGHC MITGAALWPIMTALSSQVRWVRVMPSLAYCTFLAVGLSRIFILAHFPHQVLGLITG WLMTPRVPMERELSFYGLTALALMLGTS LIYWTFLTLGLDLSWSISLAFKWCERPEWI HVDSPFPASLSRDSGAALGLGIALHSPCYAQRRAQLGNGQKIACLVLAMGLLGPLDW LGHPPIQISLFYIFNFKYTLWPCLVLALVPWAVHMFSAQEAPPIHSS		
	SEQ ID NO: 101	1386 bp	
NOV29b, CG59245-02 DNA Sequence	TGAGTCTGTACTTTCGCCCTGGAGCAAGCCGGGCTGGTCCGAGCTGGGCGCCA TGGAGTCCACGCTGGGCGCGGGCATCGTGTAGCCGAGGCGCTACAGAACAGCTAGC CTGGCTGGAGAACGTGTGGCTCTGGATCACCTTTCTGGGCGATCCCAAGATCCTCTTT CTGTTCTACTTCCCGCGGCTACTACGCTCCCGCGGTGTGGGCTGCTGCTCT GGATCAGCCTCATCACCAGTGGCTCAACCTCATCTTCAAGTGGTTTCTTTTGGAGA CAGGCCCTTTTGGTGGGTCCATGAGTCTGGTTACTACAGCCAGGCTCCAGCCCAGGTT CACCAGTTCCCTCTTCTTGTGAGACTGGTCCAGGACAGCCCTTCTGGACACTGCATGA TCACAGGAGCAGCCCTCTGGCCCATAATGACGGCCCTGTCTTCGCAAGTGGCCACTCG GGCCCGCAGCCGCTGGGTAAGGGTGATGCCTAGCCTGGCTTATTGCACCTTCTTTTG GCGGTTGGCTTGTGCGGAATCTTCATCTTAGCACATTTCCCTCACCAGGTGCTGGCTG GCCTAATAACTGGCGCTGTCTGGGCTGGCTGATGACTCCCCGAGTGCCTATGGAGCG GGAGCTAAGCTTCTATGGGTGACTGCACTGGCCCTCATGCTAGGCACCAGCCTCATC TATTGGACCCCTCTTACACTGGGCTGGATCTTTCTTGGTCCATCAGCCTAGCCTTCA AGTGGTGTGAGCGGCTGAGTGGATACAGTGGATAGCGGCCCTTTGCCTCCCTGAG CCGTGACTCAGGGCTGCCCTGGGCTGGGCATTGCCTTGCACTCTCCCTGCTATGCC CAGGTGCGTCCGGCACAGCTGGGAAATGGCCAGAAGATAGCCTGCCTTGTGCTGGCCA		

	TGGGGCTGCTGGGGCCCCCTGGACTGGCTGGGGCCACCCCTCAGATCAGCCTCTTCTA CATTTTCAATTTCCTCAAGTACACCCTCTGGCCATGCCAGTCTGGCCCTCGTGCCC TGGGCAGTGACATGTTTCTAGTGGCCAGGAAGCACCGCCATCCACTCTTCCTGACTTC TTGTGTGCCTCCCTTTCCCTTCCCTCCACAAAGCCAACACTCTGTGACCACCACACT CCAGGAGGCAGCCCCATCCCCTTCCAGCCCCCTAAGTAGGCCCTCCCTCCCTAAATCT GCTTCCGCACCACTGGTCTTAGCCCCAAAGATGGGCCTTCTCTCTCCAGATAAGTT GGTCTCCCTCTGCCTTTCTCTCAAGCCCCAAAGAGCAAAGGCAACAGCAAGACCA GCGGGTTCTTGCAACACTGTGAGGGGCAGCCAGGGCGGAAAGTACAGACTCA		
	ORF Start: ATG at 58		ORF Stop: TGA at 1096
	SEQ ID NO: 102	346 aa	MW at 38718.0kD
NOV29b, CG59245-02 Protein Sequence	MESTLGAGIVIAEALQNQLAWLENVWLWITFLGDPKILFLFYFPAAYASRRVGI AVL WISLITEWLNLI FKWFLPGDRPFWWHESGYYSQAPQVHQFPSSCETGPGSPSGHCM ITGAALWPIMTALSSQVATRRSRWVRVMPSLAYCTFLLAVGLSRIFILAHFPHQVLA GLITGAVLGWLMTPRVPMERELSFYGLTALALMLGTS LIYWTLFTLGLDLSWSISLAF KWCEPWEIHWDSRPFASLSRDSGAALGLGIALHSPCYAQVRRALQNGQKIACLVLA MGLLGPLDWLGHPPIQISLFYIFNFKYTLWPCFVLALVPWAVHMFSAQEAPPIHSS		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 29B.

Table 29B. Comparison of NOV29a against NOV29b.		
Protein Sequence	NOV29a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV29b	1..337	335/347 (96%)
	1..346	335/347 (96%)

Further analysis of the NOV29a protein yielded the following properties shown in Table 29C.

Table 29C. Protein Sequence Properties NOV29a	
PSort analysis:	0.6850 probability located in endoplasmic reticulum (membrane); 0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 41 and 42

A search of the NOV29a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 29D.

Table 29D. Geneseq Results for NOV29a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV29a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79500	Human protein SEQ ID NO 3146 - Homo sapiens, 382 aa. [WO200157190-A2, 09-AUG-2001]	1..337 37..382	336/347 (96%) 336/347 (96%)	0.0
AAB42637	Human ORFX ORF2401 polypeptide sequence SEQ ID NO:4802 - Homo sapiens, 377 aa. [WO200058473-A2, 05-OCT-2000]	1..337 31..377	328/348 (94%) 328/348 (94%)	0.0
AAB85355	Human phosphatase (PP) (clone ID 1269556CD1) - Homo sapiens, 385 aa. [WO200153469-A2, 26-JUL-2001]	1..305 1..314	297/315 (94%) 298/315 (94%)	e-174
AAM78516	Human protein SEQ ID NO 1178 - Homo sapiens, 404 aa. [WO200157190-A2, 09-AUG-2001]	1..337 125..404	266/341 (78%) 272/341 (79%)	e-146
AAB25679	Human secreted protein sequence encoded by gene 15 SEQ ID NO:68 - Homo sapiens, 141 aa. [WO200043495-A2, 27-JUL-2000]	198..337 1..140	140/140 (100%) 140/140 (100%)	6e-81

In a BLAST search of public sequence databases, the NOV29a protein was found to have homology to the proteins shown in the BLASTP data in Table 29E.

Table 29E. Public BLASTP Results for NOV29a				
Protein Accession Number	Protein/Organism/Length	NOV29a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAH21574	HYPOTHETICAL 38.7 KDA PROTEIN - Homo sapiens (Human), 346 aa.	1..337 1..346	336/347 (96%) 336/347 (96%)	0.0
Q9BUM1	HYPOTHETICAL 40.1 KDA PROTEIN - Homo sapiens (Human), 360 aa (fragment).	1..337 15..360	336/347 (96%) 336/347 (96%)	0.0
O42153	Glucose-6-phosphatase (EC 3.1.3.9) (G6Pase) (G-6-Pase) - Haplochromis nubilus, 352 aa.	8..323 8..339	127/333 (38%) 184/333 (55%)	1e-59

Q98UF8	GLUCOSE-6-PHOSPHATASE - Sparus aurata (Gilthead sea bream), 350 aa.	8..323 8..337	123/333 (36%) 185/333 (54%)	2e-57
Q9Z186	GLUCOSE-6-PHOSPHATASE - Mus musculus (Mouse), 355 aa.	7..325 7..345	128/343 (37%) 188/343 (54%)	5e-56

PFam analysis predicts that the NOV29a protein contains the domains shown in the Table 29F.

Table 29F. Domain Analysis of NOV29a			
Pfam Domain	NOV29a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PAP2: domain 1 of 1	51..190	38/175 (22%) 95/175 (54%)	0.00037

Example 30.

The NOV30 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 30A.

Table 30A. NOV30 Sequence Analysis			
	SEQ ID NO: 103	1624 bp	
NOV30a, CG59241-01 DNA Sequence	ATGGAAGTGAAGGCCGAGGAGGAGGAGGTGGGTGGCGTCCAGCCGGTGGACTTGGTGG CCTTTGCCAACAGTGCACCCCTCCATGGCACCAACCACATTTTGTGGAGGGGGTCC AGGGCCAAGGCAGGTGCTGTGGGCGGTGGCCCTTTGTCTGGCACTGGGTGCCTTCCTG TGCCAGGTAGGGGACCGGTTGCTTATTACCTCAGCTACCCACAGTGACCCCTCTCTAA ACGAAGTGGCCACCAAGAGCTGGCCCTTCCGGCAGTCACCCCTGTGCAACACTAATGC TGTGCGGCTGTCCAGCTCAGCTACCCCTGACTTGCTTTATTTGGCCCCATGCTGGGA CTGGATGAAAGTGATGACCCCGGGGTGCCCTCGCTCCACCGGGCCCTGAGGCCTTCT CTGGGGAGCCCTTTAACTGCACCGCTTCTACAATCGCTCCTGCCACCGGCTGGAGGA CATGCTGCTCTATTGCTCCTACCAAGGGGACCCCTGCGGCCCTCACAACTTCTCAGTG GTGTTACACGCTATGGAAGTGCTACACGTTCAACTCGGGCCGAGATGGGCGGCCGC GGCTGAAGACCATGAAGGGTGGGACGGGCAATGGGCTGGAAATCATGCTGGACATCCA GCAGGACGAGTACCTGCTGTGTGGGGGAGACTGACGAGACGTCCTTCAAGCAGGC ATCAAAGTGCAGATCCATAGTCAGGATGAACCTCCTTTTCATCGACGAGCTGGGCTTTG GCGTGGCCCCAGGCTTCCAGACCTTTGTGGCCTGCCAGGAGCAGCGGATCTACCTGCC CCCACCTGGGGCACCTGCAAAGCTGTTACCATGGACTCGGATTTCTTCGACTCCTAC AGCATCACTGCCTGCCGCATCGACTGTGAGACGCGCTACCTGGTGGAGAAGTGCAACT GCCGATGGTGACATGCCAGGTGATGCCCATACTGTACTCCAGAGCAGTACAAGGA GTGTGCAGATCCTGCTCTGGACTTCTGTGGAGAAGGACCAGGAGTACTGCGTGTGT GAAATGCCTTGCAACTGACCCGCTATGGCAAAGAGCTGTCCATGGTCAAGATCCCCA GCAAAGCCTCAGCCAAGTACCTGGCCAAGAAGTTCAACAAATCTGAGCAATACATAGG GGAGAACATCCTGGTGTGGACATTTTCTTTGAAGTCTCAACTATGAGACCATTTGAA CAGAAGAAGGCCTATGAGATTGCAGGGCTCCTGGGTGACATCGGGGGCCAGATGGGGC TGTTTCATCGGGGCCAGCATCCTCACGGTGTGAGCTCTTTGACTACGCCTACGAGGT AGTCATTAAACACAAGCTGTGCCGACGAGGAAATGCCAGAAGGAGGCCAAAAGGAGC AGTGGGACAAGGGCGTGGCCCTCAGCCTGGACGACGTCAAAAGACACAACCCGTGGC AGAGCCTTCGGGGCCACCCTGCCGGGATGACATACGCTGCCAATCTTACCTCACCA TCCGGCCCGAGGCACGTTTCAGGACTTTACCTGCTGAGCCCCGAGGCCCGCTGAACCA AAGGCCTAGATGGGAGGACTAGGAGAGCGAGGGGGCCCCAGCTGCCTCCTCACATC		
	ORF Start: ATG at 1	ORF Stop: TGA at 1543	
	SEQ ID NO: 104	514 aa	MW at 57221.7kD
NOV30a,	MELKAEVEEVGGVQPDVLVAFANSCTLHGTNHFVEGGPGPRQVLWAVFVLALGAPL CQVGDRVAYYLSYPHVTLLNEVATTELAFFAVTLCNTNAVRLSQLSYPDLLYLAPMLG		

CG59241-01 Protein Sequence	LDESDDPGVPLAPPGPEAFSGEPFNLHRFYNRSHRLEDMLLYCSYQGGPCGPHNFSV VFTRYGKCYTFNSGRDGRPLKTMKGGTGNGLIIMLDIQQDEYLPVWGETDETSFEAG IKVQIHSQDEPPFIDQLGFGVAPGFQTFVACQEQRIYLPWPWGTCKAVTMSDFDSDSY SITACRIDCETRYLVENCNCRMVHMPGDAPYCTPEQYKECADPALDFLVEKDQEYCV EMPCNLTRYGKELSMVKIPSKASAKYLAKKFNKSEQYIGENILVLDIFFEVLNYETIE QKKAYEIAGLLDIGGQMLFIGASILTVLELFDYAYEVVVIKHKLCRRGKQKEAKRS SADKGVALLDDVVRHNPCESLRGHPAGMTYAANILPHHPARGTFEDFTC
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Further analysis of the NOV30a protein yielded the following properties shown in Table 30B.

Table 30B. Protein Sequence Properties NOV30a	
PSort analysis:	0.7900 probability located in plasma membrane; 0.3000 probability located in Golgi body; 0.2000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 60 and 61

A search of the NOV30a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 30C.

Table 30C. Geneseq Results for NOV30a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV30a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY69178	A rat acid-sensitive cationic channel 1B (rASIC1B) - Rattus sp, 559 aa. [WO200008149-A2, 17-FEB-2000]	1..514 47..559	488/515 (94%) 497/515 (95%)	0.0
AAY03186	Rat Acid sensitive ion channel protein sequence - Rattus sp, 513 aa. [WO9911784-A1, 11-MAR-1999]	1..514 1..513	488/515 (94%) 498/515 (95%)	0.0
AAW68507	Rat acid sensing ionic channel 1B - Rattus sp, 559 aa. [WO9835034-A1, 13-AUG-1998]	1..514 47..559	488/515 (94%) 497/515 (95%)	0.0
AAY69175	A rat acid-sensitive cationic channel 1A (rASIC1A) - Rattus sp, 526 aa. [WO200008149-A2, 17-FEB-2000]	1..514 1..526	416/527 (78%) 445/527 (83%)	0.0
AAY03188	Rat Acid sensitive ion channel alpha protein sequence - Rattus sp, 526 aa. [WO9911784-A1, 11-MAR-1999]	1..514 1..526	416/527 (78%) 445/527 (83%)	0.0

In a BLAST search of public sequence databases, the NOV30a protein was found to have homology to the proteins shown in the BLASTP data in Table 30D.

Table 30D. Public BLASTP Results for NOV30a				
Protein Accession Number	Protein/Organism/Length	NOV30a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q91YB8	ION CHANNEL - Rattus norvegicus (Rat), 559 aa.	1..514 47..559	489/515 (94%) 498/515 (95%)	0.0
O88762	ASIC-BETA - Rattus norvegicus (Rat), 513 aa.	1..514 1..513	488/515 (94%) 498/515 (95%)	0.0
P55926	Amiloride-sensitive brain sodium channel BNaC2 (Amiloride-sensitive cation channel neuronal 2) (Proton gated cation channel ASIC1) - Rattus norvegicus (Rat), 526 aa.	1..514 1..526	416/527 (78%) 445/527 (83%)	0.0
P78348	Amiloride-sensitive brain sodium channel BNaC2 (Amiloride-sensitive cation channel neuronal 2) - Homo sapiens (Human), 574 aa.	1..514 1..574	421/575 (73%) 447/575 (77%)	0.0
Q99NA1	PROTON-GATED CATION CHANNEL SUBUNIT ASIC-BETA2 - Rattus norvegicus (Rat), 425 aa.	175..514 86..425	334/341 (97%) 337/341 (97%)	0.0

PFam analysis predicts that the NOV30a protein contains the domains shown in the Table 30E.

Table 30E. Domain Analysis of NOV30a			
Pfam Domain	NOV30a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ASC: domain 1 of 2	21..118	34/106 (32%) 79/106 (75%)	1.6e-29
ASC: domain 2 of 2	145..442	133/351 (38%) 281/351 (80%)	2.1e-139

Example 31.

The NOV31 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 31A.

Table 31A. NOV31 Sequence Analysis			
	SEQ ID NO: 105	1949 bp	
NOV31a, CG58602-01 DNA Sequence	TGCCTGGCTATGGCCGACTGCTCAGGTCTGCAACCTGGGAGCTGTTCCCTGGAGGG GCTACTGCTCCCAGTCCCTGCAGGGAGAGCTCTGCAGGGACTTCGTAGAGGCTCTGAA GGCCGTGGTGGGCGGCTCCACGTGTCCACTGCCGCGGTGGTCCGAGAGCAGCACGGG CGCGATGAGTCGGTGACAGGTGCGAACCCTCTGATGCTGTGGTGTGGCCCCAGAACG TGGAGCAGGTGAGCCGGCTGGCAGCCCTGTGCTATCGCCAAGGTGGTGGCCATCATCCC ATTCCGCACCGGCACCGGGCTTGAGGGTGGCGTCTGTGCTGTGACAGGGCGGCGTCTGC GTTAACCTGACGCATATGGACCGAATCCTGGAGCTGAACCAGGAGGACTTCTCTGTGG TGGTGGAGCCAGGTGTCACCCGCAAAGCCCTCAACGCCCACTTCCGGGACAGCGGCCT CTGGTTTCTCCAGACCCAGGCGCGGACGCCTCTCTGTGGCATGGCGGCCACCGGG GCGTCCGGGACCAACGCGGTCCGCTACGGCACCATGCGGGACAACGTGCTCAACCTGG AGGTGGTGTGCCCGACGGGCGGCTGCTGCACACGGCGGGCCGAGGCTCATCACAGA TTCCACTGCTGCATTCCCCACATCAGCCCCACTGAGTGTCTTTCCAGGGGCCAGGG CCTCATGTCAATTCTCCTCACCCTGCCCCTGAGGGCCACAGTGGCGGCCACGTGTGCGT TCCCCAGTGTCCAGGCTGCTGTGGACAGCACTGTACACATCTCCAGGCTGCAGTGCC CGTAGCCCCGATTGAGTTCCTGGATGAAGTCATGATGGATGCCTGCAACAGGTACAGC AAGCTGAATTGCTTAGTGGCGCCCACTCTTCTGGAGTTCCATGGCTCCGACGAGG CACTGGAGGAGCAGCTGCAGCGCACAGAGGAGATAGTCCAGCAGAACGGAGGCTCTGA CTTCTCCTGGGCCAAGGAGGCGGAGAGCGCAGCCGGCTTTGGACAGCACGGCACAAT GCCTGGTACGCAGCCCTGGCCACGCGGCCAGGCTGCAAGGGCTACTCCACGGATGTGT GTGTGCCCATCTCCGGCTGCGGAGATCGTGGTGCAGACCAAGGAGGATCTGAATGC CTCAGGACTCACAGGAAGCATTGTCCGGCATGTGGGTGACGGCAACTTCCACTGCATC CTGTCTGGTCAACCTGATGACGCCGAGGAAGTGGGCGGGTCAAGGCTTTTGACAGAAC AGCTGGGCAAGCGGGCACTGGCTCTCCACGGAACGTGCACGGGGAGCATGGCATCGG AATGGGCAAGCGGCACTGCTGCAGGAGGAGGTGGGCGCGCTGGGCGGTGGAGACCATG CGGCAGCTCAAGGCCGTGTAGACCCCCAAGGCCTCATGAATCCAGGCAAAGTGTCTGT GAAGGGGGTCTGAGCACTTAGCCCCAAGTTCCCTGACTACGGAGCCGGTCTTGGAACT TTTTCTTCATGCCACGGCCCCCTGCAAGGAAATAGATGCTGAGGCAGTCTTCTGCCAG CGAGCCCACTGTATCTGGGCCCCAAGGCCAGAGGGCCAGAGAGAAGCCTGAGCACCGT GTTACCTCCCTGGCCCTCTGGCTGGCCCCAGGAGCCTTTGGTTTCAGTAAACGACCCAG GGTGGTTCCCAGCAAAGCTGCTTCTCTCTGCTCCTACGCATCCTGTCTGGCGGGGAA GAGAGCGTCTGGTCCATTCAAGACTCTGATGACACCCCTCCCGAGGCTCCCTCACTG CCGGGGTCCCAGGACCCCTTCCCCCTTCACTGGTGACAGGAACACTCCTTTCTGGTA TGGAACGTGAGCTCCCGTGACATGATGATAGGTCTTCTCCTTGGGGCTCCCCCAATA AATCTGTAATAAACCTGAAACCCACCTACAGCTAA		
	ORF Start: ATG at 10	ORF Stop: TGA at 1450	
	SEQ ID NO: 106	480 aa	MW at 51629.1kD
NOV31a, CG58602-01 Protein Sequence	MARLLRSATWELFPWRGYCSQSLQGLCRDFVEALKAVVGGSHVSTAADVREQHGRDE SVHRCEPPDAVVVPQNVQVSRLLAALCYRQGVPIIPFGTGTGLEGGVCAVQGGVVCNVL THMDRILELNQEDFSVVVEPGVTRKALNAHLRDSGLWFFPDGADASLCGMAATGASG TNAVRYGTRMDNVNLNLEVVLPDGRLLHTAGRGLITDSTAAPPHISPTECFSQGPVPHV NSPHPAPEATVAATCAFPVQAAVDSTVHILQAAVPVARI EFLDEVMDACNRYSKLN CLVAPTLFLEPHGSQQAEEQLQRTEEIVQONGASDFSWAKRAEERSRLWTARHNAWY		

	AALATRPGCKGYSTDVCPISRLPEIVVQTKEDLNASGLTGSIVGHVGDGNFHCILLV NPDDAEELGRVKAFABEQLGRRALALHGTCTGSHGIGMGRQLLQEEVGAVGVETMRQL KAVLDPQGLMNPQKVL
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Further analysis of the NOV31a protein yielded the following properties shown in Table 31B.

Table 31B. Protein Sequence Properties NOV31a	
PSort analysis:	0.6574 probability located in mitochondrial matrix space; 0.3502 probability located in mitochondrial inner membrane; 0.3502 probability located in mitochondrial intermembrane space; 0.3502 probability located in mitochondrial outer membrane
SignalP analysis:	Likely cleavage site between residues 20 and 21

A search of the NOV31a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 31C.

Table 31C. Geneseq Results for NOV31a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV31a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABB10446	Human cDNA SEQ ID NO: 754 - Homo sapiens, 115 aa. [WO200154474-A2, 02-AUG-2001]	1..96 15..110	91/96 (94%) 92/96 (95%)	8e-49
AAE09597	Human gene 5 encoded novel protein HDPMT22, SEQ ID NO:33 - Homo sapiens, 115 aa. [WO200155311-A2, 02-AUG-2001]	1..96 15..110	91/96 (94%) 92/96 (95%)	8e-49
AAM52368	GIP12-C4 protein - Arabidopsis thaliana, 159 aa. [FR2806095-A1, 14-SEP-2001]	66..203 3..140	69/138 (50%) 98/138 (71%)	9e-34
AAG92286	C glutamicum protein fragment SEQ ID NO: 6040 - Corynebacterium glutamicum, 948 aa. [EP1108790-A2, 20-JUN-2001]	46..477 25..502	108/486 (22%) 186/486 (38%)	2e-22
AAB79309	Corynebacterium glutamicum SMP protein sequence SEQ ID NO:134 - Corynebacterium glutamicum, 945 aa. [WO200100844-A2, 04-JAN-2001]	46..477 22..499	108/486 (22%) 186/486 (38%)	2e-22

In a BLAST search of public sequence databases, the NOV31a protein was found to have homology to the proteins shown in the BLASTP data in Table 31D.

Table 31D. Public BLASTP Results for NOV31a				
Protein Accession Number	Protein/Organism/Length	NOV31a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9D635	4733401P21RIK PROTEIN - Mus musculus (Mouse), 481 aa.	1..480 1..481	394/483 (81%) 423/483 (87%)	0.0
Q19965	F32D8.4 PROTEIN - Caenorhabditis elegans, 912 aa.	20..480 445..909	221/466 (47%) 307/466 (65%)	e-121
CAD16371	PUTATIVE D-LACTATE DEHYDROGENASE (CYTOCHROME) OXIDOREDUCTASE PROTEIN (EC 1.1.2.4) - Ralstonia solanacearum (Pseudomonas solanacearum), 472 aa.	32..479 20..469	226/454 (49%) 300/454 (65%)	e-119
A89201	protein F32D8.4 [imported] - Caenorhabditis elegans, 870 aa.	30..480 399..867	214/469 (45%) 296/469 (62%)	e-115
AAL51780	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4) - Brucella melitensis, 468 aa.	41..480 28..467	209/444 (47%) 286/444 (64%)	e-114

Pfam analysis predicts that the NOV31a protein contains the domains shown in the Table 31E.

Table 31E. Domain Analysis of NOV31a			
Pfam Domain	NOV31a Match Region	Identities/ Similarities for the Matched Region	Expect Value
FAD_binding_4: domain 1 of 1	33..214	70/208 (34%) 154/208 (74%)	3.7e-56
FAD-oxidase_C: domain 1 of 1	206..479	91/307 (30%) 210/307 (68%)	1.3e-58

Example 32.

The NOV32 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 32A.

Table 32A. NOV32 Sequence Analysis			
	SEQ ID NO: 107	698 bp	
NOV32a, CG58468-01 DNA Sequence	CTCCTTCCTGTGCTCTTTATATGGACCAACAACCTTCTCGTCCTTGGGGTCTCTGTGCA AATATCAATTTTTTCACATTATCTTTTCTCCACAGACATGAGAGGGAAGGCATTATTATT TTCCCTCAAGAATCAGCTACAGTCTATGTGTCCCTGATCCCCAAGGTGAAGAAGCCCC TGAAGAACTTCAAGCTTTGCCTGAAAACCTTCACAGACTTCACCTGCCCTTATAGCCT CTTCTACAGCACTCGGTCCCAGGACAATGAGCTGCTTCTCCTTGTCAACAAAATGGGA ATGTATCTGCTGCACATTGGAAATGCTGCGGTCACTTTCAATGGCCCCACCCCTGCC CTCGATCTCCTTATGCTTCGACCCATGTCAATGTGAGCTGGGAGTCTGCCTCTGGAAT TGCTACACTCTGGGCAAATGGGAAGCTGGTGGGGAGGAAGGGTGTGTGGAAGGGGTAC TCTGTGGGAGAAGAGGCTAAGATCATCCTGGGACAAGAGCAGGATTCTTTGGGGGAC ATTTTGATGAAAATCAATCCTTTGTTGGGGTGATATGGGATGTGTTTTGTGGGATCA TGTGCTCCCTCCAAAGGAGATGTGTGACTCCTGTTACAGCGGCAGCCTCCTGAATCGG CATACCCTGACTTATGAAGATAATGGCTATGTGGTAACTAAGCCCAAGGTGTGGGCTT AA		
	ORF Start: ATG at 21	ORF Stop: TAA at 696	
	SEQ ID NO: 108	225 aa	MW at 25265.8kD
NOV32a, CG58468-01 Protein Sequence	MDQQLVLVGVSVQISIFSHYLFSTDMRGKAFIPQESATVYVSLIPKVKKPLKNFKLC LKTFDFTCPYSLFYSTRSQDNELLLLNVNKMGMYLLHIGNAAVTFNGPTPCPRSPYAS THVNVSWESASGIATLWANGKLVGRKGWVKGVSVGBEAKIILGQEQDSFGGHFDENQS FVGVIWDVFLWDHVLPPKEMCDSCYSGSLNLRHTLTIEDNGYVVTKPKVWA		

Further analysis of the NOV32a protein yielded the following properties shown in Table 32B.

Table 32B. Protein Sequence Properties NOV32a	
PSort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.3200 probability located in microbody (peroxisome); 0.2368 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV32a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 32C.

Table 32C. Geneseq Results for NOV32a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV32a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAR74763	Sermun amyloid P component, promoter sapm - Homo sapiens, 204 aa. [WO9505394-A, 23-FEB-1995]	24..224 2..203	98/207 (47%) 136/207 (65%)	4e-48
AAR29923	SAP - Homo sapiens, 223 aa. [WO9221364-A, 10-DEC-1992]	7..224 5..222	101/224 (45%) 143/224 (63%)	3e-47

AAR29922	CRP - Homo sapiens, 225 aa. [WO9221364-A, 10-DEC-1992]	14..224 11..224	100/218 (45%) 132/218 (59%)	2e-43
AAR74769	Female hamster protein, 1 fhp - Cricetus cricetus, 210 aa. [WO9505394-A, 23-FEB-1995]	24..222 1..199	95/206 (46%) 132/206 (63%)	6e-43
AAY76844	Human C reactive protein (CRP) sequence - Homo sapiens, 206 aa. [JP2000014388-A, 18-JAN-2000]	24..224 2..205	98/208 (47%) 128/208 (61%)	1e-42

In a BLAST search of public sequence databases, the NOV32a protein was found to have homology to the proteins shown in the BLASTP data in Table 32D.

Table 32D. Public BLASTP Results for NOV32a				
Protein Accession Number	Protein/Organism/Length	NOV32a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9D8J8	1810030J14RIK PROTEIN - Mus musculus (Mouse), 219 aa.	6..224 4..218	130/220 (59%) 166/220 (75%)	5e-72
Q9D8V2	1810030J14RIK PROTEIN - Mus musculus (Mouse), 200 aa.	6..190 20..200	110/186 (59%) 139/186 (74%)	2e-58
Q63913	SERUM AMYLOID P - Cricetulus migratorius (Armenian hamster), 223 aa.	1..224 1..222	109/231 (47%) 152/231 (65%)	4e-51
P23680	Serum amyloid P-component precursor (SAP) - Rattus norvegicus (Rat), 228 aa.	6..224 4..223	105/224 (46%) 145/224 (63%)	7e-50
P15697	Female protein precursor (FP) (Serum amyloid P-component) - Cricetulus migratorius (Armenian hamster), 231 aa.	1..222 1..220	108/229 (47%) 151/229 (65%)	7e-50

PFam analysis predicts that the NOV32a protein contains the domains shown in the Table 32E.

Table 32E. Domain Analysis of NOV32a			
Pfam Domain	NOV32a Match Region	Identities/ Similarities for the Matched Region	Expect Value
pentaxin: domain 1 of 1	29..221	103/214 (48%) 156/214 (73%)	8e-76

Example 33.

The NOV33 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 33A.

Table 33A. NOV33 Sequence Analysis		
	SEQ ID NO: 109	3350 bp
NOV33a, CG58183-01 DNA Sequence	<p>TAATGAGGAGACTGAGTTTGTGGTGGCTGCTGAGCAGGGTCTGTCTGCTGTTGCCGCC GCCCTGCGCACTGGTGTGGCCGGGGTGCCAGCTCCTCTCGCACCCGAGCCCTGC CAGATCCTCAAGCGCATCGGGCACGCGGTGAGGGTGGGCGCGGTGCACCTTGACGCCCT GGACCACCGCCCCCGCGCGGCCAGCCGCGCTCCGGACGACAGCCGAGCAGGAGCCCA GAGGGATGAGCCGAGCCAGGGACTAGGCGGTCCCCGGCGCCCTCGCCGGGCGCACGC TGGTTGGGGAGCACCTGCATGGCCGGGGCGCGGGCTCCCGTAAGCCCGGGGAGG GCGCCAGGGCGGAGGCCCTGTGGCCACGGGACGCCCTCCTATTGCGGTGGACAACCT GAACCGCGTGAAGGGCTGCTACCCTACAACCTGTCTTGAAGTAGTGATGGCCATC GAGGCAGGCCTGGGCGATCTGCCACTTTTGCCCTTCTCCTCCCTAGTTCCGCATGGA GCAGTGACCTTTCTCCTTCTGCAAGTGTGTGCCATACCGTGGTGGTGCAAGGGGT GTGGCGCTGCTCGCCTTCCCCAGAGCCAGGGCGAAATGATGGAGCTCGACTTGGTC AGCTTAGTCTGACATTCAGTGATCAGCATCGTGCACGAGTTTCCACGGGAGA GTCAGAATCCCCTTACCTACAAGTGTAGTAAATTCATTAGTTCTGATGCTGA TGTCACTGTCTCACTGACCATGAACAAGTGTGTAATTTAGCTTGTGTGTC CAGGAAGACTGGAACATCACGACTTCTCCTCCTTACCCAGAATAATCCAAGTTCC ACCTTGGTTCTATCATCAACATCACCGCTAACCTCCCCTCCACCCAGGACCTCTGAG CTTCTACAGATCCAGCTTGAGAGTATTAAGAACAGCACCCACAGTGGTGTGTTT GGCTGCGCATGGAAAGTATCCGGCGGATTTCGAAATTACAACCCAGTTTGGGGTCA TGCCCCCTGAACCTTCGTGGGTGCTGGGAGATTCCAGAAATGTGGAGGAAGTGGAGC AGAGGGTCTGCCCTTAGGGCTCATTGCTCATGGAAAAACAACAGTCTGTCTTTGAG CACTACGTACAAGATGCTATGGAGCTGGTCGCAAGAGCTGTAGCCACAGCCACCATGA TCCAACCAAGACTTGTCTCATTCCCAGCAGCATGAATGCGATGGAGGTGGAACTAC AAATCTCACTTCAGGACAATATTTATCAAGGTTTCTAGCCAATACCCTTTCAGAGGC CTCAGTGGTTCCATCAGAGTAAAGGTTCCACCATCGTCAGCTCAGAAAACACTTTT TCATCTGGAATCTTCAACATGACCCCATGGGAAAGCCAATGTGGACCCGCTTGGCGAG CTGGCAGGGGGGAAAGATTGTCTAGGACTATGGAATATGGCCAGAGCAGGCCAGAGA CACAAAACCCACTTCCAACATCCAAGTAAGCTACACTTGAGAGTGGTTACCCCTGATTG AGCATCCTTTTGTCTTCAAGGGAGGTAGATGATGAAGGCTTGTGCCCTGCTGGCCA ACTCTGTCTAGACCCCATGACTAATGACTCTCCACATTGGACAGCCTTTTATGACG CTCCATAGCAGTAATGATACAGTGCCATTAAATTCAAGAAGTGTGTATGGATATT GCATTGATCTGTGGAAAAGATAGCAGAAGACATGAACCTTGACTTCGACCTCTATAT TGTAAGGGATGGAAAGTATGGAGCATGGAAAAATGGGCACTGGACTGGGCTAGTGGGT GATCTCCTGAGAGGGACTGCCACATGGCAGTCACTTCTTTAGCATCAATACTGCAC GGAGCCAGGTGATAGATTTACCCAGCCCTTCTTCTCCACAGCTTGGGCATCTTAGT GAGGACCCGAGATACAGCAGCTCCCATGGAGCCTTCATGTGGCCACTCCACTGGACA ATGTGGCTGGGGATTTTGTGGCTCTGCACATCACTGCCGTCTTCTCACTCTGTATG AATGAAGAGTCCATTTGGTTTGAATTTCAAGGGGCGAAATAGAAGTAAAGTCTTCTC CTTTTCTTCAAGCTTGAACATCTGTATGCCCTCTTGTGTGGCAGAACAGTGGCCATC AAACCTCCAAATGTGGACTGGAAGGTTTCTAATGAACCTTTGGGCCATTTTCTGTA TGTTTTCCTTTCCACATACAGGCAAACTTGGCTGCTGTATGGTAGGTGAGAAGAT CTATGAAGAGCTTCTGGAATACATGACCCCAAGTTACATCATCTTCCCAAGGATT CGCTTGGAACTGTCCGAGAAAGCAGTGTGAAGATTATGTGAGACAAAGTTTCCAG AGATGCGATGAATATATGAGAAGGTACAATGTTCCAGCCACCCCTGATGGAGTGGAGTA TCTGAAGAATGATCCAGAGAACTAGACGCCTTCATCATGGACAAAGCCCTTCTGGAT TATGAAGTGTCAATAGATGCTGACTGCAAACTTCTCACTGTGGGGAAGCCATTGGCA TAGAAGGTTACGGCATTGGCCCTCCACCCAACTCTCCATTGACCGCCAACATATCCGA GCTAATCAGTCAATACAAGTCACATGGGTTATGGATATGCTCCATGACAAGTGGTAC AGGGTGGTTCCCTGTGGCAAGAGAAGTTTGTCTGTACGGAGACTTTGCAATGGGCA</p>	

	TCAAACACTTCTCTGGGCTCTTTGTGCTGCTGTGCATTGGATTGGTCTGTCCATTTT GACCAACATTGGTGAGCACATAGTATACAGGCTGCTGCTACCACGAATCAAAAAACAAA TCCAAGCTGCAATACTGGCTCCACACCAGCCAGAGATTACACAGAGCAATAAATACAT CATTTATAGAGGAAAAGCAGCAGCATTTCAAGACCAAACGTTGGAAAAGAGATCTAA TGTGGGACCCCGTCAGCTTACCGTATGGAATACTTCCAATCTGAGTCATGACAACCGA CGGAAATACATCTTTAGTGATGAGGAAGGACAAAACAGCTGGGCATCCGGATCCACC AGGACATCCCCCTCCCTCCAAGGAGAAGAGAGCTCCCTGCCTTGGGACCACCAATGG GAAAGCAGACTCCCTAAATGTATCTCGGAACCTCAGTGATGCAGGAACCTCTCAGAGCTC GAGAAGCAGATTACAGTGATCCGTCAGGAGCTGCAGCTGGCTGTGAGCAGGAAAAACGG AGCTGGAGGATATCAAGGACAAAGTCGGACTTGTGAGTCCTAG		
	ORF Start: ATG at 3 ORF Stop: TAG at 3348		
	SEQ ID NO: 110	1115 aa	MW at 125453.7kD
NOV33a, CG58183-01 Protein Sequence	MRRLSLWLLSRVCLLLPPPCALVLAVPSSSSHPQPCQILKRIGHAVRVGAVHLQPW TTAPRAASRAPDDSRAGAQRDEPEPGTRRSPAPSPGARWLSTLHGRGPPGSRKPGEG ARAEALWPRDALLFAVDNLNRVEGLLPYNLSLEVMAIEAGLGDLPLLPFSSPSPSPWS SDPFSLQSVCHTVVVGVSALLAFPPQSQGEEMMELDLVSLVLHIPVISIVRHEFPRES QNPLHLQLSLENSLSSDADVTVSILTMNNWYNFSLLLCQEDWNITDFLLLTQNNSKFH LGSIIINITANLPSTQDLSLFLQIQLESIKNSTPTVVMFSCDMESIRRIFEITTFQFVM PPELRWVLGDSQNVLELRTEGLPLGLIAHGKTTQSVFEHYVQDAMELVARAVATATMI QPELALIPSTMNCEVETTNLTSGQYLSRFLANTTFRGLSGSIRVKGSTIVSSENNFF IWNLQHDPMGKPMWTRLGSWQGGKIVMDYGIWPEQAQRHKTTHFQHPSKLHLRVTLIE HPFVFTREVDDGLCPAGQLCLDPMTNDSSLTDSLFSLSLHSSNDTPVIFKFKCCYGYC IDLLEKIAEDMNFDFDLYIVGDGKYGAWKNGHWTGLVGDLLRGTAHMAVTSFSINTAR SQVIDFTSPFFSTSLGILVTRDTPAIPGAFMWPLHWTMWLGIFVALHITAVFLTLYE WKSPFGLTSKGRNRSKVFSFSSALNICYALLFGRTVAIKPKCWTGRFLMNLWAIFCM FCLSTYTANLAAMVGEKIYEELSGIHDPKLHHPSSQGFRTVRESSAEDYVRQSFPE MHEYMRRYNPATPDGVEYLKNDPEKLDAFIMDKALLDYEVSIDADCKLLTVGKPPAI EGYIGLPPNSPLTANISELISQYKSHGFMDMLHDKWYRVVPCGKRSFAVTETLQMG KHPSGLFVLLCIGFGLSILTTIGEHIVYRLLLPRIKNKSKLQYWLHTSQRHLHRAINTS FIEEKQHFKTQKRVKRSNVGPRQLTVWNTSNLSDNRRKYIFSDEEQNLGIRIHQ DIPLPRRRRELPAI RTTNGKADSLNVSRSNVMQELSELEKQIQVIRQELQLAVSRKTE LEEYQRTSRTCES		

Further analysis of the NOV33a protein yielded the following properties shown in Table 33B.

Table 33B. Protein Sequence Properties NOV33a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 34 and 35

A search of the NOV33a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 33C.

Table 33C. Geneseq Results for NOV33a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV33a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU02199	Human glutamate receptor-like protein, MEM4 - Homo sapiens, 1043 aa. [WO200144473-A2, 21-JUN-2001]	95..1103 6..1007	508/1047 (48%) 680/1047 (64%)	0.0
AAB42494	Human ORFX ORF2258 polypeptide sequence SEQ ID NO:4516 - Homo sapiens, 901 aa. [WO200058473-A2, 05-OCT-2000]	95..985 6..885	484/912 (53%) 635/912 (69%)	0.0
AAU02198	Human glutamate receptor-like protein, MEM3 - Homo sapiens, 971 aa. [WO200144473-A2, 21-JUN-2001]	532..1103 362..935	361/579 (62%) 448/579 (77%)	0.0
AAU02197	Human glutamate receptor-like protein, MEM2 - Homo sapiens, 965 aa. [WO200144473-A2, 21-JUN-2001]	532..1103 362..929	352/579 (60%) 437/579 (74%)	0.0
AAR44192	Rat NMDA receptor subunit, NR2A - Rattus rattus, 1464 aa. [DE4216321-A, 18-NOV-1993]	175..1023 77..911	245/873 (28%) 425/873 (48%)	2e-83

In a BLAST search of public sequence databases, the NOV33a protein was found to have homology to the proteins shown in the BLASTP data in Table 33D.

Table 33D. Public BLASTP Results for NOV33a				
Protein Accession Number	Protein/Organism/Length	NOV33a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL40734	N-METHYL-D-ASPARTATE RECEPTOR 3A - Homo sapiens (Human), 1115 aa.	1..1115 1..1115	1110/1115 (99%) 1112/1115 (99%)	0.0
Q62800	IONOTROPIC GLUTAMATE RECEPTOR - Rattus norvegicus (Rat), 1115 aa.	1..1115 1..1115	1032/1115 (92%) 1083/1115 (96%)	0.0
Q9R1M7				0.0

	RECEPTOR SPLICE VARIANT NR3A-2 - Rattus norvegicus (Rat), 1135 aa.	1..1135	1083/1135 (94%)	
CAC69380	SEQUENCE 7 FROM PATENT WO0144473 - Homo sapiens (Human), 1043 aa.	95..1103 6..1007	508/1047 (48%) 680/1047 (64%)	0.0
Q91ZU9	NMDA-TYPE GLUTAMATE RECEPTOR SUBUNIT NR3B PRECURSOR - Mus musculus (Mouse), 1003 aa.	112..1103 34..980	510/1001 (50%) 669/1001 (65%)	0.0

Pfam analysis predicts that the NOV33a protein contains the domains shown in the Table 33E.

Table 33E. Domain Analysis of NOV33a			
Pfam Domain	NOV33a Match Region	Identities/ Similarities for the Matched Region	Expect Value
lig_chan: domain 1 of 1	674..952	81/323 (25%) 232/323 (72%)	4e-95

Example 34.

The NOV34 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 34A.

Table 34A. NOV34 Sequence Analysis			
	SEQ ID NO: 111	1253 bp	
NOV34a, CG59315-01 DNA Sequence	CCCAGCGCCATGGGGAGTGGGCGTTCCTGGGCTCGCTGCTGGACGCGGTGCAGCTGCG AGTCGCCGCTCGTGGGCGCGCTCTGGCTGGTGGTCATGCTGATCTTCGCGATCCTGGT GCTGGCCACGGTGGGCGGCGCGTGTTCGAGGACGAGCAAGAGGAGTTCTGTGTGCAAC ACGCTGCAGCCGGGCTGTGCGCAGACCTGTACGACCGCGCCTTCCCGGTCTCCCACT ACCGCTTCTGGCTCTTCCACATCCTGCTGCTCTCGGCGCCCCGGTGTGTTCGTGCTG CTACTCCATGCACCGGGCAGGCAAGGAGGCGGGCGGCGCTGAGCGGCGGCGCAGTGC GCCCCCGGACTGCCCGAGGCCAGTGCAGCGCGTGCGCCCTGCGCGCCCCGCGCGCGG GCCGCTGCTACCTGCTGAGCGTGGCGCTGCGCCTGCTGGCCGAGCTGACCTTCCTGGG CGGCCAGGCGCTGCTCTACGGCTTCCGCGTGGCCCCGCACTTCGCGTGCAGCGGTCCG CCCTGCCCGCACACGGTCGACTGCTTCGTGAGCCGGCCACCGAGAAGACCGTCTTCG TGCTCTTCTATTTGCGGTGGGGCTGCTGTGCGGCTGCTCAGCGTAGCCGAGCTGGG CCACCTGCTCTGGAAGGGCGCCCGCGCGCGCGGGGAGCGTGACAACCGCTGCAACCGT GCACACGAAGAGGCGCAGAAGCTGCTCCCGCGCGCGCGCGCCACCTCCGCCACCGG CCCTGCCCTCCCGGCGCCCCGCGCCGAGCCGTGCGCCCCGCGGCTATGCGCACCC GGCGCCGGCCAGCCTCCGCGAGTGCGGCAGCGGCCGCGGCAGGAATGCGCCAATGGCT CCCAGATGTGGACGCCACCGCTTAACCCCTTACCCCCAGCCGCGCTCCCCAAGGGC CTTCAGCCTGAGCCCCGCCAACAGCAGGGAGCTCTGCCAGGTGAGAACCGCCAG GACTGGAGTCAGCGCCAGCCCGCCCCCTAGTGCCACGGACACCTCCCAACCTAGATCC TACCTGTCTTCCTTCTTGGAGCTGGAGGGGAAGGCTCATGGACACAAGAATGCAAGC ATGCATGCACACAGCTACACTGCTCCATCCCTCCCGCCGAGCTGCCAGGGTGGC CCTCCCTCGCTCCCATCTTGGCAGGGCGGGCGGCGCAGAGCGCTCCACTCCGATTTC CCCAGCCCCGAGCGTTTCGAGGCTCGACAAG		
	ORF Start: ATG at 10	ORF Stop: AG at 1252	
	SEQ ID NO: 112	414 aa	MW at 44773.0kD

NOV34a, CG59315-01 Protein Sequence	MGEWAFGLSLDAVQLQSPLVGRWLWVVMILFRILVLATVGGAVFEDEQE EFVCNTLQ PGCRTQCYDRAFPVSHYRFLHILLSSAPPVLFVVYSMHRAGKEAGGAEEAAQCAPG LPEAQCAPCALRARRARRCYLLSVALRLLAELTFLGGQALLYGFRVAPHFACAGPPCP HTVDCFVSRPTEKTVFVLFYFAVGLLSALLSVAELGHLLWKGRPRAGERDNRCNRAHE EAQKLLPPPPPPPPPPALPSRRPGPEPCAPPAYAHAPASLRECGSGRGRNAPMAPRC GRHRLTPYPPAALPQGSSSLSPANSRELCPGENQPTGVSASPLVPTDTSQPSYLS SFLEAGGEGSWTQECKHACTQLHCLPSPPADAAARVPLPRSPSWQGGRRRALHSGFPTP PSRSQART
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Further analysis of the NOV34a protein yielded the following properties shown in Table 34B.

Table 34B. Protein Sequence Properties NOV34a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.0300 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 39 and 40

A search of the NOV34a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 34C.

Table 34C. Geneseq Results for NOV34a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV34a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW49009	Mouse alpha 3 connexin protein - Mus sp, 417 aa. [WO9830677-A1, 16-JUL-1998]	1..296 1..327	121/334 (36%) 169/334 (50%)	5e-52
AAW23968	Connexin protein Cx40 - Homo sapiens, 358 aa. [WO9802150-A1, 22-JAN-1998]	1..215 1..232	93/233 (39%) 133/233 (56%)	9e-46
AAW23970	Connexin protein Cx45 - Homo sapiens, 396 aa. [WO9802150-A1, 22-JAN-1998]	4..212 3..253	93/252 (36%) 137/252 (53%)	3e-43
AAW23969	Connexin protein Cx43 - Homo sapiens, 382 aa. [WO9802150-A1, 22-JAN-1998]	1..216 1..235	86/235 (36%) 130/235 (54%)	1e-42
AAM93194	Human polypeptide, SEQ ID NO: 2573 - Homo sapiens, 370 aa. [EP1130094-A2, 05-SEP-2001]	7..384 7..360	129/409 (31%) 169/409 (40%)	8e-38

In a BLAST search of public sequence databases, the NOV34a protein was found to have homology to the proteins shown in the BLASTP data in Table 34D.

Table 34D. Public BLASTP Results for NOV34a				
Protein Accession Number	Protein/Organism/Length	NOV34a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q91YD1	CONNEXIN30.2 - Mus musculus (Mouse), 278 aa.	1..283 1..265	228/283 (80%) 240/283 (84%)	e-129
I46053	connexin44 - bovine, 402 aa.	1..397 1..396	151/418 (36%) 207/418 (49%)	1e-62
P41987	Gap junction alpha-3 protein (Connexin 44) (Cx44) - Bos taurus (Bovine), 401 aa.	2..397 1..395	150/417 (35%) 206/417 (48%)	4e-62
AAA50954	CONNEXIN44 - Bos taurus (Bovine), 407 aa.	1..398 1..402	154/429 (35%) 214/429 (48%)	1e-60
Q9TU17	GAP JUNCTION PROTEIN (CONNEXIN) - Ovis aries (Sheep), 413 aa.	1..398 1..408	147/415 (35%) 204/415 (48%)	1e-60

PFam analysis predicts that the NOV34a protein contains the domains shown in the Table 34E.

Table 34E. Domain Analysis of NOV34a			
Pfam Domain	NOV34a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DUF26: domain 1 of 1	107..152	12/56 (21%) 27/56 (48%)	1.4
connexin: domain 1 of 1	1..212	101/247 (41%) 150/247 (61%)	6.5e-75

Example 35.

The NOV35 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 35A.

Table 35A. NOV35 Sequence Analysis		
	SEQ ID NO: 113	724 bp

NOV35a, CG59203-01 DNA Sequence	<u>TAAATTCGCGGCCGCGTCGACCTTCCGCAGACTCAACTGAGAAGTCAGCCTCTGCGGC</u> <u>AGGCACCCAGGAATCTGCCTTTTCAGTTCTGTCTCCGGCAGGCTTTGAGGATGAAGGCT</u> <u>GCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACA</u> <u>CTCGTTGCAAACTGGCAAAAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTT</u> <u>CAGCCTTGGAACTGGATCTGCATGGCGTATTATGAGAGCGGCTACAACACCACAGCC</u> <u>CAGACGGTCCTGGATGACGGCAGCATCGACTACGGCATCTTCCAGATCAACAGCTTCG</u> <u>CGTGGTGACAGCGGAAAGCTGAAGGAGAACCACTGCCACGTCGCCTGCTCAGC</u> <u>CTTGGTCACTGATGACCTCACAGATGCGATTATCTGTGCCAAGAAAATTGTTAAAGAG</u> <u>ACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACACTGTGAGGGGAGAGACCTGT</u> <u>CCGACTGGAAAAAGACTGTGAGGTTTCCTAAACTGGAACCTGGACCCAGGATGCTTTG</u> <u>CAGCAACGCCCTAGGTTTGCAGTGAATGTCCAAATGCCTGTGTCATCTGTCCCGTT</u> <u>TCCTCCCAATATTCTCTCAAACCTGGAGAGGGGAAAATTAAGCTATACTTTTAAGAA</u> <u>AATAAATATTCCATTTAAATGTCAAAA</u>		
	ORF Start: ATG at 108	ORF Stop: TAA at 552	
	SEQ ID NO: 114	148 aa	MW at 16655.9kD
NOV35a, CG59203-01 Protein Sequence	MKAAGILTLLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYN TTAQTVLDDGSIDYGIQINSFAWCRRGKLENNHCHVACSALVTDLLTDAIICAKKI VKETQGMNYYQGWKKHCEGRDLSDWKKDCEVS		
	SEQ ID NO: 115	453 bp	
NOV35b, CG59203-02 DNA Sequence	<u>CATTCTGACCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACACTCGT</u> <u>TGCAAACTGGCAAAAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTTCAGCC</u> <u>TTGGAACTGGATCTGCATGGCGTATTATGAGAGCGGCTACAACACCACAGCCCAGAC</u> <u>GGTCCTGGATGACGGCAGCATCGACTACGGCATCTTCCAGATCAACAGCTTCGCGTGG</u> <u>TGCAGACGCGGAAAGCTGAAGGAGAACCACTGCCACGTCGCCTGCTCAGCCTTGG</u> <u>TCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGAGACACA</u> <u>AGGAATGAATTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCGAC</u> <u>TGGAAAAAAGGCTGTGAGGTTTCCTAAACTGGAACCTGGACCCAGGAT</u>		
	ORF Start: ATG at 134	ORF Stop: TAA at 431	
	SEQ ID NO: 116	99 aa	MW at 11288.6kD
NOV35b, CG59203-02 Protein Sequence	MAYYESGYNTTAQTVLDDGSIDYGIQINSFAWCRRGKLENNHCHVACSALVTDLLT DAIICARKIVKETQGMNYYQGWKKHCEGRDLSDWKKGCEVS		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 35B.

Table 35B. Comparison of NOV35a against NOV35b.		
Protein Sequence	NOV35a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV35b	50..148 1..99	97/99 (97%) 98/99 (98%)

Further analysis of the NOV35a protein yielded the following properties shown in Table 35C.

Table 35C. Protein Sequence Properties NOV35a	
Psort analysis:	0.3700 probability located in outside; 0.1697 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 20 and 21

A search of the NOV35a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 35D.

Table 35D. Geneseq Results for NOV35a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV35a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY57399	Human lysoenzyme LYC2 polypeptide - Homo sapiens, 148 aa. [WO200012722-A1, 09-MAR-2000]	1..148 1..148	143/148 (96%) 147/148 (98%)	3e-86
AAU29169	Human PRO polypeptide sequence #146 - Homo sapiens, 148 aa. [WO200168848-A2, 20-SEP-2001]	1..148 1..148	143/148 (96%) 146/148 (98%)	6e-86
AAB66145	Protein of the invention #57 - Unidentified, 148 aa. [WO200078961-A1, 28-DEC-2000]	1..148 1..148	143/148 (96%) 146/148 (98%)	6e-86
AAY99396	Human PRO1278 (UNQ648) amino acid sequence SEQ ID NO:203 - Homo sapiens, 148 aa. [WO200012708-A2, 09-MAR-2000]	1..148 1..148	143/148 (96%) 146/148 (98%)	6e-86
AAY71109	Human Hydrolase protein-7 (HYDRL-7) - Homo sapiens, 194 aa. [WO200028045-A2, 18-MAY-2000]	1..148 47..194	142/148 (95%) 146/148 (97%)	1e-85

In a BLAST search of public sequence databases, the NOV35a protein was found to have homology to the proteins shown in the BLASTP data in Table 35E.

Table 35E. Public BLASTP Results for NOV35a				
Protein Accession Number	Protein/Organism/Length	NOV35a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96LF2	BA14C22.1 (NOVEL PROTEIN SIMILAR TO LYSOZYME) - Homo sapiens (Human), 148 aa.	1..148 1..148	148/148 (100%) 148/148 (100%)	7e-88
Q9H1R9	BA534G20.1.1 (NOVEL PROTEIN SIMILAR TO LYSOZYME C-1 (1,4-BETA-N-ACYLMURAMIDASE C, EC 3.2.1.17) (ISOFORM 1)) - Homo sapiens (Human), 148 aa.	1..148 1..148	144/148 (97%) 147/148 (99%)	4e-86
AAH21730	HYPOTHETICAL 21.6 KDA PROTEIN - Homo sapiens (Human), 194 aa.	1..148 47..194	143/148 (96%) 146/148 (98%)	2e-85
Q9CPX3	1700038F02RIK PROTEIN - Mus musculus (Mouse), 148 aa.	1..148 1..148	110/148 (74%) 127/148 (85%)	3e-66
Q9H1R8	BA534G20.1.2 (NOVEL PROTEIN SIMILAR TO LYSOZYME C-1 (1,4-BETA-N-ACYLMURAMIDASE C, EC 3.2.1.17) (ISOFORM 2)) - Homo sapiens (Human), 106 aa (fragment).	20..125 1..106	104/106 (98%) 106/106 (99%)	1e-59

Pfam analysis predicts that the NOV35a protein contains the domains shown in the Table 35F.

Table 35F. Domain Analysis of NOV35a			
Pfam Domain	NOV35a Match Region	Identities/ Similarities for the Matched Region	Expect Value
lys: domain 1 of 1	20..145	68/129 (53%) 107/129 (83%)	8e-58

Example 36.

The NOV36 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 36A.

Table 36A. NOV36 Sequence Analysis

	SEQ ID NO: 117	712 bp
NOV36a, CG58662-01 DNA Sequence	GCAGCTATTGCACTTAATCGCGGCTGCTAGCACCATGTCCCGCGTTTGGTGCCTTGC CATGTGAAAGGCACCGTAGCCCTGCAGGTGGGGACGTATGGACCTCCCAAGGCCGGC CTAGTGTGCTGGTCATTGATGTACCTTCCCTGTGTCACTCCGTTCCGAGGGGATCAC ATTTAAGAATTATTACACAGCGTTTTTTGAGCATCCTGTCTGCAGCACACCTCAGCA CACACACCGGCCAAGTGGGTGACCTGCCTGTGGGACTACTGTCTGATGCCGACCCAC ACAGTGAGGAGGGAGCCAGGAGTATGTGTGCTGTTCAAGCAACAGATACTGTGTGA CATGGCCAGAATATCGGAGCTACACCTGATTCTGCAGCAGCCATCACCCTGTGGCTG TCTTTCACAGTGGAGGAGCTGCAGATCTATCAGCAGGGACCAAAGAGCCCTCCATGA TCTTCCCCAAGTGGCTCTCCACCCAGTGCCCTGTGAGCAACCTGCACCTCTCCATGA GGGTCTCCAGACCCAGCAGGATATCCTCTGAGGTGCAGCAGATGTGGGCACTGACA GAGATGATCCGGGCCAGTCACACCTCCGCGAGGATAGGCCACTTTGATGTAGATGGCT GTTATGACCTGAACCTACTCTCTACACTTGAGTGGTGGCTCTAGCCAAGATGTTGG CCTTCTGTGCCCACT	
	ORF Start: ATG at 35	ORF Stop: TGA at 668
	SEQ ID NO: 118	211 aa MW at 23932.3kD
NOV36a, CG58662-01 Protein Sequence	MSRVLVPCHVKGTVALQVGDVWTSQGRPSVLVIDVTFPCVTPFEGITFKNYTAFPEH PVCQHTSAHTPAKWVTCCLWDYCLMPDPHSEGAQEYVSLFKQQLCDMARISELHLIL QQPSPLWLSFTVEELQIYQQGPKSPSMIFPKWLSHPVPCPEQALLHEGLPDPSPRVSE VQQMWALTEMIRASHTSARIGHFDVDGCDLNLSSYT	
	SEQ ID NO: 119	843 bp
NOV36b, CG58662-02 DNA Sequence	CTGGCCTGAAGCCATGTCCCGCGTTCTAGCACCATGTCCCGCGTCTAGCACCATGTCC CGCGTCTAGCACCATGTCCCGCGTTCTAGCACCATGTCCCGCGTCTAGCACCATGTCC CCGCGTTCTAGCACCATGTCCCGCGTTTGGTGCCTTGCCATGTGAAAGGCTCCGTAG CCCTCCAGGTGGGCGACGTGCGGACCTCCCAAGGCCGCGCTGGCGTGTGGTCATCGA TGTACCTTCCCGAGCGTCGCTCCCTTCGAGTTGCGAGAAATCACGTTAAGAATTAC TACACAGCTTTTTTGAAGCATCCGTGTCGTCAGTACACCTCAGCACACACCTGCCA AGTGGGTGACCTGCCTTCGGGACTACTGCCTGATGCCTGACCCACACAGTGAAGAGGG AGCCAGGAGTATGTATCGCTGTTCAAGCATCAGATGCTATGTGACATGGCTAGAATA TCGGAGCTACGCTGATTCTGCGGCAGCCATCACCCTGTGGCTGTCTTTCACAGTGG AGGAGCTGCAGATCTATCAGCAGGGACCAAAGAGCCCTCCGTCACCTTTCCCAAGTG GCTCTCCACCCAGTGCCCTGTGAGCAACCTGCACCTCCTCCGTGAGGGTTTCCAGAC CCCAGCAGGATATCCTCCGAGGTGCAGCAGATGTGGGCACTGACAGAGATGATCCGGG CCAGTCACACCTCCGCAAGGATCGGCCGCTTTGATGTGGATGGCTGTTATGACCTGAC CTTGCTCTCTACACTGAATGGTTGCTCTTAGCCAAGATGTTGGCCTTTTGTGGGC ACAGAAAGGCCAACGCGGGACATGGTGCTAG	
	ORF Start: ATG at 132	ORF Stop: TGA at 771
	SEQ ID NO: 120	213 aa MW at 24222.6kD
NOV36b, CG58662-02 Protein Sequence	MSRVLVPCHVKGSVALQVGDVRTSQGRPGVLVIDVTFPSVAPPELQETFKNYTAFIL SIRVRQYTSHTPAKWVTCCLRDYCLMPDPHSEGAQEYVSLFKHQLCDMARISELRL ILRQPSPLWLSFTVEELQIYQQGPKSPSVTFPKWLSHPVPCPEQALLREGFPDPSRVSE SEVQQMWALTEMIRASHTSARIGHFDVDGCDLNLSSYT	

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 36B.

Table 36B. Comparison of NOV36a against NOV36b.		
Protein Sequence	NOV36a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV36b	1..211	188/213 (88%)
	1..213	193/213 (90%)

Further analysis of the NOV36a protein yielded the following properties shown in Table 36C.

Table 36C. Protein Sequence Properties NOV36a	
PSort analysis:	0.5666 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1562 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV36a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 36D.

Table 36D. Geneseq Results for NOV36a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV36a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG04038	Human secreted protein, SEQ ID NO: 8119 - Homo sapiens, 115 aa. [EP1033401-A2, 06-SEP-2000]	1..103 1..105	82/105 (78%) 85/105 (80%)	1e-39

In a BLAST search of public sequence databases, the NOV36a protein was found to have homology to the proteins shown in the BLASTP data in Table 36E.

Table 36E. Public BLASTP Results for NOV36a				
Protein Accession Number	Protein/Organism/Length	NOV36a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BSH3	SIMILAR TO RIKEN CDNA 1500032A17 GENE - Homo sapiens (Human), 213 aa.	1..211 1..213	190/213 (89%) 195/213 (91%)	e-107
Q9CQM0	1500032A17RIK PROTEIN - Mus musculus (Mouse), 213 aa.	1..211 1..213	174/213 (81%) 183/213 (85%)	4e-97

PFam analysis predicts that the NOV36a protein contains the domains shown in the Table 36F.

Table 36F. Domain Analysis of NOV36a			
Pfam Domain	NOV36a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 37.

The NOV37 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 37A.

Table 37A. NOV37 Sequence Analysis			
	SEQ ID NO: 121	520 bp	
NOV37a, CG58584-01 DNA Sequence	<u>CATTGCTGTCTCCTCTGCTCACCAGCAGCTGTACTGGAGCCACCCGCGAAAATTCGG</u> <u>CCAGGGTTCTCGCTCTTGTCTGTCTGTTCAAACCGGCACGGTCTGATCCGGAAATAT</u> <u>GGCCTCAATATGTGCCGCCAGTGTTCCTGTCAGTACGCGAAGGATATCGGTTTCATT</u> <u>AGAAAGACCTGAGCTGTCTTCCTTGGCACTGCCTATGGAGGTGACACCCATCTCCTCC</u> <u>ATCATGGCCATCCTGAGACCGCTCGCGAAGCCCAAGATCATCAAAAAGAGCACCAAGT</u> <u>TCACTGGGAACCACTCAGACTGATATGTCAAATTAAGGGTAACTGGTGAAACACAG</u> <u>AGGTATTGACAACAGGGTTCATAGAAGGTTTGAGGGCCAGATCTATGCCCAACATTGG</u> <u>TTATGGGAGAAACAAAAGACAAAGCACATACTGCCAGTGGCTTCTGGAAGTTCCTG</u> <u>GTCCACAACGTTAAGGAGCTGGAAGTACTGCTGGTGAGCAGAGGAGACAGCAAATG</u>		
	ORF Start: TTT at 3	ORF Stop: TGA at 216	
	SEQ ID NO: 122	71 aa	MW at 8461.8kD
NOV37a, CG58584-01 Protein Sequence	FAVSSAHQQLYWSHPRKFGQGSRSRVCNSNRHGLIRKYGLNMCRCQCFRQYAKDIGFIK KDLSCLPWHCLWR		

Further analysis of the NOV37a protein yielded the following properties shown in Table 37B.

Table 37B. Protein Sequence Properties NOV37a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV37a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 37C.

Table 37C. Geneseq Results for NOV37a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV37a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG76128	Human colon cancer antigen protein SEQ ID NO:6892 - Homo sapiens, 80 aa. [WO200122920-A2, 05-APR-2001]	7..60 2..55	46/54 (85%) 48/54 (88%)	4e-24
AAM79084	Human protein SEQ ID NO 1746 - Homo sapiens, 56 aa. [WO200157190- A2, 09-AUG-2001]	7..60 3..56	39/54 (72%) 43/54 (79%)	2e-18
AAG39921	Arabidopsis thaliana protein fragment SEQ ID NO: 49464 - Arabidopsis thaliana, 637 aa. [EP1033405-A2, 06- SEP-2000]	7..63 3..58	40/57 (70%) 45/57 (78%)	2e-18
AAM80068	Human protein SEQ ID NO 3714 - Homo sapiens, 74 aa. [WO200157190- A2, 09-AUG-2001]	7..58 22..73	38/52 (73%) 42/52 (80%)	5e-18
AAG34802	Arabidopsis thaliana protein fragment SEQ ID NO: 42406 - Arabidopsis thaliana, 56 aa. [EP1033405-A2, 06- SEP-2000]	7..58 3..54	37/52 (71%) 42/52 (80%)	1e-17

In a BLAST search of public sequence databases, the NOV37a protein was found to have homology to the proteins shown in the BLASTP data in Table 37D.

Table 37D. Public BLASTP Results for NOV37a				
Protein Accession Number	Protein/Organism/Length	NOV37a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
BAB79485	RIBOSOMAL PROTEIN S29 - Homo sapiens (Human), 56 aa.	7..60 3..56	53/54 (98%) 53/54 (98%)	1e-27
P30054	40S ribosomal protein S29 - Homo sapiens (Human),, 55 aa.	7..60 2..55	53/54 (98%) 53/54 (98%)	1e-27
Q90YP2	40S RIBOSOMAL PROTEIN S29 - Ictalurus punctatus (Channel catfish), 56 aa.	7..60 3..56	52/54 (96%) 53/54 (97%)	2e-27
AAL62474	RIBOSOMAL PROTEIN S29 - Spodoptera frugiperda (Fall armyworm), 56 aa.	7..60 3..56	41/54 (75%) 48/54 (87%)	6e-21
Q9VH69	CG8495 PROTEIN - Drosophila melanogaster (Fruit fly), 56 aa.	10..60 6..56	41/51 (80%) 46/51 (89%)	3e-20

PFam analysis predicts that the NOV37a protein contains the domains shown in the Table 37E.

Table 37E. Domain Analysis of NOV37a			
Pfam Domain	NOV37a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Ribosomal_S14: domain 1 of 1	7..61	17/60 (28%) 51/60 (85%)	7.5e-20

Example 38.

The NOV38 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 38A.

Table 38A. NOV38 Sequence Analysis		
	SEQ ID NO: 123	2039 bp
NOV38a, CG58538-01 DNA Sequence	GCAGCACACCTGCTCTGTGACTGACACTCTTGAGAGAAGTGGGGCCACTTCAGGGACAT GGACAAGGTGTTGTACCTGCTGTGCAGAGCCTGTTATCTGTTTCAGAAATGACCGAAGA AGCATGCCGAACACGGAGTCAGAAACGAGCGCTTGAACGGGACCCAACAGAGGACGAT GTGGAGAGCAAGAAAATAAAAAATGGAGAGAGGATTGTTGGCTTCAGATTAAACACTG ACGGAGACATGAGGGTGACACCTGAGCCGGGAGCAGGTCCAACCAAGGATTGCTGAG GGCAACAGAGGCCACGGCCATGGCCATGGGCAGAGGCGAAGGGCTGGTGGGCGATGGG CCCGTGGACATGCGCACCTCACACAGTGACATGAAGTCCGAGAGGAGACCCCTCAC CTGACGTGATTGTGCTCTCCGACAACGAGCAGCCCTCGAGCCGAGAGTGAATGGGCT GACCACGGTGGCCTTGAAGGAGACTAGCACCGAGGCCCTCATGAAAAGCAGTCCTGAA	

	GAACGAGAAAGGATGATCAAGCAGCTGAAGGAAGAATTGAGGTTAGAAGAAGCAAAAC TCGTGTGTTGAAAAAGTTGCGGCAGAGTCAATACAAAAGGAAGCCACGCCAGAA GCCCCACAGGTTCTGTGGGAGCACCGTGACACCCCTCCCCCGCTTGTTCGGGGCACT CAGAACATTCTGTGCTGGCAAGCCATCACTCCAGACCTCTTCAGCTCGGATGCCCGGCA GTGTATACCCCGCCCCCTGGTCCGAGGTGGGCGAGGCGCTCTCGAAGCTGGGGCC ACAGGCGAGTCAAGAGTCTGTCATGCCCCACTCGTCAGGGGGGCTCAGCAAATCCAC AGCATTAGGCAACATTCCAGCACAGGGCCACGCCCTCTCTCTGGCCCCCGGGCGT CGGTGCCAGTGTGCAGATTCAAGGACAGAGGATCATCCAGCAGGCGCTCATCCGCGT CGCCAAATGTTCCCAACACCAGCTGCTCGTCAACATCCCACAGCCACCCAGCATCA CTGAAGGGGACAAACAGCCACCTCCGCTCAGGCCAACTCCACCCCTAGTGTGGCCT CTGTGGTCACTCTGCGGAGTCTCCAGCAAGCCGACAGGCGCGCCCAAGCTGGCGCT GCGCAAACAGCTGGAGAAGACGCTACTCGAGATCCCCCAACCAAGCCCCAGCCCCA GAGATGAATTCCTGCCAGCGCCGCAACACGAGTTCATCTACCTGGTCGGCGCTGG AGGAGTGGTGCAAGACCTACTGGAGACACAAGCAGGCAGGATGTCGGCCGCACTGT GCTGTCCCGGAGCCCTACATGTGTGCACAGTGAAGACGGAATTCAGTGCCTGG CGGAGGAGAAGAGCGCGCCATCATGTGTGAGAATGCAATGACAACCAACAGAAGA AGGCGCTCAAGGTGGAGCACACCAGCGGCTGAAGGCCCTTTGTGAAGCGCTGCA GCAGGAACAGGAGATTGAGCAGCGGCTCTGTCAGCAGGCGACGGCCCTGCAACAGCC AAGGCCGAGCCACCGCTGCCCCACACCCCTGCTGAAGCAGGCTCCAGCCAGCTGT CCCCGGGTTTCGGCCACGACGCCCGAGGTGTCTGTCACAGTTCAGTCCGTCACCCAA ACTGCAGAACTCAGCCTCGGCCACAGCCTGGTCAGCAGGACCGGCAGACATTCTGAG AGAACCGTGAGCGCGGCAAGGGCAGCGCCACCTCCAACCTGGAAGAAGACGCCCTCA GCACAGGCGGGACCCCTTGCCTTGTGACCCCAAGCCTGGCGGTGCACAAGAGCTCCTC GGCCGTGGACCGCCAGCAGAGTACCTCCTGGACATGATCCACCCCGCTCCATCCCC CAGTCAGCCACGTGGAATAGTCCGAGCCAGGCCCGTGGGAAGACGGGCTCCCTCCTC CCCCACCTGGCCCCGTCTAGAAGGACCCACTGCACCACCCTCCGCTGGCTCGGGAA GACACCGTG		
	ORF Start: ATG at 106		ORF Stop: TAG at 1933
	SEQ ID NO: 124	609 aa	MW at 65295.8kD
NOV38a, CG58538-01 Protein Sequence	MTEECRTRSQKRALERDPTEDDVESKKIKMERGLLASDLNTDGMVTPPEPGAGPTQ GLLRATEATAMAMGRGEGLVGDGPVDMRTSHSDMKSERPPSPDIVVLSDNEQPSSPR VNLTTVALKETSTEALMKSSPEERERMIKQLKEELRLEEAKLVLLKKLRQSQIQKEA TAQKPTGSGVSTVTPPLVRGTQNI PAGKPSLQTSSARMPGSI PPPLVRGGQOASS KLGPQASSQVMPPLVRGAQQIHSIRQHSSTGPPPLLLAPRASVPSVQIQGQRI IQQG LIRVANVPNTSLLVNI PQTPASLKGTTATSAQANSTPTSASVVTSAESPASRQAAA KLALRKQLEKTLLEIPPKPPAPEMNF LPSAANNEFIYLVGLEEVQNLLTQAGRMS AATVLSREPYMCAQCKTDFTCRWEEKSGAIMCENCMTTNQKKALKVEHTSRLKAAFV KALQQEQEIEQRL LQQGTAPAQAQAEPTAAPHPVLKQASSQLSRGSATTPRGVLHTFS PSPKLQNSASATALVSRTGRHSERTVSAGKGSATSNWKKTPLSTGGTLAFVSPSLAVH KSSSAVDRQREYLLDMIPPRSIQSATWK		

Further analysis of the NOV38a protein yielded the following properties shown in Table 38B.

Table 38B. Protein Sequence Properties NOV38a	
PSort analysis:	0.4404 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1257 probability located in mitochondrial inner membrane; 0.1257 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV38a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 38C.

Table 38C. Geneseq Results for NOV38a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV38a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM00991	Human bone marrow protein, SEQ ID NO: 492 - Homo sapiens, 502 aa. [WO200153453-A2, 26-JUL-2001]	1..471 4..473	217/504 (43%) 290/504 (57%)	2e-87
AAM00944	Human bone marrow protein, SEQ ID NO: 420 - Homo sapiens, 546 aa. [WO200153453-A2, 26-JUL-2001]	1..471 48..517	217/504 (43%) 290/504 (57%)	2e-87
AAM00831	Human bone marrow protein, SEQ ID NO: 194 - Homo sapiens, 266 aa. [WO200153453-A2, 26-JUL-2001]	1..197 47..262	84/217 (38%) 110/217 (49%)	1e-23
AAM85818	Human immune/haematopoietic antigen SEQ ID NO:13411 - Homo sapiens, 84 aa. [WO200157182-A2, 09-AUG-2001]	417..471 1..55	41/55 (74%) 49/55 (88%)	7e-19

In a BLAST search of public sequence databases, the NOV38a protein was found to have homology to the proteins shown in the BLASTP data in Table 38D.

Table 38D. Public BLASTP Results for NOV38a				
Protein Accession Number	Protein/Organism/Length	NOV38a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
No Significant Matches Found				

PFam analysis predicts that the NOV38a protein contains the domains shown in the Table 38E.

Table 38E. Domain Analysis of NOV38a			
Pfam Domain	NOV38a Match Region	Identities/ Similarities for the Matched Region	Expect Value
GATA: domain 1 of 1	414..453	12/43 (28%) 17/43 (40%)	1.1

Example 39.

The NOV39 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 39A.

Table 39A. NOV39 Sequence Analysis			
	SEQ ID NO: 125	1421 bp	
NOV39a, CG59371-01 DNA Sequence	ACCATTTCAGAGATGCTTCCAGAAGTACCAAAGATTTAATTAAGTAAGTGGGGAT CGAAGCCTAGTAACCTCCAAATCCGAACTACATTAGAAAAATTAAGGGAGAAATTGC ACACTTAAAGACATCAGTGGATGAAATCACAAGTGGGAAAGGAAAGCTGACTGATAAA GAGAGACACAGACTTTTGGAGAAAATTCGAGTCCTTGAGGCTGAGAAGGAGAAGAATG CTTATCAACTCACAGAGAAGGACAAAGAAATACAGCGACTGAGAGACCAACTGAAGGC CAGATATAGTACTACCACATTGCTTGAACAGCTGGAAGAGACAACGAGAGAAGGAGAA AGGAGGGAGCAGGTGTTGAAAGCCTTATCTGAAGAGAAAGACGTATTGAAACAACAGT TGCTGCTGCAACCTCACGAATTGCTGAACTTGAAAGCAAAACCAATACACTCCGTTT ATCACAGACTGTGGCTCCAACTGCTTCAACTCATCAATAAATAATATTTCATGAAATG GAAATACAGCTGAAAGATGCTCTGGAGAAAAATCAGCAGTGGCTCGTGTATGATCAGC AGCGGGAAGTCTATGTAAGGAGCTTTTAGCAAAGATCTTTGAGTTGGAAAAGAAAAAC GGAAACAGCTGCTCACTTCACTCCACAGCAGACAAAAAGCCTGAATCAGAAGGTTAT CTTCAAGAAGAGAAGCAGAAATGTTACAACGATCTCTTGCCAAGTGCAAAAAAGATC TTGAGGTTGAACGACAAACCATAACTCAGCTGAGTTTTGAAGTGAAGTGAATTCGAAG AAAAATGAAGAAACCCAAAAAGAAGTTCACAATTTAAATCAGCTGTTGTATTACAA AGAAGGGCAGATGTGCAACATCTGGAAGATGATAGGCATAAAACAGAGAAGATACAAA AACTCAGGAAGAGAATGATATTGCTAGGGGAAAACCTGAAGAAGAGAAGAAGAGATC CGAAGAGCTCTTATCTCAGGTCCAGTCTCTTTACACATCTCTGCTAAAGCAGCAAGAA GAACAAACAAGGTTAGCTCTGTTGGAACAACAGATGCAGGCATGTACTTTAGACTTTG AAAATGAAAAACTCGACCGTCAACATGTGCAGCATCAATTGCATGTAATTTCTAAGGA GCTCCGAAAAGCAAGAAAAATATAACACAGTTGGAATCCTTGAACAGCTTCATGAG TTTGCCATCACAGAGCCATTAGTCACTTTCCAAGGAGAGACTGAAACAGAGAAAAAG TTGCCGCTCACCAAAAAGTCCCAGTCTGCACTCAATGGAAGCCTGGTGGAAATGTCC CAAGTGCAATATACAGTATCCAGCCACTGAGCATCGCGATCTGCTTCCATGTGGAA TACTGTTCAAAGTAGCAAAATAAGTATT		
	ORF Start: ATG at 13	ORF Stop: TAG at 1405	
	SEQ ID NO: 126	464 aa	MW at 54045.6kD
NOV39a, CG59371-01 Protein Sequence	MSSRSTKDLISKWGSKPSNSKSETTLEKLKGEIAHLKTSVDEITSGKGKLTDKERHR LLEKIRVLEAEKEKNAYQLTEKDKEIQRLRDQLKARYSTTTLLEQLEETTREGERREQ VLKALSEEKDVLLKQQLSAATSRIAELESKNTNLRSLQTVAPNCFNNSINNIHMEIQL KDALEKNQQLVVDQREVYVKGLLAKIFELEKKTETAHSLPQQTKKPESEGYLQEE KQKCYNDLLASAKKDLEVERQTITQLSFELSEFRRKYEETQKEVHNLNQLLYSQRRAD VQHLEDDRHKTEKIQKLREENDIARGKLEEEKRSEELLSQVQSLYTSLLKQEEQTR VALLEQQMQACTLDFENEKLDROHVQHQHLHVILKELRKARKNITQLESKQLHEFAIT EPLVTFQGETENREKVAASPKSPTAALNGSLVECPKCNIQYPATEHRDLLVHVEYCSK		

Further analysis of the NOV39a protein yielded the following properties shown in Table 39B.

Table 39B. Protein Sequence Properties NOV39a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV39a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 39C.

Table 39C. Geneseq Results for NOV39a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV39a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB92925	Human protein sequence SEQ ID NO:11576 - Homo sapiens, 231 aa. [EP1074617-A2, 07-FEB-2001]	170..392 1..223	222/223 (99%) 222/223 (99%)	e-122
AAG75490	Human colon cancer antigen protein SEQ ID NO:6254 - Homo sapiens, 165 aa. [WO200122920-A2, 05-APR-2001]	1..67 99..165	64/67 (95%) 64/67 (95%)	1e-28
AAM78520	Human protein SEQ ID NO 1182 - Homo sapiens, 990 aa. [WO200157190-A2, 09-AUG-2001]	6..394 515..929	96/421 (22%) 182/421 (42%)	3e-12
AAM41000	Human polypeptide SEQ ID NO 5931 - Homo sapiens, 1988 aa. [WO200153312-A1, 26-JUL-2001]	70..420 852..1203	90/384 (23%) 161/384 (41%)	3e-12
AAM40999	Human polypeptide SEQ ID NO 5930 - Homo sapiens, 1988 aa. [WO200153312-A1, 26-JUL-2001]	70..420 852..1203	90/384 (23%) 161/384 (41%)	3e-12

In a BLAST search of public sequence databases, the NOV39a protein was found to have homology to the proteins shown in the BLASTP data in Table 39D.

Table 39D. Public BLASTP Results for NOV39a				
Protein Accession Number	Protein/Organism/Length	NOV39a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96H32	SIMILAR TO RIKEN CDNA 1200008O12 GENE - Homo sapiens (Human), 464 aa.	1..464 1..464	458/464 (98%) 458/464 (98%)	0.0
Q9DBZ8	1200008O12RIK PROTEIN - Mus musculus (Mouse), 462 aa.	1..464 1..462	348/464 (75%) 401/464 (86%)	0.0
Q9NVS7				e-122

	NT2RP2001245 - Homo sapiens (Human), 231 aa.	1..223	222/223 (99%)	
Q9CZP8	2700032M20RIK PROTEIN - Mus musculus (Mouse), 189 aa.	1..176 1..176	121/176 (68%) 150/176 (84%)	3e-63
Q9VJE5	CLIP-190 PROTEIN - Drosophila melanogaster (Fruit fly), 1690 aa.	4..439 675..1118	108/461 (23%) 203/461 (43%)	2e-16

Pfam analysis predicts that the NOV39a protein contains the domains shown in the Table 39E.

Table 39E. Domain Analysis of NOV39a			
Pfam Domain	NOV39a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 40.

The NOV40 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 40A.

Table 40A. NOV40 Sequence Analysis		
	SEQ ID NO: 127	3955 bp
NOV40a, CG59346-01 DNA Sequence	<p>TGCACCCTCGCTGCCTCCTTTTCCTCCATGCTGCCTGGATCTGGCGAGCTGGGGTGATT AATTGGCTATGATGATGAACGTCCCGCGGAGGAGCGGCCGGTGTATGATGACGGG CTACAATAATGGTCGTGTCCCGGAATTCTCTTACAGTGACTGCATTATTGAGGAG AAGACGGTGGTCTGCAGAAAAAGACAATGAGGGCTTTGGATTTCGTGCTTCGAGGGG CCAAAGCTGACACACCCATTGAAGAATTCACACCAACACCGGCTTTCCAGCCCTACA GTACCTGGAGTCCGTGGATGAAGGTGGGGTGGCGTGGCAAGCCGGAATAAGGACCGG GACTTCTTGATTGAGTTAACAATGAGAATGTTGTCAAAGTCGGCCACAGGCAGGTGG TGAACATGATCCGGCAGGGAGGGAATCACCTGGTCTTAAGGTGGTCACGGTGACCAG GAATCTGGACCCGACGACACCGCCAGGAAGAAAGCTCCCCCGCTCCAAAGCGGGCA CCGACCACAGCCCTCACCTGCGCTCCAAGTCCATGACCTCGGAGCTGGAGGAGCTCG ATAAACCCGAGGAGATAGTCCCGGCTCCAAGCCCTCCCGCTGCTGAGAACATGGC TGTGGAACCGAGGGTGGCGACCATCAAGCAGCGGCCAGCAGCCGGTCTTCCCGCG GGCTCAGACATGAACGTGAGTGGCCGTACCTTGGGACACGAGGGCGGGGGCGACGG TGCCCCCTAGGCTCTCTGGTTTGACGTCTGTGTAGCAACGCCAAGGAATCGCCGTGAT GACGCCCACTGTTCTTGGAGCCCAAGCCCGTTTCTGGGCATCCCTCGAGGTACG ATGCGAAGGCAGAAATCAATAGGAATAACAGAGGAAGAGCGGCAGTTTCTGGCTCCTC CAATGCTGAAGTTCAACAGAAGCCTGTCCATGCCGACACCTCTGAGGACATCCCCC TCCACCGCAGTCTGTGCCCCGTCCCCACCACACCTTCCCCAACCTTACAAGTGC CCCCAAGTCCCCAAGTCTACGGGACGATTAAGCCTCGTTCAATCAGAATT CTGCGGCCAAGGTGTCCCCGCCACCAGGTCCGACACCGTGGCCACCATGATGAGGGA GAAGGGGATGTACTTCAGGAGAGAGTGGACCGCTACTCTTGGACTCTGAAGACCTC TACAGTCGGAATGCCGCCCGCAAGCCAATTCCGCAACAAGAGAGGCCAGATGCCAG AAAACCCATACTCAGAGGTGGGAAGATCGCCAGCAAAGCCGTCTACGTCCCGCCAA GCCCGCCAGGCGGAAGGGATGCTGGTGAAGCAGTCCAACGTGGAGGACAGCCCCGAG AAGACGTGCTCCATCCCTATCCCGACCATCATCGTGAAGGAGCCGTCCACCAGCAGCA GCGGCAAGAGCAGCGGAGGGCAGCAGCATGGAGATCGACCCCAAGGCCCGGAGCACC GAGCCAGCTGCGGCTGACGAAAGCCTGACCGTCAGCAGCCCCCTTGGCGCGCCATC GCCGGAGCGTCCGCGACCGTGAGAAGCGGCTGGAAGCCAGGAGGAATCCCCGGCT TCCTCTCCACAGACCTGGGGATGAGGATGTGGGCTGGGGCCACCGCCCCCAGGAC GCGGCCCTCCATGTTCCCGAGGAGGGGATTTGCTGACGAGGACAGCGCCGAGCAGC CTGTCTATCCCCATGCCGAGTGCCACGCCAGGAGCCGAAAACCATTTCTGGGGTG GCGCGAGGCGAGTGTCCGGGTGAGGCTGGGAGGCGCTGAATTCACGTCCAAAGC CCAGGGGCCGAGAGCAGCCAGCAGTGCCCTCCCGAGCAGCGGCACAGCCGCCCC GGGAATTATGTCCACCACTCACAGGGCGGCTGCTTGATCCAGCTCCCGCTGGCCC</p>	

	<p>TGGCACTCTCCGCAAGGGACCGAGCCATGAAGGAGTCTCAACAGGGACCCAAAGGGGA GGCCCCCAAGGCCGACCTCAACAAACCTCTTTACATTGATACCAAATCGGGCCCAGC CTGGATGCCGGCTTCCCTACGGTCACCGAGCAGAACACCCGGGGACCCCTGAGGCGGC AGGAGACGGAGAACAAGTACGAGACCGACCTGGGCCGAGACCGGAAAGGCGATGACAA GAAGAACATGCTGATCGACATCATGGACACGTCACGAGCAGAGTCCGGCTGGCCTGCTG ATGGTGCCACCGTGGACGCCACTAAGCTGGACAACGCCCTGCAGGAAGAGGACGAGA AGGCAGAGGTGGAGATGAAGCCAGACAGCTCGCCGTCGAGGTGCCAGAAGGTGTTTC CGAAACCGAAGGTGCTTTACAGATCTCCGCTGCCCGGAGCCACCACCGTGCCCGGC AGAACCATCGTCGGGTGGGCTCCATGGAAGAGGCGGTGATTTTGCCATTCCGCATCC CTCCTCCCCCTCTGGCATCGTGGACTTGGATGAGGATTTTATTTTACAGAGCCATT GCCTCCTCCCCGGAATTTGCAAATAGTTTGTATATCCCCGATGACCGGGCAGCTTCT GTCCCCGCTCTCTCAGACTTAGTGAAGCAGAAGAAAGCGACACCCCTCAGTCCCCCTT CGTTGAACTCCAGCCAACCAACCACTCTGCAGACAGCAAGAAGCCAGCCAGTCTTTC AAACTGTCTGCCTGCCTCATTCTGACCCCTGAAAGCTTTGAGCCGTGCGCGAC TCTGGGATCGAGGAGGTGGACAGCCGAGTAGCAGCGACACCACCTCGAGACGACCA GCACTATCTCCACCGTGTCTAGCATCTCCACCTGTCTTCCGAAGGTGGAGAGATGT GGACACCTGCACAGTCTATGCAGATGGGCAAGCATTATGGTTGACAAACCCAGTA CCTCCTAAGCCAAATGAAGCCATCATTCAAAAGCAATGCACTTATCAAGAGC CGCTCGTGAAGAAGATGTAGATAGCTTGTATCCCCCGCCGCTCCCCGCCCCC GCCGGGCGAGTGCCAGCCTGGGATGGCAAGGTTCTCCAGCAAGGACCTCAAGTTG TGGGGCGAGCTCACAGAGATCAAAAGCCGATCTCTCAGGCCCAAGGCAAGCGTTA TTAGTGAATTGAACTCTATCTACAGCAAATGAACCGAGAGAAATGGCAAAGCCGGG GGAAGGACTGGATTACCAATGGGAGCCAAGTCCGCGCAGCTCGCTCCAGAAGCCCG GAGATCATGAGCACCATCTCAGGTACACGGAGCACGACGGTCACCTTCACTGTTCCGC CCGGCACCTCCAGCCCATCACCTGCAGAGCCGGCCCCCGACTATGAAGACGAGGAC CTCAGGAACAAGACGTGCCCAAGCCCTGTGGTCTCGCCAACAGAGATGAACAAAGAG ACCCCTGCCCGCCCCCTGTCTGCTGCCACCGCCTCTCCTTCTCCGCTCTCTCAGATG TCTTTAGCCTTCCAAGCCAGCCCCCTTCTGGGGATCTATTGGCTTGAACCCAGCGGG ACGCACTAGGTGCGCATCCCCCTCGATACTGCAACAGCCAATCTCAAAATGAAGCCTTT ACAACTAAACCTGTCCACCTGTGGACTAAACAGATGTGGCCGATGGCTGGAAGTC TAAACTTGGGTGAACATAAAGAGGCCCTTATGGACAATGAGATCGATGGCAGTCACTT ACCAAACTGCAGAAGGAGGACCTCATCGATCTGGGGTAACTCGAGTCGGGCACAGA ATGAACATAGAAGGGCTTTGAAACAGCTGTGGACAGATAAGGACCGGCTGCTTCCA CCTCGCAGACTGCTTGTATTATAAGTAGAGATGGGCTCGTGCTGAAACATCTGAATGC CAAGCGAAGTC</p>
	<p>ORF Start: ATG at 67 ORF Stop: TAA at 3868</p>
	<p>SEQ ID NO: 128 1267 aa MW at 136108.7kD</p>
<p>NOV40a, CG59346-01 Protein Sequence</p>	<p>MMNVPPGGAAAVMMTGYNNGRCPRNSLYSDCIIEEKTVVQLKKDNEGFVFLRGAKA DTPIEEFTPTPAFFALQYLESVDEGGVAWQAGLRGTGDFLIEVNNENVKVGHQVVM IRQGGNHLVLKVTVTRNLDPDDTARKKAPPPKRAPTTALTLSKSMSELELDKP EEIVPASKPSRAENMAVEPRVATIKQRPSRCFPAGSDMNVSGRTLGRGRGPTVPP RLSLGLQSVYERQGIAMVTPTPVPGSPKAPFLGIPRGTMRRQKSIGITEERQFLAPML KFTRSLSPDTSEDI PPPQSVPPSPPPSPPTTNCPSPTPRVYGTIKPAFNQNSAA KVSPATRSDTVATMMREKGMFRRELDRLDSEDLYSRNAGPQANFRNRKGQMPENP YSEVGKIASKAVYVPAKPARRKGMVLKQSNVEDSPEKTCISIPIPTIIVKEPSTSSSGK SSQSSMEIDPOAPEPPSQLRPDESLTVSSPFAAIIAGAVRDREKRLEARRNSPAFLS TDLGDEDVGLGPPAPRTRPSMFPEEGDFAEDSAEQLSSPMPSATPREPENHFVGGAE ASAPGEAGRPLNSTSKAQGPSSPAVPSASSGTAGPGNYVHPLTGRLLDPSSPLALAL SARDRAMKESQQGPKGEAPKADLNKPLYIDTKMRPSLDAGFPPTVRQNRGRLRRQET ENKYETDLGRDRKGDDKNMLIDIMDTSQQKSAGLLMVHTVDATKLDNALQEEDKAE VEMKPDSSPSEVPEGVSETEGALQISAAPEPTTVPGRTIVAVGSMEEAVILPFRIPPP PLASVDLDEDFIFTEPLPPPLEFANSFDIPDDRAASVPALSDLVKQKSDTPQSPSLN SSQPTNSADSKKPASLNSCLPASFLPPPEFSDAVADSGIEEVDSSRSDSHLETTSTI STVSSISTLSSEGGENVDTCTVYADGQAFMVDKPPVPPKPKMKPIIHKSNALYQDALV EEDVDSFVI PPPAPPPPPGSAQPGMAKVLPRTSKLWGDVTEIKSPILSGPKANVISE LNSILQQMNRKLAKPGEGLDSPMGAKSASLAPRSPEIMSTISGTRSTTVTFVRPGT SQPITLQSRPPDYESRTSGTRRAPSPVVSPTMKNKETLPAPLSAATASPSALSDVFS LPSQPPSGDLFGLNPAGRSRSPSPSILQQPISNKPFTTKPVHLWTKPDVADWLLESLNL GEHKEAFMDNEIDGSHLPNLQKEDLIDLGVTRVGHMNIERALKQLLDR</p>

Further analysis of the NOV40a protein yielded the following properties shown in Table 40B.

Table 40B. Protein Sequence Properties NOV40a

PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV40a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 40C.

Table 40C. Geneseq Results for NOV40a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV40a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79240	Human protein SEQ ID NO 1902 - Homo sapiens, 1248 aa. [WO200157190-A2, 09-AUG-2001]	14..1267 1..1248	1231/1271 (96%) 1231/1271 (96%)	0.0
AAB31518	Amino acid sequence of the rat Shank2 polypeptide - Rattus sp, 1470 aa. [WO200078921-A2, 28-DEC-2000]	30..1267 240..1470	1078/1255 (85%) 1132/1255 (89%)	0.0
AAM80224	Human protein SEQ ID NO 3870 - Homo sapiens, 1161 aa. [WO200157190-A2, 09-AUG-2001]	172..1267 82..1161	1071/1103 (97%) 1071/1103 (97%)	0.0
AAB31517	Amino acid sequence of the rat Shank3a polypeptide - Rattus sp, 1740 aa. [WO200078921-A2, 28-DEC-2000]	18..1264 550..1737	496/1349 (36%) 673/1349 (49%)	0.0
AAY83017	Rat shank 3a - Rattus rattus, 1740 aa. [WO200011204-A2, 02-MAR-2000]	18..1264 550..1737	496/1349 (36%) 673/1349 (49%)	0.0

In a BLAST search of public sequence databases, the NOV40a protein was found to have homology to the proteins shown in the BLASTP data in Table 40D.

Table 40D. Public BLASTP Results for NOV40a				
Protein Accession Number	Protein/Organism/Length	NOV40a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UPX8	KIAA1022 PROTEIN - Homo sapiens (Human), 1131 aa (fragment).	124..1267 1..1131	1121/1154 (97%) 1121/1154 (97%)	0.0
Q9QX93	PROLINE RICH SYNAPSE ASSOCIATED PROTEIN 1 - Rattus norvegicus (Rat), 1252 aa.	2..1267 1..1252	1103/1276 (86%) 1158/1276 (90%)	0.0
O70470	CORTACTIN-BINDING PROTEIN 1 - Rattus norvegicus (Rat), 1252 aa.	2..1267 1..1252	1102/1276 (86%) 1158/1276 (90%)	0.0
Q9WUV9	PROLINE RICH SYNAPSE ASSOCIATED PROTEIN 1 - Rattus norvegicus (Rat), 1259 aa.	2..1267 1..1259	1103/1283 (85%) 1158/1283 (89%)	0.0
Q9WUW0	PROLINE RICH SYNAPSE ASSOCIATED PROTEIN 1 - Rattus norvegicus (Rat), 1250 aa.	2..1267 1..1250	1095/1276 (85%) 1151/1276 (89%)	0.0

PFam analysis predicts that the NOV40a protein contains the domains shown in the Table 40E.

Table 40E. Domain Analysis of NOV40a			
Pfam Domain	NOV40a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PDZ: domain 1 of 1	38..131	23/97 (24%) 70/97 (72%)	1e-07
SAM: domain 1 of 1	1202..1265	27/68 (40%) 53/68 (78%)	9.8e-22

Example 41.

The NOV41 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 41A.

Table 41A. NOV41 Sequence Analysis

	SEQ ID NO: 129	2069 bp
NOV41a, CG57814-01 DNA Sequence	GGACACTGACATGGACTGAAGGAGTAGAAAGCACTATAAATGTCCTTCTCTATCTGTG TGTACTCTTATCTCACTGTTCTATTTTTCTCCTCATTTATATTAACTCTTCTTACC TTTTTTCTGAACCTCTAGGCCTTCTCTTCCAGAACTGGTGAAGACAATGAAACG GCCAAGATGGTAAGAAACAAGCCGCACTTCTCCTTGGGGAGACTGATAATTTAAAGG TTGTGTGTGCAGAAACATTTCCAGCTTCATCACCACCCCTTCTCTCCACCTCTGCC CACTGGAGACCACTTACATCCCGAAGCGGACGCGGCAGCTGAAGTCAGGAAACCATGC ATCACATTAGCAGGAGCCAACTGCAGACTTTAAACTCCGTTCAACATGTGGATGCGGC AGAGAAATGACCTGTCCAGACAAGCCGGGGCAGCTCATAAAGTGGTTCATCTGCTCCC TGTGCGTCCCGCGGTGCGTAAGCTCTGGAGCAGCCGGCGTCCAAGGACCCGGAGAAA CCTTCTGCTGGGCACTGCGTGTGCCATCTACTGGGCTTCTGCTGAGCCAGGTGGG AGGGCTCTCTCCAGCATGGACAGGCGGTGAGAGGGGCGACATCGACCCGCGACA CCGCCGAGCCATCCTTCCCTGAGATACCCCTGGATGGTACCTGGCCCTTCCAGATC CCAGGGCAATGGGTCCACTCTGCAGCCCAATGTGGTGTACATTACCTACGCTCCGAG CGCAGCAAGCCGGCAATATCCGTGGCACCCTGAAGCCCAAGCGCAGGAAAAAGCATG CAGTGGCATCGGCTGCCCCAGGGCAGGAGGCTTGGTCCGACCATCCCTTCAGCCGCA GGAAGCGGCAAGGAAGCTGATGCTGTAGCACTGGGTACCTCAGGGAGCAAACTCTG GTTAAGATTGGAGAGCGACCTGGAGGTGGTGGGGGTCCGGAGTGGCAGCCGGGG GCCCCAGACTTCTGAGCCAGCTCCAGGGAGAGCAACATTAGGATCTACAGCGAGAG CGCCCCCTCTGGCTGAGCAAGATGACATCCGAAGAATGCGACTCTGGCGGACAGC GCAGTGGCAGGGCTCCGGCTGTGTCTCTAGGAGCGGAGCCGCTTGTGCTGGTCTGG AGGGGGGCGCACCTGGCGTGTGCTCCGCTGTGGCCCTAGCCCTGTGGGCTTCTCAA GCAGCCCTTGGACATGAGTGAGGTGTTGCTTCCACCTAGACAGGATCTCTGGGCTC AACAGGACCTGCGCTGTGTGAGCAGGAAAGCAGAGTTCATCAAGATGGCCGCCCT GCCCATCATTTCTTGGGATGCATCTTATCTTACGCAAGTAAATGACACCCATTCTTC TGTTAAGCTCACCTGGGGAATTATCAGCAGTTGCTGAAACAGAATGCTGGCAGAAT GGCCGAGTACCCAAGCTGAATCAGGTGTACTGAAATACATCATCATGAGTGGTCCA AGATGGCACTCTTTGATTTTTGTTACAGATTATAATCGTTAGATACAAATTGCTG TGGATTACAGCCTCGAAGGAAGATGCCTGTGTACAGAATGGATTAGGCCAAAATGT GATGACCAAGGTTCTGCGCTCTAGCACACATTATCCAGCGAAAGCATGACCCAGGC ATTTGGTTTTTATAGACAACAAGGTTTCTTTGACAGGAGTGAAGATAACTTAAACT CAAAATGTTTAGAAGGCATCAAAGAGTTTCCAGCTTCTGCACTTCTGTTTGAAGAGC CAGCACTTACGGCAGAACTTCTTCACTCTGTTTCTTGATAAAGTGTATTGGGAAA GTCAAGGAGGTAGACAAGGAATTGAAAGCTTATCGATGTAATAGAACACAGAGCCAA AATCTTATCACCTATATCAATGCACACGGGGTCAAAGTATTACCTATGAATGAATGA CAAAAGAATCTTCTGGCTAGGGTGTAGATATATTATGCATTTTGGTTTGTGTTTT AAATCAAGCACATCAACCTCAAGCCCGTTTAGCAATGAG	
	ORF Start: ATG at 413	ORF Stop: TGA at 1970
	SEQ ID NO: 130	519 aa MW at 57552.4kD
NOV41a, CG57814-01 Protein Sequence	MTCPPKPGQLINWFCISLCVPRVRKLWSSRRPRTNRNLLLTACAIYLGFLVSQVGRA SLQHQAEEKGPFRSRDTPAEPSPFELPDGTLAPPESQNGSTLQPNVYITLRSERS KPNIRGTVPKRRKKHAVASAAPGQEAALVGPQLPQEAAREADAVAPGYAQGANLVK IGERPWLVRGPGVRAGGPDFLQPSRESNIRIYESAPWSLKKDDIRMRLLADSAV AGLRPVSSRSRGLLVLEGGAPGAVLRGCPSPCGLLKQPLDMSEVFAPHLDRILGLNR TLPSVSRKAEIFQDGRPCPIILWDASLSSASNDTHSSVKLTWGTYYQLLKQKQWQNGR VPKPESGCTEIHHEWSKMALEDFLLQIYNRLDTNCCGFRPRKEADACVQNGLRPKCDD QGSAAALAHIIQRKHDPRLVFIIDNKGFDRSEDNLNFKLLEGIKEFPASAVSVLKSQH LRQKLLQSLFLDKVWESQGGRGIEKLIDVIEHRAKILITYINAHGVKVLPMNE	
	SEQ ID NO: 131	1740 bp
NOV41b, CG57814-02 DNA Sequence	GGCAGCTGAAGTCAGGAACCATGCATCACATTAGCAGGAGCCAACTGCAGACTTTAA ACTCCGTTCAACATGTGGATGCGGCAGAGAAATGACCTGTCCAGACAAGCCGGGCGAG CTCATAAACTGGTTCATCTGCTCCCTGTGCGTCCCGCGGTGCGTAAGCTCTGGAGCA CGCCGGCTCCAAGGACCCGAGAAACCTTCTGCTGGGCACTGCGTGTGCCATCTACTT GGGCTTCCGTGTGAGCCAGGTGGGAGGGCTCTCTCCAGCATGGACAGCGCGCTGAG AAGGGGCCACATCGCAGCCGACACCGCGAGCCATCCTTCCCTGAGATACCCCTGG ATGGTACCTGGCCCTCCAGAGTCCAGGGCAATGGGTCCACTCTGCAGCCCAATGT GGTGTACATTACCTACGCTCCAAGCGCAGCAAGCCGGCCAATATCCGTGGCACCGTG AAGCCCAAGCGCAGGAAAAGCATGCAGTGGCATCGGCTGCCCGGCGAGGAGGCTT TGGTCCGACCATCCCTTACCGCAAGAAGCGGCAAGGGAAGCTGATGCTGTAGCACT GGGTACGCTCAGGAGCAAACTGGTTAAGATGGAGAGCGACCTGAAGGTGGTGGGGG TCGGGAGTGCAGCGCGGGGGCCAGACTTCTGCGAGCCAGCTCCAGGGAGAGCAACA TTAGGATCTACAGCGAGAGCGCCCCCTCTGGCTGAGCAAGATGACATCCGAAGAAT GCGACTCTTGGCGGACAGCGCAGTGGCAGGGCTCCGGCTGTGTCTCTAGGAGCGGA GCCCCGTTGCTGGTGTGGAGGGGGCGCACCTGGCGCTGTGCTCCGCTGTGGCCCTA GCCCTGTGGGCTTCTCAAGCAGCCCTTGGACATGAGTGAAGTGTGTGCTTCCACCT AGACAGGATCTGGGGCTCAACAGGACCTGCCGTCTGTGAGCAGGAAGCAGAGTTC	

	ATCCAAGATGGCCGCCCATGCCCCATCATTCTTTGGGATGCATCTTTATCTTCAGCAA GTAATGACACCCATTCTTCTGTTAAGCTCACCTGGGGAATTATCAGCAGTTGCTGAA ACAGAAATGCTGGCAGAAATGGCCGAGTACCCAAGCCTGAATCAGGTTGTACTGAAATA CATCATCATGAGTGGTCCAAGATGGCACTCTTTGATTTTTTGTACAGATTATAATC GCTTAGATACAAATGCTGTGGATTACAGACCTCGCAAGGAAGATGCCTGTGTACAGAA TGGATTGAGGCCAAAATGTGATGACCAAGGTTCTGCGGCTCTAGCACACATTATCCAG CGAAAGCATGACCCAAGGCATTGTTTATAGACAACAAGGGTTCTTTGACAGGA GTGAAGATAACTTAAACTTCAAATGTTAGAAGGCATCAAAGAGTTCCAGCTTCTGTC AGTTTCTGTTTTGAAGAGCCAGCACTTACGGCAGAACTTCTTCAGTCTCTGTTTCTT GATAAAGTGTTATTGGGAAAGTCAAGGAGGTAGACAAGGAATTGAAAAGCTTATCGATG TAATAGAACACAGAGCCAAAATTCTTATCACCTATATCAATGCACACGGGGTCAAAGT ATTACCTATGAATGAATGACAAAAGAATCTTCTGGCTAGGGTGTAGATATATTTATG CATTTTGGTTTTGTTTTTAAATCAAGCACATCAACCTCAAGCCCGTTTAGCAATGAG		
	ORF Start: ATG at 90	ORF Stop: TGA at 1641	
	SEQ ID NO: 132	517 aa	MW at 57179.9kD
NOV41b, CG57814-02 Protein Sequence	MTCPPDKPQLINWFICSLCVRVRKLWSSRRPRTRNLLLTACAIYLGFLVSQVGRA SLQHGGAAEKGPHRSRDTAEPSPFEIPLDGTLPAPESQNGSTLQPNVVYITLRSKRS KPNIRGTGTVKPKRRKHAVASAAQGEALVGPQLQPQEAAREADAVALGTLRSKLVKM ESDPEGAGSGVRAGGPDFLQPSRESNIRIYSESAPSWLSKDDIRRMRLADSAVAG LRPVSSRSGARLLVLEGGAPGAVLRGSPSPCGLLKQPLDMSEVFAPHLDIRLGLNRTL PSVSRKAEFIQGRPCPIILWDASLSSASNDTHSSVKLTWGTYQQLLKQKQWQNGRVP KPESGCTEIHHEWSKMALFDLLQIYNRLDTNCCGFRPRKEDACVQNGLRPKCDDQG SAALAHIIQRKHPRLVFDNKGFFDRSEDNLNFKLLEGIKEFPASAVSVLKSQHLR QKLLQSLFLDKVYWESQGGRGQIEKLIDVIEHRAKILITYINAHGVKVLPMNE		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 41B.

Table 41B. Comparison of NOV41a against NOV41b.		
Protein Sequence	NOV41a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV41b	1..519	493/519 (94%)
	1..517	497/519 (94%)

Further analysis of the NOV41a protein yielded the following properties shown in Table 41C.

Table 41C. Protein Sequence Properties NOV41a	
PSort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.2404 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	Likely cleavage site between residues 59 and 60

A search of the NOV41a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 41D.

Table 41D. Geneseq Results for NOV41a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV41a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU12276	Human PRO6001 polypeptide sequence - Homo sapiens, 519 aa. [WO200140466-A2, 07-JUN-2001]	1..519 1..519	518/519 (99%) 519/519 (99%)	0.0
AAM39125	Human polypeptide SEQ ID NO 2270 - Homo sapiens, 519 aa. [WO200153312-A1, 26-JUL-2001]	1..519 1..519	518/519 (99%) 519/519 (99%)	0.0
AAM40911	Human polypeptide SEQ ID NO 5842 - Homo sapiens, 537 aa. [WO200153312-A1, 26-JUL-2001]	1..519 19..537	491/527 (93%) 495/527 (93%)	0.0
AAM41373	Human polypeptide SEQ ID NO 6304 - Homo sapiens, 479 aa. [WO200153312-A1, 26-JUL-2001]	212..512 161..471	130/316 (41%) 180/316 (56%)	1e-64
AAM39587	Human polypeptide SEQ ID NO 2732 - Homo sapiens, 397 aa. [WO200153312-A1, 26-JUL-2001]	212..512 79..389	130/316 (41%) 180/316 (56%)	1e-64

In a BLAST search of public sequence databases, the NOV41a protein was found to have homology to the proteins shown in the BLASTP data in Table 41E.

Table 41E. Public BLASTP Results for NOV41a				
Protein Accession Number	Protein/Organism/Length	NOV41a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9ET25	HYPOTHETICAL BASIC PROTEIN I-19 - Mus musculus (Mouse), 517 aa.	1..519 1..517	431/519 (83%) 462/519 (88%)	0.0
Q9NYZ0	AD021 PROTEIN - Homo sapiens (Human), 246 aa.	274..519 1..246	246/246 (100%) 246/246 (100%)	e-145
Q9UFP1	HYPOTHETICAL 49.5 KDA PROTEIN - Homo sapiens (Human), 448 aa (fragment).	212..512 130..440	129/316 (40%) 179/316 (55%)	2e-63

PFam analysis predicts that the NOV41a protein contains the domains shown in the Table 41F.

Table 41F. Domain Analysis of NOV41a			
Pfam Domain	NOV41a Match Region	Identities/ Similarities for the Matched Region	Expect Value
SQS_PSY: domain 1 of 1	109..145	8/37 (22%) 29/37 (78%)	9.9

Example 42.

The NOV42 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 42A.

Table 42A. NOV42 Sequence Analysis			
	SEQ ID NO: 133	1294 bp	
NOV42a, CG59327-01 DNA Sequence	GATGGCCACCTTGAACGTTGTACTGATGTTGATGCCCTTGCCAGTACATTTTCCAT TGTTTTATAACTGTGCTACTGAAGTACTTGTGTGCAGAGTATGGCTGGAGGAATGCCA TGTTGATCCAAGGCGCGCTTTCCTTAAACCTGTTTGTGTTTTGGGACCTCATGAGGC CCTCCCTCTCGGAAAAACCCAAATGACCCAGAAGAGAAAGATCTGCGCGTCTGCCC GCGCACTCCACAGAGTCTGTAATGTCAAATGGACAGCAGGGAAGAATAGAAGAGAAG ATGGCGGGTCTGGGAACGAGGAGACCTCTGTGACCTGCAAGCCAGGAGTGAAGCC CAGGAGTGCCCCGATCAGGCCAGATCATGTGCGCTTTCGGTTCGAAGACGGTCAGC TGGCTCATTATGAGAGTCAAGAAGGGCTTCGAGGATTGGTACTCAGGCTATTTGGGA CAGCCAGCCTATTACAAATCGAATGTTTGTAGCCTTTGTTTTCTGGGCTCATTTCG ATACAGCAGCTTTGTCTATCTCCTTTATTCATCTCCCAGAAATCGTCAATTTGTATAAC TTATTGGAGCAAACGAAGGTTTTCCCTCTGACTTCAATTATAGCAATAGTTCACATTG TTGGAAAGTGATCCTGGGCGTCATAGCTGACTTACCTTGCCATCAGTGTTTGGAATGT CTTCCTGTGGCCAGCTTCGTTCTTGTCTCCTCAGTATTTTGTGTTGCTGCCTTTGATG CATATGTACGCTGGCCTGGTGGTCATCTGCACACTGACAGGGTTTCCAGCGGTTATT TCTCCCTAATGCCCATAGTGACTGAAGACTTGGTTGGCATTGAACATTGGCCAAATGC CTACGGCATCATCATCTGTGCTAATGGCATCTCTGCGTTGTTGGGACCACCTTTTGCA GGTAAACTGTCTGAGGTTTTAAGAGTTCATAGTGCATATAGATACGGTGTGTTAGCTC TGCGAGGAGACGGATGCAGAGCACTCACATCTTCTCTTATACATAGAAGTGAATGGC TTTCTAAAGTTAGATCACTGGCCAGAGTTTTTGAGTCACAAGAGCTATTCCACAGATT TCCTTTAGAAAAACAATCAACCACTGGCAGTCCACTTCAGTGACACAGAATGGGTTGCA GAACCTTGCTTACTTATGTGACACATTCAACCTGCTCAATGAACCTCAATCTGTCACTTC AGGGGAGAAAGGACAACCTGTGTTCAAGTCAGCAAATAAAGTGGCTACATTCAAACCAA ACTGGAATTACGGGGGTG		
	ORF Start: ATG at 2	ORF Stop: TAA at 1049	
	SEQ ID NO: 134	349 aa	MW at 38694.2kD
NOV42a, CG59327-01 Protein Sequence	MATLNVLMLMPLAQYIFHCFITVLLKYLCAEYGWRNAMLIQGAVSLNLFVFGTLMRP LPPGKNPNDPEEKDLRVLPASTESVMSNGQQGRIEEKDGGSGNEETLCDLQAQECKP RSAPIRPDHVRFPVLKTVSWLIMRVKKGFDWYSGYFGTASLFTNRMFVAFVFWASFA YSSFVISFIHLPEIVNLNLEQTKVPLTSSIIAIVHIVGKVLGVIALDLPISVWNV FLLASFVLVLSIFVLLPLMHMYAGLVVICTLTGFSSGYFSLMPVITEDLVGIEHLANA YGIICANGISALLGPPFAGKLSEVLRVHSAYRYGVLLRGDGCRAITSSLIHRSEMA F		

Further analysis of the NOV42a protein yielded the following properties shown in Table 42B.

Table 42B. Protein Sequence Properties NOV42a	

analysis:	probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 32 and 33

A search of the NOV42a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 42C.

Table 42C. Geneseq Results for NOV42a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV42a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAO07132	Human polypeptide SEQ ID NO 21024 - Homo sapiens, 107 aa. [WO200164835-A2, 07-SEP-2001]	257..331 5..81	49/77 (63%) 58/77 (74%)	6e-20
AAY31642	Human transport-associated protein-4 (TRANP-4) - Homo sapiens, 465 aa. [WO9941373-A2, 19-AUG-1999]	157..342 221..401	54/197 (27%) 86/197 (43%)	1e-07
AAY02737	Human secreted protein encoded by gene 88 clone HKAFB88 - Homo sapiens, 229 aa. [WO9902546-A1, 21-JAN-1999]	198..342 24..164	41/147 (27%) 65/147 (43%)	9e-06

In a BLAST search of public sequence databases, the NOV42a protein was found to have homology to the proteins shown in the BLASTP data in Table 42D.

Table 42D. Public BLASTP Results for NOV42a				
Protein Accession Number	Protein/Organism/Length	NOV42a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96NI7	CDNA FLJ30794 FIS, CLONE FEBRA2001093, WEAKLY SIMILAR TO MONOCARBOXYLATE TRANSPORTER 4 - Homo sapiens (Human), 336 aa.	22..331 1..310	250/312 (80%) 266/312 (85%)	e-138
Q9D1K0	1110004H10RIK PROTEIN - Mus musculus (Mouse), 336 aa.	22..331 1..310	220/312 (70%) 250/312 (79%)	e-119

AAL39716	LD30953P - <i>Drosophila melanogaster</i> (Fruit fly), 894 aa.	142..314 665..843	50/180 (27%) 89/180 (48%)	2e-15
Q9V9B3	CG3409 PROTEIN - <i>Drosophila melanogaster</i> (Fruit fly), 800 aa.	142..314 571..749	50/180 (27%) 89/180 (48%)	2e-15
Q9W0L6	CG13907 PROTEIN - <i>Drosophila melanogaster</i> (Fruit fly), 816 aa.	157..331 565..738	55/178 (30%) 91/178 (50%)	1e-14

PFam analysis predicts that the NOV42a protein contains the domains shown in the Table 42E.

Table 42E. Domain Analysis of NOV42a			
Pfam Domain	NOV42a Match Region	Identities/ Similarities for the Matched Region	Expect Value
oxidored_q3: domain 1 of 1	197..314	25/177 (14%) 73/177 (41%)	9.1

Example 43.

The NOV43 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 43A.

Table 43A. NOV43 Sequence Analysis			
	SEQ ID NO: 135	455 bp	
NOV43a, CG59494-01 DNA Sequence	TAGAACTGTGTTGAGCTCTCACCCATCAGCATGAGCAACAAATCTTGGGAACCTGGGA AGCTGGTCTCCAGTGAAAACCTTTGAGGATTACATGAAAGAACTGGGAGTGAATTTCCG AGCCCGGAACATGGCAGGGTTAGTGAACCCGACAGTAACTATTAGTGTGATGGGAAP ATGATGACCATAAGAACAGAAAGTTCTTTCCAGGACACTAAGATCTCCTTCAAGCTGG GGGAAGAATTGATGAAACTACAGCAGACAACCGGAAAGTAAAGAGCACCATAACATT AGAGAATGGCTCAATGATTCACGTCCAAAAATGGCTTGGCAAAGAGACAACAATCAAP AGAAAAATTGTGGATGAAAAAATGGTAGTGAATGTAAATGAATAATATTGTCAGCA CCAGAATCTACGAAAAGGTCTGAAAAATCATTTCTTCATTGAAGTGGCT		
	ORF Start: ATG at 31	ORF Stop: TGA at 427	
	SEQ ID NO: 136	132 aa	MW at 15096.4kD
NOV43a, CG59494-01 Protein Sequence	MSNKFGLGTWKLVSSENFEDYMKELGVNFAARNMAGLVKPTVTISVDGKMMTIRTESSE QDTKISFKLGEFEFDETTADNRKVKSTITLENGSMIHVQKWLKETTIRKIVDEKMMV ECKMNNIVSTRIYEKV		

Further analysis of the NOV43a protein yielded the following properties shown in Table 43B.

Table 43B. Protein Sequence Properties NOV43a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0053 probability located in microbody (peroxisome)

SignalP analysis:	No Known Signal Sequence Predicted
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A search of the NOV43a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 43C.

Table 43C. Geneseq Results for NOV43a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV43a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW40227	Human myelin P2 protein - Homo sapiens, 136 aa. [WO9803647-A2, 29-JAN-1998]	1..130 1..130	89/130 (68%) 107/130 (81%)	2e-47
AAW40228	Bovine myelin P2 protein - Bos taurus, 136 aa. [WO9803647-A2, 29-JAN-1998]	1..130 1..130	89/130 (68%) 106/130 (81%)	9e-47
AAY90320	Human AFABP protein sequence - Homo sapiens, 132 aa. [WO200047734-A1, 17-AUG-2000]	1..131 1..131	84/131 (64%) 110/131 (83%)	3e-46
AAY90319	Mouse AFABP protein sequence - Mus sp, 132 aa. [WO200047734-A1, 17-AUG-2000]	1..131 1..131	83/131 (63%) 108/131 (82%)	7e-45
AAG66576	Mouse MDGI polypeptide - Mus sp, 133 aa. [US6232291-B1, 15-MAY-2001]	1..131 1..131	73/131 (55%) 103/131 (77%)	6e-40

In a BLAST search of public sequence databases, the NOV43a protein was found to have homology to the proteins shown in the BLASTP data in Table 43D.

Table 43D. Public BLASTP Results for NOV43a				
Protein Accession Number	Protein/Organism/Length	NOV43a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
MPRB2	myelin P2 protein - rabbit, 132 aa.	1..132 1..132	95/132 (71%) 109/132 (81%)	3e-49
P02691	Myelin P2 protein - Oryctolagus cuniculus (Rabbit), 131 aa.	2..132 1..131	94/131 (71%) 108/131 (81%)	1e-48
MPHU2	myelin P2 protein [validated] - human, 132 aa.	1..132 1..132	92/132 (69%) 109/132 (81%)	3e-48
Q90X56	ADIPOCYTE FATTY ACID BINDING PROTEIN - Gallus gallus (Chicken), 132 aa.	1..131 1..131	86/131 (65%) 113/131 (85%)	1e-47
P02689	Myelin P2 protein - Homo sapiens (Human), 131 aa.	2..132 1..131	91/131 (69%) 108/131 (81%)	1e-47

Pfam analysis predicts that the NOV43a protein contains the domains shown in the Table 43E.

Table 43E. Domain Analysis of NOV43a			
Pfam Domain	NOV43a Match Region	Identities/ Similarities for the Matched Region	Expect Value
lipocalin: domain 1 of 1	4..132	45/157 (29%) 113/157 (72%)	3.2e-36

Example 44.

The NOV44 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 44A.

Table 44A. NOV44 Sequence Analysis		
	SEQ ID NO: 137	1561 bp
NOV44a, CG59432-01 DNA Sequence	AAGAATTGTAGCTCTCCACTGAATTGCAGGGGTTCTTGAATGTGTCAACATTTGGAG GCAGTTGGAGGAGGGAGCTCTATTGATGAAAAATGGCTACATATTCAAATTTCAAGTG TATACCAGGAAGATAATTCATTCATCTCTGGCTTACCCAAAGAATCTTGGAGTTAC TGCCAATGAGGAAATCCCAGGGTCTAATAAAAAATATCTTTAGGAGTGAAGCAGTTAA CTGAGTGTGTAAGCTTTATCTTCTGTCCAATGGACTTGTGGTTTGCTTATAAACTCT CCAGTAAATAATTGTTAGAGACCTGTCATTGATAGCAGTTGCTAGTTGCTGCCTTTTA AGAGCTCGTTGATTCTCTGCAAGGTGGTGCAGCATCCTCTGTCCCTTCATTCAATTC AGATCTACTCAGGTCTCCCTGTAACAGATCTCTCGGATCAATAAGCATGAATGACGA AGACTACAGCACCATCTATGACACAATCCAAATGAGAGGACGTATGAGGTTCCAGAC CAGCCAGAAGAAAAATGAAAGTCCCATTTATGATGATGTCCATGAGTACTTAAGGCCAG AAAAATGATTTATATGCACTCAGCTGAATACCATGAGTATGATTTTGTGTCAGTCTA TACCATTAAGGGTGAAGAGACCAGCTTGGCCTCTGTCCAGTCAGAAGACAGAGGGCTAC	

	<div>CTCCTCGCTGATGAGATATACTCTGAACTCCAGGAGGCTCATCCAGGTGAGCCCCAGG AGGCAGGGGCATCTCAATGGAAGGGTTATATTCATCAACCCAGGACCAGCAACTCTG CGCAGCAGAAGTCCAGGAGAATGGGAGTGTGATGAAGGAAGATCTGCCTTCTCCTTCA AGCTTCACCATTCAGCACAGTAAGGCCTTCTCTACCACCAAGTATTCTGCTATTCTG ATGCTGAAGGTTTGAAGAAAAGGAGGGAGCTCACATGAACCTTGAGATTACCTCTT TGTGAAGGTAAGGTCTGCCTCTGACAGGCATACCCTGTTTCATGTCAGATATTATGGCTG GTGTTTTATTTTGTCTCTGAATGACCAGGGAAGATTATAATGCCATGGTCTCTGGAT CTCAATACATATTACAGGAGTCGGAGGGGACTAAATCAGTCATTAGAGTGTACTCAGCTC TTCACAAAATTAGAGGAATTGGAAGGTGCATTTAAAGCACGTATTTAATCACTGACTT TTACATACCATGGGCAAAGTATTTTTCAAACGGTTTCACATAAGTGAGCCATAACTGC TGCCCAAATCCTTGCCATTGTGGCTGACATTAAGTACATTTTTCTGTCTGGTTAAATT TCCTTTGTGACATGTTTTAAAGTGAAACCAAAGCTTGTGAAAGAAAGACCTTCTTGT GCTTCTAAGGTACAGATTTGTGAGATAGGTGGTCAATAAAGGCTATCTCTGTCACTA GCTTGCCCTTTGGCACCAATATAACTAAAAATTTGATGAAGTCAAATGATTTTCAGTA GTAGTAAGACACTACCAGTGTTAATGTTTAATACTTACGATATCTAAACAGAA</div>		
	ORF Start: ATG at 454		ORF Stop: TAA at 1132
	SEQ ID NO: 138	226 aa	MW at 26132.2kD
NOV44a, CG59432-01 Protein Sequence	<div>MNDEDYSTIYDTIQNERTYEVDPQPEENESPHYDDVHEYLRPENDLYATQLNTHEYDF VSVYTIKGEETSLASVQSEDRGYLLPDEIYSELQEAHPGEPQEDRGISMEGLYSTQD QQLCAAELEQENGSMKEDLPSPSSFTIQHSAFSTTKYSCYSDAEGLEEKEGAMHNPE IYLFVKVRSASDRHTLFMQILWLVFYFALNDQGKIHNAMVLGSQYIFRSRRD</div>		
	SEQ ID NO: 139	809 bp	
NOV44b, CG59432-02 DNA Sequence	<div>ATCCTCTGTCCCTTCATTCATTTAGATCTACTCAGGTCTCCCTGTAAACAGATCTCT CGGATCAATAAGCATGAATGACGAAGACTACGGCACCATCTATGACACAATCCAAAT GAGAGGACGTATGAGGTTCCAGACCAGCCAGAAGAAAATGAAAGTCCCCATTATGATG ATGTCCATGAGTACTTAAGGCCAGAAAATGATTTATATGCCACTCAGCTGAATACCCA TGAGTATGATTTTGTGTGCTATACCATTAAGGGTGAAGAGACCAGCTTGGCCTCT GTCCAGTCAGAAGACAGAGGCTACCTCCTGCCTGATGAGATATACTCTGAATCCAGG AGGCTCATCCAGGTGAGCCCCAGGAGGACAGGGGCATCTCAATGGAAGGGTTATATTC ATCAACCCAGGACCAGCAACTCTGCGCAGCAGAACTCCAGGAGAATGGGAGTGTGATG AAGGAAGATCTGCCTTCTCCTTCAAGCTTCACCATTACGACAGTAAGGCCTTCTCTA CCACCAAGTATTCTGCTATTCTGATGCTGAAGGTTTGAAGAAAAGGAGGGAGCTCA CATGAACCTGAGATTTACCTCTTTGTGAAGGTAAGGTCTGCCTCTGACAGGCATACC CTGTTTCATGCAGATATTATGGCTGGTGTGTTTTATTTTGTCTGAATGACCAGGGAAGA TTCATAATGCCATGGTCTCTGGATCTCAATACATATTACGAGTCGGAGGGACTAAAT CAGTCATTAGAGTGTACTCAGCTCTTCACAAAATTAGAGGAATTGGAAGGTGCAT</div>		
	ORF Start: ATG at 72		ORF Stop: TAA at 750
	SEQ ID NO: 140	226 aa	MW at 26102.2kD
NOV44b, CG59432-02 Protein Sequence	<div>MNDEDYGTIYDTIQNERTYEVDPQPEENESPHYDDVHEYLRPENDLYATQLNTHEYDF VSVYTIKGEETSLASVQSEDRGYLLPDEIYSELQEAHPGEPQEDRGISMEGLYSTQD QQLCAAELEQENGSMKEDLPSPSSFTIQHSAFSTTKYSCYSDAEGLEEKEGAMHNPE IYLFVKVRSASDRHTLFMQILWLVFYFALNDQGKIHNAMVLGSQYIFRSRRD</div>		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 44B.

Table 44B. Comparison of NOV44a against NOV44b.		
Protein Sequence	NOV44a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV44b	1..226	225/226 (99%)
	1..226	225/226 (99%)

Further analysis of the NOV44a protein yielded the following properties shown in Table 44C.

Table 44C. Protein Sequence Properties NOV44a

PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV44a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 44D.

Table 44D. Geneseq Results for NOV44a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV44a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found				

In a BLAST search of public sequence databases, the NOV44a protein was found to have homology to the proteins shown in the BLASTP data in Table 44E.

Table 44E. Public BLASTP Results for NOV44a				
Protein Accession Number	Protein/Organism/Length	NOV44a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96JT5	CLIC5B - Homo sapiens (Human), 410 aa.	1..200 1..202	185/202 (91%) 191/202 (93%)	e-104
Q9NPY9	DJ447E21.4 (SIMILAR TO BOVINE CHLORIDE CHANNEL PROTEIN (P64)) - Homo sapiens (Human), 180 aa (fragment).	1..180 1..180	180/180 (100%) 180/180 (100%)	e-103
A47104	chloride channel 64K chain - bovine, 437 aa.	1..197 1..229	104/231 (45%) 133/231 (57%)	1e-39
P35526	Chlorine channel protein p64 - Bos taurus (Bovine), 437 aa.	1..197 1..229	103/231 (44%) 131/231 (56%)	1e-38

PFam analysis predicts that the NOV44a protein contains the domains shown in the Table 44F.

Table 44F. Domain Analysis of NOV44a			
Pfam Domain	NOV44a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 45.

The NOV45 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 45A.

Table 45A. NOV45 Sequence Analysis			
	SEQ ID NO: 141	877 bp	
NOV45a, CG59394-01 DNA Sequence	ACTTTGTCCTCTTGGGCTTCACACAGAATCCAAAGGAGCAGAAAGTACTTTTGTATT GTTCTTGCTCTTCTACATTTTGACCATGGTGGGCAACCTGCTCATTTGTAGTGACCGT ACTGTCAGTGAGACCCTGGGCTCACCAATGTACTTCTTTCTTGCTGGCTTATCATTT TAGATATCATTTATTCTTCATCCATTTCCCCCAGATTGATTTCAGGCTGTCTTTGG GAATAATCCATATCCTTCCAATCTTGCATGGCCAGCTCTTTATCGAGCACATTTTC GGTGGGTCAGAGGTCTTTCTCCTGTTGGTGATGGCCTATGACTGCTATGTGGCCATC GTAAGCCCTTGCATTATTGGTTATCATGAGACAATGGGTGTGTGTTGTGCTGCTGGT AGTGTCTCTGGGTGGAGGATTTCTGCACTCAGTATTTCAACTTAGCATTTATTTATGG CTCCCATCTGTGGCCCAATGTGCTATTGATCATTTTCTGTGACATGTATCCCTTAT TGAAACTGGTCTGCACTGACCCCATGCTATTGGCCTCTTAGTGGTGGCCAATGGAG ACTGGCTTGCACTATTGTGTTTCTGCTCTTACTCATCTCTTATGGTGTCTATCTTGCA TCTTTAAAGAACCTTAGTCAGAAAGGGAGGCAAAAGCCCTCTCAACCTGCAGTTCC ACATGACTGTGGTGTGCTCTTCTTCTTTGTTCTTGTATTTTATGTATGCTAGACCTG TAGGACCTTCCCCATTGACAAATCAGTGAGTGTGTTTATACAGTCATAACCCCAAT CTGAACCCCTTAATCTACACTCTGAGAAATCTGAGATGACAAGTGTCTATGAAGAAG TTTAGAG		
	ORF Start: TTT at 3	ORF Stop: TAG at 873	
	SEQ ID NO: 142	290 aa	MW at 32485.7kD
NOV45a, CG59394-01 Protein Sequence	FVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTVTSETLGSPMYFFLAGLSF DIIYSSSISPRLISGLFFGNNSISFQSCMAQLFIEHIFGGSEVFLLVMAYDCYVAIC KPLHYLVIMRQWVCVLLVVSWSVGGFLHSVFQLSIIYGLPFCGPNVIDHFFCDMPYPL KLVCTDTHAIGLLVVANGGLACTIVFLLLLISYGVILHSLKNLSQKGRQKALSTCSSH MTVVVFVFFVPCI FMYARPARTFPIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL		

Further analysis of the NOV45a protein yielded the following properties shown in Table 45B.

Table 45B. Protein Sequence Properties NOV45a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 42 and 43

A search of the NOV45a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 45C.

Table 45C. Geneseq Results for NOV45a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV45a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU24536	Human olfactory receptor AOLFR21 - Homo sapiens, 299 aa. [WO200168805-A2, 20-SEP-2001]	1..290 10..299	273/290 (94%) 278/290 (95%)	e-155
AAG71950	Human olfactory receptor polypeptide, SEQ ID NO: 1631 - Homo sapiens, 299 aa. [WO200127158-A2, 19-APR-2001]	1..290 10..299	273/290 (94%) 278/290 (95%)	e-155
AAG72258	Human olfactory receptor polypeptide, SEQ ID NO: 1939 - Homo sapiens, 262 aa. [WO200127158-A2, 19-APR-2001]	33..290 1..250	234/258 (90%) 240/258 (92%)	e-131
AAG72553	Human OR-like polypeptide query sequence, SEQ ID NO: 2234 - Homo sapiens, 327 aa. [WO200127158-A2, 19-APR-2001]	1..290 10..299	198/290 (68%) 242/290 (83%)	e-121
AAG71909	Human olfactory receptor polypeptide, SEQ ID NO: 1590 - Homo sapiens, 327 aa. [WO200127158-A2, 19-APR-2001]	1..290 10..299	198/290 (68%) 242/290 (83%)	e-121

In a BLAST search of public sequence databases, the NOV45a protein was found to have homology to the proteins shown in the BLASTP data in Table 45D.

Table 45D. Public BLASTP Results for NOV45a				
Protein Accession Number	Protein/Organism/Length	NOV45a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9QW37	OR18=ODORANT RECEPTOR - Rattus sp, 307 aa.	1..290 10..299	192/290 (66%) 237/290 (81%)	e-115
Q96R66	OLFACTORY RECEPTOR - Homo.sapiens (Human), 213 aa (fragment).	57..269 1..213	198/213 (92%) 202/213 (93%)	e-111
Q9R0K2	ODORANT RECEPTOR MOR18 - Mus musculus (Mouse), 308 aa.	1..290 10..299	177/290 (61%) 229/290 (78%)	e-105

Q9R0K1	ODORANT RECEPTOR A16 - Mus musculus (Mouse), 302 aa.	1..290 10..299	171/290 (58%) 226/290 (76%)	e-102
CAC88333	SEQUENCE 34 FROM PATENT WO0164879 - Homo sapiens (Human), 309 aa.	1..290 10..299	167/290 (57%) 221/290 (75%)	5e-99

PFam analysis predicts that the NOV45a protein contains the domains shown in the Table 45E.

Table 45E. Domain Analysis of NOV45a			
Pfam Domain	NOV45a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	30..276	50/268 (19%) 174/268 (65%)	4.4e-23

Example 46.

The NOV46 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 46A.

Table 46A. NOV46 Sequence Analysis			
	SEQ ID NO: 143	1746 bp	
NOV46a, CG59383-01 DNA Sequence	ATAATT CAGTTT GAAAAC CAGTGG TTTCTCTTTCCTTCCCTATAGGTGTAAGAATAT CCAGCTGGTGGCTACAGTTCCCCCTCTGGTTTGGTGCCATGCATCCTGGGCGAACTA CTGGTAAAGGGCCCTCTACTCACACTCAGATTGACCAGCAACCTCCACGGCTTCTCAT TGTGCACATTGCTCTACCGTCTGGGCTGACATCTGCACCAACCTCTGTGAGGCTCTG CAGAACTTCTTCTCTCTAGCCTGCAGCTTGATGGGCCCCAGCCGCATGCTCCCTGTTCTC GTTTATACATGGTACAAGATCAGCATGAGTGCATCCTCCCTTTTGTGCAAGTGAAAGG GAACTTTGCTAGGTTGCAGACCTGCATCTCAGAACTCCGCATGTTACAGAGAGAAGGG TGTTTCAGATCACAAGGTGCTTCTCTGCGGCTGGCAGTAGAGGATGGGCTCCAGCAAT TCAAACAATACAGCAGACATGTGACCACAAGGGCAGCTCTGACCTATACTCCCTCGGA GATTACTATTCTGACTTCTCAGCCTGGAAAAGAGGTGGTCAAACAGTTGGAGGAAGGG TTGAAAGATACAGACCTAGCCAGAGTCAGGAGGTTTCAGGTCGTTGAGGTCACAAAGG GAATCCTAGAGCACGTGGACTCAGCGTCTCCTGTTGAGGATACCAGCAATGATGAGAG TTCTATTCTGGGAACCTGACATTGACCTTCAGACTATAGACAATGATATCGTCAGCATG GAGATTTTCTTCAAAGCCTGGCTACATAACAGTGGAAACAGACCAAGAACAAATCCATC TTCTTCTTTCTTTCACAGTGTTCAGCAACATTTCCAGACCCAGAGATAATCCAATGTG TCTGAAATGTGATCTCCAAGAGCGACTGCTCTGCCATCCCTACTCGCTGGCAGACGT GACGGCTCCTTGAGAAATGGATGACCCTAAAGGAGACTTCATCACACTCTACCAGATGG CTTCCCAAGTCATCGGCCCTCTCATTACAAGCTCCAAGTGATCAAGGCTTTAAAAATCTAG CGGGCTCTGCGAGTCATTGACATATGGACTCCCGTTTCATCCTCAGACCTACAAGCTGT TGGCAGCTGGACTGGGATGAGCTGGGAGCAAATCAGCAACATTTCCATGCTTTGTGTG ACAGCCTGCTGAAAAGGGAATGGCTGCTGTAGCCAAGGGGGAACACCGGGGCCAGG ACACAGCCAGAGAATTCTTGCCAGCACCTTCTATGTGATCATGCCGTACACTCCCTC ACACTGCTGGTAAAGCGGTGGCCACGCGGGAAGTGTGCTGCCAGCACCTTCCCC TGCTACCTGAGGACCCACATGATGATAGCCTTAAGAATAGCATGCTGGACAGCCTGGGA GCTGGAGCCACCTACAACCCCTTGATGTTCAAAGCCACCTGTACTCACACTGAGC AGCATCTATGCCAAGCCTCAGGGGGCGGCTCCACCCACACTGGGAGAGCCGAGCTCCGA GAAAGACTGGGCAGTTGCAGACCAACCGAGCTCGAGCTACTGTGGCCCCCTGCTGAT GACTCCTGTCCCAGGCAGAGCCTCCAAGATGCCAGCAGCCAGCAAATCTTCTCAGAT GCCTTCTTCTGCTTTCAGAGTGGGAGAAGGATCCCTCAAGGCCCTAAGTCACCAGCA CCAGAGCCCAAGCTGCCAGCTTAACCATATCCATGCTCAGGTTACATAATGGCTATC TGTGGT		
	ORF Start: ATG at 98	ORF Stop: TAA at 1670	
	SEQ ID NO: 144	524 aa	MW at 58691.3kD

NOV46a, CG59383-01 Protein Sequence	MHPGRTTGGKPSHTHTQIDQPPRLLIHVHIALPSWADICTNLCEALQNFFSLACSLMGP SRMSLFSLYMVQDQHECILPFVQVKGNFARLQTCISELRMLQREGCFRSGASLR LAV EDGLQQFKQYSRHVTTAAALTYTSLEITILTSQPGKEVVVKQLEEGLKDTDLARVRRFQ VVEVTGKGLLEHVDASAPVEDTSNDESSILGTDIDLQTIIDNDIVSMIEFFKAWLHNSGT DQEQIHLHLLSSQCFSNISRPRDNPMLCKDLQERLLCPSLLAGTADGSLRMDDPKGFQ ITLYQMASQSSASHYKLQVIKALKSSGLCESLTYGLPFIILRPTSCWQLDWDLELTNQ HFHALCHSLLKREWLLAKGEPPGPGHSQRIPASTFYVIMPSHSLTLVKA VATRELM LPSTFPLLPEDPHDDSLKNSMLDSLELEPTYNPLHVQSHLYSHLSSIYAKPQGR LPH WESRAPRKTGQLQTNRARATVAPLPMTFVPGRAKMPAASKSSSDAFFLPSEWKDPS RP
	SEQ ID NO: 1451647 bp
NOV46b, CG59383-02 DNA Sequence	AAAGAATATCCAGCTGGTGGCTACAGTTCCCCCTCTGGTTTTGCTGCCATGCATCCTG GGCGAACTACTGGTAAAGGGCCCTCTACTCACACTCAGATTGACCAGCAACCTCCAGC GCTTCTCATTTGTGCACATTGCTCTACCGTCTGGGCTGACATCTGCACCAACCTCTGT GAGGCTCTGCAGAACTTCTTCTCTCTAGCCTGCAGCTTGATGGGCCCCAGCCGATGT CCCTGTTTCACTTTATACATGGTACAAGATCAGCATGAGTGCATCCTCCCTTTTGTGCA AGTGAAAGGGAACCTTGTAGGTTGCAGACCTGCATCTCAGAACTCCGATGTTTACAG AGAGAAGGGTGTTTCAGATCACAAGGTGCTTCTCTGCGGCTGGCAGTAGAGGATGGGC TCCAGCAATTCAAACAATACAGCAGACATGTGACCACAAGGGCAGCTCTGACCTATAC TCCCTGGAGATTACTATTCTGACTTCTCAGCCTGGAAAAGAGGTGGTCAAACAGTTG GAGGAAGGGTTGAAAGATACAGACCTAGCCAGAGTCAGGAGGTTTCAGGTCGTTGAGG TCACAAAGGGAATCCTAGAGCACGTGGACTCAGCGTCTCCTGTTGAGGATACACAGCAA TGATGAGAGTTCTATTCTGGGAAGTGCATTGACCTTCAGACTATAGACAATGATATC GTACAGATGGAGATTTTCTTCAAAGCCTGGCTACATAACAGTCGGAACCCAGCAAGAAC AAATCCATCTTCTTCTTCTTCTCACAGTGTTTCAGCAACATTTCCAGACCCAGAGATAA TCCAATGTGTCGAAATGTGATCTCCAAGAGCGACTGCTCTGCCATCCCTACTCGCT GGCAGAGCTGACGGCTCCTTGAGAATGGATGACCTAAAGGAGACTCATCAGCACTCC ACCAGATGGCTTCCCAGTCATCGGCCTCTCATTACAAGCTCCAAGTGATCAAGGCTTT AAAATCTAGCGGGCTCTGCGAGTCATTGACATATGGACTCCCGTTCATCCTCAGACCT ACAAGCTGTTGGCAGCTGGACTGGGATGAGCTGGAGACAAATCAGCAACATTTCCATG CTTTGTGTCACAGCCTGCTGAAAAGGGAATGGCTGCTGTTAGCCAAAGGGGGAACCA GGGCCCAGGACACAGCCAGAGAATTCTGCCAGCACCTTCTATGTGATCATGCCGTCA CACTTCCCTCACACTGCTGGTAAAGGCGGTGGCCACGCGGGAATCATGTGCTGCCAGCA CCTTCCCTGCTGCTGAGGAGCCACATGATGATAGCCTTAAGAAATGTGGAGAGCAT GCTGGACAGCCTGGAGCTGGAGCCACCTACAACCCCTTGATGTTCAAAGCCACCTG TACTCACACCTGAGCAGCATCTATGCCAAGCCTCAGGGGCGCTCCACCCACACTGGG AGAGCCGAGCTCCGAGAAAGCATCCCTGCAAGACTGGGCAGTTGCAGACCAACAGCAG TCGAGCTCTGAGGCCCCCTGCCTATGACTCCTGTCAGGAGCAGAGCTTCAAGATG CCAGCAGCCAGCAAATCTTCTCAGATGCCTTCTTCTGCTTTCAGAGTGGGAGAAGG ATCCCTCAAGGCCCTAAGTCAAC
	ORF Start: ATG at 49ORF Stop: TAA at 1639
	SEQ ID NO: 146530 aaMW at 59359.1kD
NOV46b, CG59383-02 Protein Sequence	MHPGRTTGGKPSHTHTQIDQPPRLLIHVHIALPSWADICTNLCEALQNFFSLACSLMGP SRMSLFSLYMVQDQHECILPFVQVKGNFARLQTCISELRMLQREGCFRSGASLR LAV EDGLQQFKQYSRHVTTAAALTYTSLEITILTSQPGKEVVVKQLEEGLKDTDLARVRRFQ VVEVTGKGLLEHVDASAPVEDTSNDESSILGTDIDLQTIIDNDIVSMIEFFKAWLHNSGT DQEQIHLHLLSSQCFSNISRPRDNPMLCKDLQERLLCPSLLAGTADGSLRMDDPKGFQ ITLHQMASQSSASHYKLQVIKALKSSGLCESLTYGLPFIILRPTSCWQLDWDLELTNQ HFHALCHSLLKREWLLAKGEPPGPGHSQRIPASTFYVIMPSHSLTLVKA VATRELM LPSTFPLLPEDPHDDSLKNVESMLDSLELEPTYNPLHVQSHLYSHLSSIYAKPQGR LPH PHWESRAPRKHPCKTGQLQTNRARATVAPLPMTFVPGRAKMPAASKSSSDAFFLPSE WEKDPSPR

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 46B.

Protein Sequence	NOV46a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV46b	1..524	509/530 (96%)
	1..530	510/530 (96%)

Further analysis of the NOV46a protein yielded the following properties shown in Table 46C.

Table 46C. Protein Sequence Properties NOV46a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV46a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 46D.

Table 46D. Geneseq Results for NOV46a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV46a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM34317	Peptide #8354 encoded by probe for measuring placental gene expression - Homo sapiens, 52 aa. [WO200157272-A2, 09-AUG-2001]	259..310 1..52	52/52 (100%) 52/52 (100%)	7e-23
ABB18624	Protein #623 encoded by probe for measuring heart cell gene expression - Homo sapiens, 42 aa. [WO200157274-A2, 09-AUG-2001]	101..142 1..42	42/42 (100%) 42/42 (100%)	2e-16
AAM66343	Human bone marrow expressed probe encoded protein SEQ ID NO: 26649 - Homo sapiens, 42 aa. [WO200157276-A2, 09-AUG-2001]	101..142 1..42	42/42 (100%) 42/42 (100%)	2e-16
AAM53955	Human brain expressed single exon probe encoded protein SEQ ID NO: 26060 - Homo sapiens, 42 aa. [WO200157275-A2, 09-AUG-2001]	101..142 1..42	42/42 (100%) 42/42 (100%)	2e-16
AAM26622	Peptide #659 encoded by probe for measuring placental gene expression - Homo sapiens, 42 aa. [WO200157272-A2, 09-AUG-2001]	101..142 1..42	42/42 (100%) 42/42 (100%)	2e-16

In a BLAST search of public sequence databases, the NOV46a protein was found to have homology to the proteins shown in the BLASTP data in Table 46E.

Table 46E. Public BLASTP Results for NOV46a				
Protein Accession Number	Protein/Organism/Length	NOV46a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9Z0E1	D6MM5E PROTEIN - Mus musculus (Mouse), 529 aa.	1..524 1..526	380/526 (72%) 423/526 (80%)	0.0
Q96L07	SIMILAR TO DNA SEGMENT, CHR 6, MIRIAM MEISLER 5, EXPRESSED - Homo sapiens (Human), 365 aa.	1..358 1..358	358/358 (100%) 358/358 (100%)	0.0

PFam analysis predicts that the NOV46a protein contains the domains shown in the Table 46F.

Table 46F. Domain Analysis of NOV46a			
Pfam Domain	NOV46a Match Region	Identities/ Similarities for the Matched Region	Expect Value
RA: domain 1 of 1	124..214	18/115 (16%) 65/115 (57%)	8.4

Example 47.

The NOV47 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 47A.

Table 47A. NOV47 Sequence Analysis		
	SEQ ID NO: 147	960 bp
NOV47a, CG58526-01 DNA Sequence	AGGACTAAATAAAATGGCCTAAATTAAATATGGATTGGGATTCCATTCTCTTGCAG ATGCCCAGAACCAAGAAGAGGTCTGCCTGGTTTTCTTCCTGGAGCTCCAGACCCAGA CCAAAGCCTTCTGCCTCTTCCAATCCAGGGAACCAAGCATGGCAGCTGAGTCTCCCT CTGCCAAGCAGTTTCTGCCAACAGTCAGTCTCCCTCCTGGTCTAGAATATTTAAGCC AGTTAGACCTGATAATTATACACCAGCAGGTGGAGCTGCTTGTGATACTTGGTACTGA GACCTCCAACAAATATGAGATTAATAACAGCTTGGGACAAAGAATTACTTTGCAGTG GAGGAAAGCATCTGCTTCAATCGTACTTTCTGTTCCACTCTGCGATCTTGACCCCTGA GGATCACAGATAACTCAGGTCGAGAGGTCTTACAGTGAACAGGCCCTTGAGATGTAA CAGCTGCTGGTGCCCTTGCTACCTACAAGAGTTAGAAATCCAAGCCCTCCTGGTACT ATAGTTGGTTACGTTACGCAGAAGTGGGACCCCTTCTGCCTAAATTCACAATCCAAA ATGCAACAAAGAAGATATTTGAAAATTGTTGGTCTTGTGTGACATGTGGCTGTTT TGGCGATGTGGATTTTGAAGAGGTGAAACCAATTAATGAAAGCTTACAATTGGGAAG ATTTCAAAGTACTGGTCAGGATTTGTAATGATGTCTTCACAAATGCTGACAATTTGCG GAATTCATGTTCTGCAGATCTAGATGTAACAGTCAAAGCAGCAATGATCGGTGCCCTG TTTTCTCTTTGTAAGTATGGGCTTTGAGAGCCAGCCCTCCAAGATGAGAAAGAGTCA GTGTGGCAATCAAAAATCAGAGTGCCCTCTCACCTCCAACAAGCCACTTGTGTC	

	CCAGCGATGGTTCTTAGCCAGACTGAAATGAC		
	ORF Start: ATG at 31	ORF Stop: TAG at 943	
	SEQ ID NO: 148	304 aa	MW at 33794.2kD
NOV47a, CG58526-01 Protein Sequence	MDWDFHSLADAQNQRRLPGFLPGAPDPDQSLPASSNPGNQAWQLSLPLPSSFLPTVS LPPGLELYLSQLDLIIHQQVELLVILGTETSNKYEIKNSLGQRIYFAVEESICFNRTF CSTLRSCITLRITDNSGREVITVNRPLRCNSWCPCYLQELEIQAPPGTIVGYVTQKWD PFLPKFTIQANKEDILKIVGPCVTCGCFGDVDFEKVKTINEKLTIGKISKYWSGFVN DVFTNADNFGIHVPADLDVTVKAAMIGACFLFVSMGFESPALQDEKESVWQFKKSECP LTSKQAHLPSPDGS		

Further analysis of the NOV47a protein yielded the following properties shown in Table 47B.

Table 47B. Protein Sequence Properties NOV47a	
PSort analysis:	0.8500 probability located in endoplasmic reticulum (membrane); 0.4400 probability located in plasma membrane; 0.4244 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV47a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 47C.

Table 47C. Geneseq Results for NOV47a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV47a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG78341	Human Mm-1 cell line derived transplantability-associated gene 1b - Homo sapiens, 318 aa. [WO200164894-A2, 07-SEP-2001]	24..282 60..318	152/263 (57%) 187/263 (70%)	5e-84
AAB24113	Human phospholipid scramblase HPLS protein sequence - Homo sapiens, 318 aa. [CN1259574-A, 12-JUL-2000]	24..282 60..318	152/263 (57%) 187/263 (70%)	5e-84
AAB24112	Mouse phospholipid scramblase MPLS protein sequence - Mus sp, 318 aa. [CN1259574-A, 12-JUL-2000]	24..282 60..318	152/263 (57%) 187/263 (70%)	5e-84
AA09309	Human phospholipid scramblase -	24..282 60..318	152/263 (57%) 187/263 (70%)	5e-84

	A2, 22-APR-1999]			
AA29323	Human PL scramblase - Homo sapiens, 318 aa. [WO9936536-A2, 22-JUL-1999]	24..282 60..318	152/263 (57%) 187/263 (70%)	5e-84

In a BLAST search of public sequence databases, the NOV47a protein was found to have homology to the proteins shown in the BLASTP data in Table 47D.

Table 47D. Public BLASTP Results for NOV47a				
Protein Accession Number	Protein/Organism/Length	NOV47a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JJ00	Phospholipid scramblase 1 (PL scramblase 1) (Transplantability associated protein 1) (TRA1) (NOR1) - Mus musculus (Mouse), 328 aa.	20..283 66..328	150/267 (56%) 191/267 (71%)	4e-84
Q99M50	PHOSPHOLIPID SCRAMBLASE 1 - Mus musculus (Mouse), 327 aa.	20..282 66..327	150/266 (56%) 191/266 (71%)	6e-84
O15162	Phospholipid scramblase 1 (PL scramblase 1) (Erythrocyte phospholipid scramblase) (Ca ²⁺ dependent phospholipid scramblase 1) (MmTRA1b) - Homo sapiens (Human), 318 aa.	24..282 60..318	152/263 (57%) 187/263 (70%)	2e-83
P58195	Phospholipid scramblase 1 (PL scramblase 1) (Ca ²⁺ dependent phospholipid scramblase 1) - Rattus norvegicus (Rat), 335 aa.	28..282 84..335	145/256 (56%) 183/256 (70%)	3e-81
Q9NRY7	Phospholipid scramblase 2 (PL scramblase 2) (Ca ²⁺ dependent phospholipid scramblase 2) - Homo sapiens (Human), 224 aa.	55..270 6..221	135/217 (62%) 164/217 (75%)	1e-75

PFam analysis predicts that the NOV47a protein contains the domains shown in the Table 47E.

Table 47E. Domain Analysis of NOV47a			
Pfam Domain	NOV47a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 48.

The NOV48 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 48A.

Table 48A. NOV48 Sequence Analysis			
	SEQ ID NO: 149	957 bp	
NOV48a, CG57851-01 DNA Sequence	CCCCTGCTGGTGCCCAAGACCACCGTGGGAAGGAATGGCTAAAGAGGAGACAAGTGAGT TAGAATGGGGCTTGTTACCCCCAGAAGAATTTTCCCAAGTGAATGGAATCATTTCTTCA AAAGAAAATGTGCGATTCTCTGGGATAAGATCTGGAACTTCCAAGCCAAGCCTGATGAC CTGCTCATTGCTTCTTACCCCAAAGCAGGTACCACTTGGACACAGGAAATTTAGATCT TGATACAAATGATGGCGATATTGAGAAAAGCAGGCGCGCTTCCATTCAACTTCAACA CCCTTCTCTGGAGTGGATAAGAATGACACACGCCAGGAAAATTTTGCAGGGATTGAC CAGGCTAACACAATGCCTTCCCCAAGGACCCCTGAAAACATCATCTTCTGTACAACTAC TGCTTCCATCCTTCTGGGAGGAAAACCTGTAAGATAATCTATGTGGCAAGAAATGCCAA GGATAACCTGGTGTCTTACTACCATTTTCAAAGGATGAGCAAAGCACTCCCTGACGTT TTGACAGTGGGAGAATACATTATGTGTGGGGAAGTGTGTGGGGAATATGGGAAGAGA TTCGGACTTGGCAACTGCATAGGTTGTTCTGCTGGTTCTTTGATCATGCTTCTGAGAA TCCTAGAAAGTTCAAAGGATAATGGAATTTATGGGGAATAAACTAGATGAAGATCCT GTCAAAGAATTGTTTCAGCACACATCTTTGAAAGTAAGAAGAAAACAGATGACCA ACTATGTAATGATAACCTGTGACATCATGGACCACTCCATCTCCCCATTTATGAGGAA AGGGACCGTTGGAGAGTGAAGGATTACTTCTCAGCAGCACAGAATAAGAGATTTGAT GAAGACAGGAAAATGGCTGACTCTTCTCTGACCTTCCACACGGAGCTCTAAAGAGAGA GAGACAAAGTCTATACTACACAGGGGCAC		
	ORF Start: ATG at 34	ORF Stop: TAA at 919	
	SEQ ID NO: 150	295 aa	MW at 34853.7kD
NOV48a, CG57851-01 Protein Sequence	MAKEETSELEWGLLPPEEFSQVNGIILQKKMCD FWDKIWNFQAKPDDLIIASYPKAGT TWTQEIVDLIQNDGDIEKSRASIQLQHPFLEWIRMTARKIFAGIDQANTMPSRTL KTHLPVQLLPSPFWEENCKIIYVARNAKDNLSYYHFQRMKALPDVLTVGEYIMCGE VLWGIWEEIRTWQLHRLFCWFFDHASENPRKFRIMEFMGNKLDEDPVKRIVQHTSFE SKKKNQMTNYVMITCDIMDHSISPFRMKGTVGEWKDYFSAAQNKRFDEDRKMADSSLT FHTEL		

Further analysis of the NOV48a protein yielded the following properties shown in Table 48B.

Table 48B. Protein Sequence Properties NOV48a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV48a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 48C.

Table 48C. Geneseq Results for NOV48a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV48a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE12209	Human ST drug-metabolising protein 2 encoded by DNA transcript 2 - Homo sapiens, 304 aa. [WO200172977-A2, 04-OCT-2001]	16..295 15..304	137/293 (46%) 200/293 (67%)	9e-74
AAE12210	Human ST drug-metabolising protein 3 encoded by cDNA - Homo sapiens, 304 aa. [WO200172977-A2, 04-OCT-2001]	16..295 15..304	129/293 (44%) 190/293 (64%)	1e-67
AAE12208	Human ST drug-metabolising protein 1 encoded by DNA transcript 1 - Homo sapiens, 304 aa. [WO200172977-A2, 04-OCT-2001]	16..295 15..304	128/293 (43%) 190/293 (64%)	6e-67
AAE05178	Human drug metabolising enzyme (DME-9) protein - Homo sapiens, 304 aa. [WO200151638-A2, 19-JUL-2001]	16..295 15..304	128/293 (43%) 189/293 (63%)	1e-66
AAY67294	Human STP2 (phenol sulphotransferase 2) amino acid sequence - Homo sapiens, 295 aa. [WO9964630-A1, 16-DEC-1999]	15..295 10..295	133/292 (45%) 186/292 (63%)	5e-66

In a BLAST search of public sequence databases, the NOV48a protein was found to have homology to the proteins shown in the BLASTP data in Table 48D.

Table 48D. Public BLASTP Results for NOV48a				
Protein Accession Number	Protein/Organism/Length	NOV48a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q90WR6	SULFOTRANSFERASE 1C - Gallus gallus (Chicken), 307 aa.	3..295 5..307	170/304 (55%) 218/304 (70%)	3e-94
P50237				3e-92

	(EC 2.8.2.-) (HAST-I) - <i>Rattus norvegicus</i> (Rat), 304 aa.	1..304	222/308 (71%)	
O70262	PHENOL SULFOTRANSFERASE - <i>Mus musculus</i> (Mouse), 304 aa.	18..295 19..304	164/289 (56%) 215/289 (73%)	1e-91
O75897	Sulfotransferase 1C2 (EC 2.8.2.-) (SULT1C) (SULT1C#2) - <i>Homo sapiens</i> (Human), 302 aa.	22..292 22..299	160/282 (56%) 203/282 (71%)	1e-87
O00338	Sulfotransferase 1C1 (EC 2.8.2.-) (SULT1C#1) (ST1C2) (humSULTC2) - <i>Homo sapiens</i> (Human), 296 aa.	18..295 12..296	149/289 (51%) 201/289 (68%)	1e-80

PFam analysis predicts that the NOV48a protein contains the domains shown in the Table 48E.

Table 48E. Domain Analysis of NOV48a			
Pfam Domain	NOV48a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Sulfotransfer: domain 1 of 1	23..285	116/298 (39%) 207/298 (69%)	6.2e-82

Example 49.

The NOV49 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 49A.

Table 49A. NOV49 Sequence Analysis		
	SEQ ID NO: 151	1934 bp
NOV49a, CG59377-01 DNA Sequence	<p>CTTGATTACGGAGACTGAACCTTCATAGGGTGCGCACTTACCAAGGACAGGAAGGTTT CTCTGTTTGAAGGGCTTTAACTTATAACAAAGAAAATAAAATGACGACTTCGTCTA TCAGACGGCAGATGAAAAACATCGTGAACAATTACTCAGAGGCAGAAATCAAAGTCCG GGAAGCCACCTCCAATGACCCGTGGGGCCCGTCCAGTTCTCTGATGACCGAGATTGCC GACCTGACCTACAACGTGGTGGCCTTCTCGGAGATCATGAGCATGGTGTGGAAGCGGC TGAATGACCATGGCAAGAACTGGCGGCATGTGTACAAGGCGCTGACCTGCTGGACTA CCTCATCAAGACAGGCTCCGAACGTGTGGCCAGCAGTGCCGGGAGAACATCTTCGCC ATCCAGACCCTGAAGGACTTCCAGTACATTGACCGAGATGGCAAGGACCAGGGCATCA ATGTGCGTGAGAAGTCAAAGCAACTGGTGGCTCTCCTCAAGGACGAGGAACGGTTGAA GGCTGAGAGGGCCAGGCTCTCAAACCAAAGAGCGCATGGCCAGGTTGCCACTGGC ATGGGCAGCAACCAGATCACCTTTGGGCGAGGCTCCAGCCAGCCCAACCTCTCCACCA GCCACTCGGAGCAGGATATGGCAAGGCCGGGGCTCCCGGCCTCCTACCATGGCTC CACCTCCCGCAGTGTCTCCGAGCTGGAGCAAGCCCGGCCAGACTAGTGGAGAA GAGGAGCTTCAGCTGCACTGGCACTTGCCATGAGCAGAGAAGTGGCTGAGCAGGAAG AACGCCTCAGGCGGGTGATGACCTCAGATTACAGATGGCCCTGGAAGAAAGCCGAAG GGACACAGTTAAATTCAAAAAAGAAAGAGCAGACTACGCTGTTGGATTAAATGGAT GCTCTCCCGAGCTCGGGCCCCCGCGCCAGAAAGCAGAGCCCTGGGGCCCGTCAGCCT CCACTAACCAGACCAACCCCTGGGGCGGGCCAGCGGCTCCTGCGAGTACTTCAGACCC CTGGCCATCGTTTGGTACCAAGCCAGCTGCCTCCATTGACCCATGGGGGGTGCCCACT GGAGCCACCGCACAACTGTGCCCCAAGAACTCGGACCCCTGGGCAGCTTCACAGCAGC CTGCCTCCAGTGCTGGGAAAAGAGCTTCTGACGCGTGGGGCGCAGTCTCCACCACCAA GCCCGTGTCTGTCTGCGGTCTTTGAGCTCTTCAGTAATCTGAATGGTACAATTTAA</p>	

	GATGACTTTTCTGAATTTGACAACCTTCGGACTTCAAAAAAACAGCCGAATCTGTGA CCTCTCTGCCATCCCAAAACAATGGAACCTACCAGCCCTGACCCCTTGGAGTCTCAACC CCTGACTGTGCGCTCAAGCAAGCCAGCAGTGGCCGAAACACCTGAGTCTCTCTG GGCCCCAACGGGGCTGGTGAACCTGGACTCACTGGTGACAGGCTGCCACCAG CCCAGTCCCTCAACCTTTCTTGGCACCAGGTGCTCCCGCCACCTCGGCCCTGTAA CCCTTTCCAGGTGAACCAAGCCCGAGCGCTGACACTGAACAGCTTCGGGGGAGCCCA GTCCTGGGGACCAGCACATCTTTGGGCTGGCCAGGAGTGGAGTCCATGGCTGTGG CCTCGATGACTCCGCGGCCCCACAGCCAGCTCTGGGGGCACTGGTCTCTCTGAC ACCACTGGGCCCTGCAATGATGAACATGGTGGGCAGTGTGGGTATACCCCATCAGCA GCCAGGCCACTGGCACAAACACCTTTCTTCTCTAGTGCCTGGGCCCTGGGACCCA CCCAGAGCACCTGTGCTGGAGGATGCCGAGCAGGGACTCTCGTCTGTGGGACGGGATC CAAGAGTTTGGGGATTAGGG		
	ORF Start: ATG at 101	ORF Stop: TAG at 1835	
	SEQ ID NO: 152	578 aa	MW at 61651.2kD
NOV49a, CG59377-01 Protein Sequence	MTSSIRRMKNIVMNYSEAEIKVREATSNDPWGPSSSLMTEIADLTYNVVFSEIMS MVWKRINDHGKNWRHVYKALTLLDYLKTGSEVAQQCRENIFAIQTLKDFQYIDRDG KDQGINVREKSKQLVALLKDEERLKAERAQALKTKERMAQVATGMGSNQITFGRSSQ PNLSTSHSEQYEGKAGGSPASVHGSTSPRVSSLEQARPQTSGEELQLQALAMSRE VAEQEERLRRGDDLRLQMALEESRDTVKIPKKKEQTLLDLMDALPSSGPAQAEP WGPSASTNQTNPWGGPAPASTSDPWPSFGTKPAASIDPWGPTGATAQSVKNSDPW AASQQPASSAGKRASDANGAVSTTKPVSVSGSFELFNLNGTIKDDFSEFDNLRSSK TAESVTSPLSQNNGTTSPPFESQPLTVASSKPPSARKTPESFLGPNAALVNLDLST RPAPPAQSLNPFLLAPGAPATSAPVNPQVNPQPLTLNQLRGSPVLGTSFSGPGPV ESMAVASMTSAAPQALGATGSSSLTPLGPAMNMVGSVGI PPSAAQATGTNPFLL		

Further analysis of the NOV49a protein yielded the following properties shown in Table 49B.

Table 49B. Protein Sequence Properties NOV49a	
PSort analysis:	0.4936 probability located in mitochondrial matrix space; 0.3000 probability located in nucleus; 0.2087 probability located in mitochondrial inner membrane; 0.2087 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV49a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 49C.

Table 49C. Geneseq Results for NOV49a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV49a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB93525	Human protein sequence SEQ ID NO:12872 - Homo sapiens, 584 aa. [EP1074617-A2, 07-FEB-2001]	1..578 1..584	578/584 (98%) 578/584 (98%)	0.0
AAB95663	Human protein sequence SEQ ID	40..403 1..370	364/370 (98%) 364/370 (98%)	0.0

	[EP1074617-A2, 07-FEB-2001]			
AAB93011	Human protein sequence SEQ ID NO:11762 - Homo sapiens, 484 aa. [EP1074617-A2, 07-FEB-2001]	1..407 1..470	385/470 (81%) 390/470 (82%)	0.0
AAB42049	Human ORFX ORF1813 polypeptide sequence SEQ ID NO:3626 - Homo sapiens, 551 aa. [WO200058473-A2, 05-OCT-2000]	1..578 1..551	306/636 (48%) 370/636 (58%)	e-141
AAB95100	Human protein sequence SEQ ID NO:17064 - Homo sapiens, 576 aa. [EP1074617-A2, 07-FEB-2001]	1..578 1..576	298/636 (46%) 371/636 (57%)	e-137

In a BLAST search of public sequence databases, the NOV49a protein was found to have homology to the proteins shown in the BLASTP data in Table 49D.

Table 49D. Public BLASTP Results for NOV49a				
Protein Accession Number	Protein/Organism/Length	NOV49a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O95207	EPSIN 2A - Homo sapiens (Human), 584 aa.	1..578 1..584	576/584 (98%) 576/584 (98%)	0.0
Q9UPT7	KIAA1065 PROTEIN - Homo sapiens (Human), 641 aa.	1..578 1..641	557/641 (86%) 562/641 (86%)	0.0
O95208	EPSIN 2B - Homo sapiens (Human), 642 aa.	1..578 1..642	556/642 (86%) 560/642 (86%)	0.0
Q9Z1Z3	EH DOMAIN BINDING PROTEIN EPSIN 2 - Rattus norvegicus (Rat), 583 aa.	1..578 1..583	512/590 (86%) 526/590 (88%)	0.0
O70447	INTERSECTIN-EH BINDING PROTEIN IBP2 - Mus musculus (Mouse), 509 aa (fragment).	76..578 2..509	438/515 (85%) 459/515 (89%)	0.0

PFam analysis predicts that the NOV49a protein contains the domains shown in the Table 49E.

Table 49E. Domain Analysis of NOV49a		
Pfam Domain	NOV49a Match Region	Expect Value

		Similarities for the Matched Region	
ENTH: domain 1 of 1	17..140	70/131 (53%) 117/131 (89%)	7.9e-68
VHS: domain 1 of 1	14..158	33/160 (21%) 90/160 (56%)	3.3
UIM: domain 1 of 2	217..234	11/18 (61%) 16/18 (89%)	0.043
UIM: domain 2 of 2	242..259	5/18 (28%) 12/18 (67%)	80

Example 50.

The NOV50 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 50A.

Table 50A. NOV50 Sequence Analysis		
	SEQ ID NO: 153	2580 bp
NOV50a, CG59258-01 DNA Sequence	ATGCTGCTGGCCCCCTTTATTGCTGGGTGTGTGCCCATGCTGCTGGCCCCCTTTTAT TGCTGGGCAGTGACAACTGTACCATCAGTGGCTCTCCACTGTCGGAAAGGAAGTGG AGCAATTCTGAATACTGTAAAGACAAAGCAAATCCGGCCATGAAGACTGTCTACAAG TTCGACATTGCCGAGAAATGGCTGCGCCCCCACCAGAGAGCAGCTGCCAAAGACTG CACCGTCCCCACTGGTGGAGGCCAAGGACCCCAAGCTCCGAGAAGACCGGCGGCCAAT CACAGTCCACTTTGGACAGGACCAAGTCTGAGATGTCTTTAGCTCAGCACTCACTCAC GGCAAAGAGAGTCCCCGACCCAGCCGGAGAGAGTCTGTTGACAGGACTGGCGAGCCCC TGAATCCTGAGCGCGTCTCTCCGGAGATCATCTCGGCCTGTTACGCACTTGCTCTG GGCAACCCTGGGCAAGTCTTTGCTTGCCTCATCTGTGAAATGGGTAGCAGCCCTCGT TCCCTGCAGAGAGCCCTTGCGCTGCTGGGGACACCCAGCTTATTGGGAAACTGCAA CCACCATGCGCGATGGCCCCACCACGCCCTGTCTAGGAAGCAGAGGCCTCCACAGCAG CGTGTCCACTGTGCCCTGGCCCTGCGTGAAGTGCCATCAGATGCCCGCATCCCTGC AGCAGGGCCCTCGTACTGGCCTCAGATGAGGACACAGAGGCCAGGGAAGTCACT TGCTTGCCAAAGTCACTCAGCAAACCATGTCTGTCTGGCTCTCAGAAATGGGAAAGA AGCCTGGGCATTGAGCCATGAGGGAGCCACGGCTGTAGCCAGTGGAAATGACGTACCT CAGTCCAGGATGTGACCCGGGCGAGCCAGGTCCACAGCCACTACTTTCTTGCCCCCA CCAGTGTCCACAGTTCACAGAACTCAGTCTCCAGATCTGGGCTCCAGGATGCAGAG GCTGTCTCAGGCCTGGTAAAGCCCTTGCGACACTATGCGGTCTTCTCTCCGAAGAC TCCTCTGATGATGAATGCCAGCGGAAGAGGGCCCCAGCTCTGCTTACCCGAGAGCT TTTTCTTCTCCGCTCCCTTTGAATGGCCGAGCCGTATCGGACACTCAGGAGTCA CAGCGCGAAGGGCAGAGGAGAGTCCAGAGCAGCAAGTGGGAAGTCCACAGGC CCTGTCCAGCTCCCCCTGACCGGGCTGCCAGCATCGACCTTCTGGAAGACGTCTTCA GCAACCTGGACATGGAGGCCGCACTGCAGCCACTGGGCCAGGCCAAGAGCTTAGAGGA CCTTCGTGCCCCCAAGACCTGAGGGAGCAGCCAGGGACCTTTGACTATCAGAGGCTG GATCTGGGCGGAGTGAGAGGAGCCGCGGGGTGACAGTGGCCTTGAAGCTTACCCACC CGTACAACAAGCTCTGGAGCCTGGGCCAGGACGACATGGCCATCCCCAGCAAGCCCC AGCTGCCTCCCCTGAGAAGCCCTCAGCCCTGCTCGGAACTCCCTGGCCCTGCCTCGA AGGCCCCAGAACCGGGACAGCATCCTGAACCCAGTGACAAGGAGGAGGTGCCACCC CTACTTGGGCAGCATCACCATCCCCCGGCCCCAAGGCAGGAAGACCCAGAGCTGGG CATCGTGCTCCACCGCCATTCCTCCGCCCCGCAAGCTCCAGGCTGCGGGCGCCGCA CTTGGTGACGTCTCAGAGCGGCTGCAGACGGATCGGGACAGGCGAGCTGCCCTGAGTC CAGGCTCCTGCTGGTGTGTGTCCTCCCAAGGCCCACTGAACCTGCTCCAGCCGCTCAG CCCTGGCCCCGGGGCTGCAGGCACGAGCAGTGACGCCCTGCTCGCCCTCTGGAACCG CTCAGCACAGCCTGGTCAAGCAGACCCCTCCCGTCACGCCCCGCCACCCCAATGTAG CCACCCCATTCACCCCAATTGAGCTTCCCCCTGCAGGGACACCCACCCCATTCCTCC ACAGCCCACTCAACCCCTTGTCCCATCCATGCCAGCAGCCCCACCCACCTGCCCT CTGGTCTCCACACAGCCGGGCTTTCGGGGCCCTCCAGCTTCCCTGGGGCGGCTT TTGCGTCCGGCTCCTGCTGTCCAGTGTGGCTTCTGTGCCCTCAGAGTCTCAGCC CAACCTCTCGGCCCTTCCATGCCCCAACCTCTTTGGCCAGATGCCCATGCCACCCAC ACGAGCCCCCTACAGCCGCTGGGTCCCCCAGCAGTTGCCCGTCGAGGATCCGAACGT TGCCCTTGCGCCGCTCAAGTGCCAGGGCTGCTGAGACCAAGCAGGGGTGCGCCCTGAG GCCTGGAGACCCCGCTTCTGCTCCAGGCCCTCAAGGCTGGAGCCAACTG CAGCCCTCTGCTCTCAACAGGCCAGAGACCCCTTTGAGGATTGTTACAGAAAACCA AGCAAGAGCTGAGCCCGAGTCCGGCCCTGGCCCCGGCCCCAGACTCGTGGAGCAGCT	

	CAGGAAGCAGTGGGAGACCTTCGAGTGA		
	ORF Start: ATG at 1	ORF Stop: TGA at 2578	
	SEQ ID NO: 154	859 aa	MW at 91746.7kD
NOV50a, CG59258-01 Protein Sequence	MLLAPFYCWCAHAAGPLLLGSDKLYHQWLSTVRKGSAILNTVKTKANPAMKTVYK FDIAENGCAPTPEEQLPKTAPSPLEAKDPKLRDRRPITVHFGQDQSEMSFSSALTH GKESARTQPERVVDRTGEPLNPERALSGDHLWFPVTHLLWATLGKSLALICEMGSSPR SLQRLALILGTPLIWEATTMADGPTTCLGSRGLPSSVSTVPLALREVPSDAPHPC SRALVTGLTDEDETAQGSHELLAKVTQQTMSVWLSENGKEAWAFSHEGATAVASGMTYP QSRMCTRAARSHSHYFLAPTPTVPTVPTQSPDLGSRMQRLSSGLVKPLRHAVFLSED SSDDECQREEGPSSGFTESEFFSAPFEWPPYRTLRSDSAEGDEAESPEQQVRKSTG PVPAPPDRAASIDLLEDVFSNLDMEALQPLGQAKSLEDLRAPKDLREQPGTFDYQRL DLGGSERSRGVTVALKLTHPYNKLWSLQDDMAIPSKPPAASPEKPSALLGNLALPR RPQNRDSILNPSDKKEVPTPTLGSITIPRPQGRKTPELGIVPPPIPRPAKLQAGAA LGDVSERLQTDRRRAALSPGLLPGVVFPQGPTELLQPLSPGPGAAGTSSDALLALLDP LSTAWSGSTLPSRPATPNVATPFTPQFSFPAGTPTFPQPPLNPFVPSMPAAEPPTLP LVSTPAGPFGAPPASLGPASFAGLLSSAGFCAPHRSPQNLSSALSMPLNLFQGMPMGTH TSPLQLGPPAVAFSRIRTLPLARSSARAAETKQGLALRPDGPLLPFPFPQGLEPTL QPSAPQQRDPFEDLLQKTKQDVSPSPALAPAPDSVEQLRKQWETFE		

Further analysis of the NOV50a protein yielded the following properties shown in Table 50B.

Table 50B. Protein Sequence Properties NOV50a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1940 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	Likely cleavage site between residues 15 and 16

A search of the NOV50a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 50C.

Table 50C. Geneseq Results for NOV50a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV50a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41501	Human polypeptide SEQ ID NO 6432 - Homo sapiens, 545 aa. [WO200153312-A1, 26-JUL-2001]	22..103 401..482	82/82 (100%) 82/82 (100%)	2e-42
AAM39715	Human polypeptide SEQ ID NO 2860 - Homo sapiens, 559 aa. [WO200153312-A1, 26-JUL-2001]	22..103 396..496	82/101 (81%) 82/101 (81%)	6e-39
AAW31855	Mycobacterium tuberculosis 55 kDa protein - Mycobacterium tuberculosis, 572 aa. [WO9741252-A2, 06-NOV-1997]	498..845 71..389	96/358 (26%) 125/358 (34%)	8e-12

AAW31852	Mycobacterium tuberculosis 74 kDa protein - Mycobacterium tuberculosis, 763 aa. [WO9741252-A2, 06-NOV-1997]	498..845 262..580	96/358 (26%) 125/358 (34%)	8e-12
AAB50363	Human SRCAP - Homo sapiens, 2972 aa. [WO200073467-A1, 07-DEC-2000]	501..845 1235..1575	112/369 (30%) 141/369 (37%)	1e-11

In a BLAST search of public sequence databases, the NOV50a protein was found to have homology to the proteins shown in the BLASTP data in Table 50D.

Table 50D. Public BLASTP Results for NOV50a				
Protein Accession Number	Protein/Organism/Length	NOV50a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9HCG4	KIAA1608 PROTEIN - Homo sapiens (Human), 603 aa (fragment).	309..859 62..603	501/555 (90%) 510/555 (91%)	0.0
Q9H796	CDNA: FLJ21129 FIS, CLONE CAS06266 - Homo sapiens (Human), 559 aa.	22..103 396..496	81/101 (80%) 81/101 (80%)	2e-37
AAK44515	HYPOTHETICAL 58.5 KDA PROTEIN - Mycobacterium tuberculosis CDC1551, 598 aa.	499..845 299..562	104/354 (29%) 121/354 (33%)	8e-14
Q9SN46	EXTENSIN-LIKE PROTEIN - Arabidopsis thaliana (Mouse-ear cress), 839 aa.	604..848 407..626	73/249 (29%) 100/249 (39%)	3e-12
Q41805	EXTENSIN-LIKE PROTEIN PRECURSOR - Zea mays (Maize), 1188 aa.	492..848 415..749	88/361 (24%) 124/361 (33%)	5e-12

PFam analysis predicts that the NOV50a protein contains the domains shown in the Table 50E.

Table 50E. Domain Analysis of NOV50a			
Pfam Domain	NOV50a Match Region		Expect Value

		Similarities for the Matched Region	
No Significant Matches Found			

Example 51.

The NOV51 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 51A.

Table 51A. NOV51 Sequence Analysis			
	SEQ ID NO: 155	1394 bp	
NOV51a, CG59492-01 DNA Sequence	GTGGCCTGCTCCTGCAGCAATCCCAGGACCCCTGCTCATGGGGCTGTTCTCTACTAA CCCCAAAGAGAAGACCCAGGAGGAACCCCTGGCCAGAGCAGGGCCCTGTGTTGACC GTGGTGTCCAAGTTCAGGCCCTCACTGGAGCAGCTTCTGCAGGTCTTACACAGCACCA CGCCCCACTACATTCTGCTGCATCAAGCCCAACAGCCAGGGCCAGGCGCAGACCTTTCT CCAAGAGGAGGTCCTGAGCCAGCTGGAGGCCTGTGGCCTCGTGGAGACCATCCATATC AGTGCTGCTGGCTTCCCATCCGGTCTCTCACCGAACTTTGTAGAACGATACAAGT TACTAAGAAGGCTTCATCCTTGACATCCTCTGGCCCCGACAGCCCATATCTCGCCAA AGGGCTCCCTGAATGGTGTCCACACAGCGAGGAAGCCACGCTTGAACCTCTCATCCAG GACATTCTCCCACTCTGCCGGTCTAACTCAGGCAGCAGCCATAACTGGTGACTCGG CTGAGGCCATGCCAGCCCCATGCACTGTGGCAGGACCAAGGTGTTTCACTGACTGACTC TATGCTGGAGCTTCTGGAATGTGGGCGTGCCCGGTGCTGGAGCAGTGTGCCCGCTGC ATCCAGGTGGCTGGAGGCGCACCCGGCACCGAGAGCAGGAGCGGCAGTGGCGGGCCG TCATGCTCATCCAGGCAGCCATTCTGTTCTGGTTAACTCGGAAACACATCCAGAGGCT GCATGCAGCTGCCACAGTCATCAAGCGTGCATGGCAGAAGTGGAGAATCAGAATGGCC TGCCCTTGCTGCTAAAGAGCTGGATGGTGTGGAAGAAAAACACTTCTCTCAAGCTCCCT GTTCCCTGAGCACCTCGCCGCTGCAGACCAGGCTCCTGGAGGCAATAATCCGCTTCTG GCCCTTGGGACTGGTCTTGCCAAATACGGCTATGGGTGTAGGCAGCTTTCAGAGGAAA TTAGTGGTCTGGGCTTGCCCTCCAGCTCCCCAGGGGCAGCCCCAGTAGCTACACTGTCC AGACAGCACAGAACCAGGCTGGTGTACGTCATCCGAGCGTGCCTCAGGGATCGAT AAAGTTTCACTGCAGAAAGTCTCCACTGCGGTATGCTGACATCTGCCCTGAACCTTCA CCCTACAGCATTGCAGGCTTTAATCAGATTCTGCTGGAAGACACAGGCTGATCCAGC TGACCTCTTCTGCCTTCACTGGGCTGGGGTGATCCTTGGTGCCTTTGTTTCCACAAGG CCTTTTCTGCCCCCTGCCTTGCCAAAGACATTTAATCAGCACACAGCTGCCAGACTA TTCCACAGTGTCTCAAATGCACATGAACAACAGTGACGGCTCCAGCCTTCGACCCAG AG		
	ORF Start: ATG at 39	ORF Stop: TGA at 1248	
	SEQ ID NO: 156	403 aa	MW at 45142.8kD
NOV51a, CG59492-01 Protein Sequence	MGLFPTNPKEKTQEEPPQSRAPVLTVVSKFKASLEQLQLVLHSTTPHYIRCIKPSNQ GQAQTFLEEVLSQLEACGLVETIHSAGFPPIRVSHRNFFVERYKLLRRLHPCTSSGP DSPYPAKGLPEWCPHSEETLEPLIQDILHTLPVLTQAAAITGDSAEAMPAPMHCGRT KVFMTDSMLELLECGRARVLEQCARCIQGWRRHRHREQERQWRAVMLIQAAIRSWLT RKHIQRLHAAATVIKRAWQKWRIRMACLAAKELDGVEEKHFSQAPCSLSTSPQLRLL EAIIRFWPLGLVLANTAMGVGSFQRKLVVWACLQLPRGSPSSYTVQTAQDQAGVTSIR ALPQGSIKFHCRKSPRYADICPEPSPYSIAGFNQILLERHRLIHVTSSAFTGLG		

Further analysis of the NOV51a protein yielded the following properties shown in Table 51B.

Table 51B. Protein Sequence Properties NOV51a	
PSort analysis:	0.3000 probability located in nucleus; 0.2029 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space; 0.0320 probability located in microbody (peroxisome)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV51a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 51C.

Table 51C. Geneseq Results for NOV51a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV51a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY94290	Human myosin heavy chain homologue - Homo sapiens, 612 aa. [WO200026372-A1, 11-MAY-2000]	1..403 210..612	401/403 (99%) 401/403 (99%)	0.0
AAU23676	Novel human enzyme polypeptide #762 - Homo sapiens, 387 aa. [WO200155301-A2, 02-AUG-2001]	17..403 1..387	384/387 (99%) 384/387 (99%)	0.0
ABB10243	Human cDNA SEQ ID NO: 551 - Homo sapiens, 570 aa. [WO200154474-A2, 02-AUG-2001]	1..365 206..570	365/365 (100%) 365/365 (100%)	0.0
AAU23123	Novel human enzyme polypeptide #209 - Homo sapiens, 567 aa. [WO200155301-A2, 02-AUG-2001]	1..365 203..567	364/365 (99%) 364/365 (99%)	0.0
AAM23563	Human EST encoded protein SEQ ID NO: 1088 - Homo sapiens, 477 aa. [WO200154477-A2, 02-AUG-2001]	1..189 288..476	188/189 (99%) 188/189 (99%)	e-108

In a BLAST search of public sequence databases, the NOV51a protein was found to have homology to the proteins shown in the BLASTP data in Table 51D.

Table 51D. Public BLASTP Results for NOV51a				
Protein Accession Number	Protein/Organism/Length	NOV51a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96H55	HYPOTHETICAL 86.7 KDA PROTEIN - Homo sapiens (Human), 770 aa.	72..403 439..770	330/332 (99%) 330/332 (99%)	0.0
Q9D2Z3	1110055A02RIK PROTEIN (RIKEN CDNA 1110055A02 GENE) - Mus musculus (Mouse), 395 aa.	3..394 2..395	288/394 (73%) 320/394 (81%)	e-162
Q948A2	PUTATIVE MYOSIN HEAVY CHAIN - Oryza sativa (Rice), 1601 aa.	2..255 663..876	84/258 (32%) 125/258 (47%)	1e-23
O74805	HYPOTHETICAL MYOSIN-LIKE PROTEIN C2D10.14C IN CHROMOSOME II - Schizosaccharomyces pombe (Fission yeast), 1471 aa.	20..347 615..903	96/340 (28%) 152/340 (44%)	1e-21
T30148	hypothetical protein E02C12.1 - Caenorhabditis elegans, 1019 aa.	5..249 619..830	74/248 (29%) 119/248 (47%)	6e-21

PFam analysis predicts that the NOV51a protein contains the domains shown in the Table 51E.

Table 51E. Domain Analysis of NOV51a			
Pfam Domain	NOV51a Match Region	Identities/ Similarities for the Matched Region	Expect Value
myosin_head: domain 1 of 1	26..105	37/81 (46%) 60/81 (74%)	5.1e-25

Example 52.

The NOV52 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 52A.

Table 52A. NOV52 Sequence Analysis

	SEQ ID NO: 157	1380 bp
NOV52a, CG59564-01 DNA Sequence	TAGAATTCCAGCGGCCGCTGAAATCCTCACTCGGTGAGTTCTCGGGCGAGTTACGGG GACGACCTGCGGGAGCAGCGGGCAGTGGCCGGACGCTGAAGCCAGGAGAGCGATGG AGACGTATGCGGAGGTTGGGAAGGAGGGCAAGCCTTCCTGTGCATCGGTGGATCTGCA GGGAGACAGCTCCTTACAGGTGGAGATTTCTGACGAGTGAAGTGAAGCGGAGTTCTCAG AAATTCAGTGTTCAAACAAGAGCTGCCTCCCTCACTTCGCCCAGACCGAGTTCTCAG TCGTGGCGGAGCAGGAGGATTCATCTGGCTGCATGATGCTACGTGGAGAATGAGGA GTACGCCGGCCTCATCATCCCCCAGCCCCCTCCGAGGCCAGACTTTGAGGCTTCGAGG GAAAAGCTACAGAAATTGGGCGAGGGGACAGCTCTGTCACTCGGGAAGAGTTTGCCA AGATGAAGCAGGAGCTGGAAGCGGAGTACCTGGCCATCTTTAAGAAGACAGTTGCGAT GCACGAAGTCTTTCTGCAGCGCTGGCGGCCACCCACCTCGCTCGAGACCACAAC TTCTTTGTGTTTTTGAATATGGACAGGATCTGAGTGTCCGGGGGAAGAACAGGAAGG AGCTCCTCGAGGGTTTCTGAGGAATATTGTGAAGTCCGCGGATGAAGCCCTCATCCA GGGCATGTGAGGGCTCAAGGAGGTGGATGACTTCTTTGAGCATGAGAGACCTTCCTG TTGAGTATCACACCGGTATCCGAGATGCCTGCCTGCGGGCCGACCGCGTCATGCGCG CCCACAAGTGCCTGGCAGACGATTATATCCCTATCTCAGCTGCGCTGAGCAGTCTGGG AACACAGGAAGTCAACCAGCTAAGGACGAGCTTCTCAAATTGGCAGAGCTCTTTGAC CGGCTGAGGAAGCTGGAGGGCCGGGTGGCTTCCGATGAGGACCTGAAGCTGTGACACA TGCTGAGGTACTACATGCGTGACTCACAGGCAGCCAAGGACCTGCTGTACCGCGCGGT GCGGGCACTGGCCGACTACGAGAATGCCAACAGGCGCTGGACAAGGCGCGCACAGG AACCGGGAGGTGCGGCCCGCGAGAGCCACCAGCAGCTGTGCTGCCAACGCTTCGAGC GCCTCTCGACTCCGCCAAGCAAGAGCTCATGGACTTCAAGTCCGCCCGGGTCTCCTC TTTTCGAAAGAATCTATTGAGCTGGCAGAGCTGGAGCTCAAACACGCCAAGGCCAGC ACCCTGATTCTCGGAACACCCTTGTGCGCTAAAGGGGAGCCCTTAGAGTAGCCAGA GCTCAGCCAGACCTAATCTGGGATCTCCAGTGACCAGGGTATCCC	
	ORF Start: ATG at 113	ORF Stop: TAG at 1322
	SEQ ID NO: 158	403 aa MW at 46384.2kD
NOV52a, CG59564-01 Protein Sequence	METYAEVKGEGKPCASVDLQGDSSLQVEISDAVSEKDKVKFTVQTKSCLPHFAQTEF SVVRQHEEPIWLHDAYVENEYAGLIIPAPPRPDFEASREKLQKLGEEDSSVTRREEF AKMKQLEAEYLAIFFKKTVMHEVFLQRLAAHPTLRDHNFFVFLEYGQDLSVRGKNR KELGGLRNIVKSADEALITGMSGLKEVDFFFEHERTFLLEYHTRIRDACLRAADRV RAHKCLADDYIPISAAALSSLTQEVNQLRTSFLKLAELFDRLRLKLEGRVASDEDLKLS DMLRYMRDSQAADLLYRRLRALADYENANKALDKARTNRNREVRPAESHQQLCCQRF ERLSDSAKQELMDFKSRVSSFRKNLIELAELELKHAKASTLIILRNTLVALKGEF	

Further analysis of the NOV52a protein yielded the following properties shown in Table 52B.

Table 52B. Protein Sequence Properties NOV52a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV52a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 52C.

Table 52C. Geneseq Results for NOV52a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV52a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY94209	Human TRAF four associated factor TFAF2 - Homo sapiens, 406 aa. [CA2245340-A1, 19-FEB-2000]	17..402 23..405	273/386 (70%) 333/386 (85%)	e-160
AAB07856	Amino acid sequence of Smad1 interactor protein clone S1+12-2 - Homo sapiens, 414 aa. [WO200047102-A2, 17-AUG-2000]	17..402 31..413	273/386 (70%) 333/386 (85%)	e-160
AAB43157	Human ORFX ORF2921 polypeptide sequence SEQ ID NO:5842 - Homo sapiens, 460 aa. [WO200058473-A2, 05-OCT-2000]	17..402 77..459	273/386 (70%) 333/386 (85%)	e-160
AAB58368	Lung cancer associated polypeptide sequence SEQ ID 706 - Homo sapiens, 414 aa. [WO200055180-A2, 21-SEP-2000]	17..402 31..413	273/386 (70%) 333/386 (85%)	e-160
AAO13507	Human polypeptide SEQ ID NO 27399 - Homo sapiens, 443 aa. [WO200164835-A2, 07-SEP-2001]	17..400 61..441	242/384 (63%) 317/384 (82%)	e-144

In a BLAST search of public sequence databases, the NOV52a protein was found to have homology to the proteins shown in the BLASTP data in Table 52D.

Table 52D. Public BLASTP Results for NOV52a				
Protein Accession Number	Protein/Organism/Length	NOV52a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UNH7	Sorting nexin 6 (TRAF4-associated factor 2) - Homo sapiens (Human), 406 aa.	17..402 23..405	273/386 (70%) 333/386 (85%)	e-159
Q9CZ03	2810425K19RIK PROTEIN - Mus musculus (Mouse), 406 aa.	17..402 23..405	271/386 (70%) 333/386 (86%)	e-159
Q9Y5X3	Sorting nexin 5 - Homo sapiens (Human), 404 aa.	17..400 22..402	242/384 (63%) 317/384 (82%)	e-143

Q9D8U8	Sorting nexin 5 - Mus musculus (Mouse), 404 aa.	17..400 22..402	241/384 (62%) 314/384 (81%)	e-142
Q96NG4	CDNA FLJ30934 FIS, CLONE FEBRA2007017, MODERATELY SIMILAR TO HOMO SAPIENS TRAF4-ASSOCIATED FACTOR 2 MRNA - Homo sapiens (Human), 277 aa.	1..237 1..237	236/237 (99%) 236/237 (99%)	e-134

PFam analysis predicts that the NOV52a protein contains the domains shown in the Table 52E.

Table 52E. Domain Analysis of NOV52a			
Pfam Domain	NOV52a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PX: domain 1 of 1	23..164	39/160 (24%) 103/160 (64%)	1.6e-15

Example 53.

The NOV53 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 53A.

Table 53A. NOV53 Sequence Analysis		
	SEQ ID NO: 159	3056 bp
NOV53a, CG59553-01 DNA Sequence	CTCCTGCGGGGTCAAATACAGAATTACGCACCCTTGGCTTCCTTGGAGCCTAGCGGC TCTCCCGCGTCCAAGATGGCGGCAGAAGCAGCTGGTGGGAAATACAGAAGCACAGTC AGCAAAAGCAAAGACCCTCGGGGCTGCTCATCTCTGTGATCAGGACTCTGTCTACTA GTGACGATGTCGAAGACAGGGAATGAAAAGGGTCGCCTTGAAGAAGCCTACGAGAA ATGTGACCGTGACCTGGATGAATTGATTGTACAGCACTACACAGAATTGACGACAGCC ATTGCGACATACCAGAGCATCACAGAGCGCATCACTAACTCCCGAAATAAAATAAAGC AGGTAAAGAGAACCTGCTTTCATGCAAGATGCTGCTGCACTGCAACCGGGATGAGCT TCGGAACCTGTGGATTGAAGGAATTGAGCATAAGCATGCTGAACTGTGTGGATGAA ATTGAGAAATATCAAGCAAGTGCCCTCAAAGCTGGAACAGTGCTGCGCCAGCAAGCACT ATCTCAGTGCCACTGACATGTTGGTGTGAGCAGTTGAGTCTTTGGAGGGCCCCCTGCT CCAGGTGGAAGGACTGAGTGACCTTCGACTAGAGCTTCACAGCAAGAAGATGAACCTT CACTTGGTTCTCATAGATGAATACACCGGCACCTGTACATCAAATCGACTAGCCGAG TTGTGCAGCGTAACAAGGAAAAAGGAAAAATCAGCTCCCTCGTGAAAGATGCTTCTGT TCCTCTGATTGATGTTACAAACCTCCCTACTCCTCGAAAATTCCTTGATACCTCTCAC TATTCTACTGTGGAAGCTCAAGTGTGAGGAGATAAATCTGCAGGACATCAAGGAAG ATTAGAAATGGATCCAGAGAAAACAGCACCTGTTTATGGGTATCCTCATTAAGGG CTTGGCGAAACTGAAGAAGATCCCAAGAACAGTTAAGGCAATCATAGACGCTTGGAG CAGGAGTTGAAGCAATTTGTAAGAGGTCTACAACCCAGGTGGCAGACAGTGGCTATC AGCGGGGGGAGAACGTTACTGTGGAGAACCAACCAAGTTGCTTCTAGAACTGCTGGA GTTACTGTTTGACAAGTTTAAATGCTGTAGCCGCTGCACACTCTGTGGTCTCTGGGATAC CTGCAGGACACTGTAGTGACTCCACTGACTCAGCAGGAAGATACAACTGTATGATA TGGCAGATGTATGGGTGAAGATCCAAGATGTTCTACAGATGCTATTAACTGAGTACTT GGATATGAAAAATACTCGTACGGCCTCTGAACCATCAGCTCAACTAAGCTATGCCAGC ACTGGACGAGAGTTTGACGCTTTTGTGCAAGAAGAAACCTCAAAGGCCAAAAATTT CTCTTTTCAAGTTCGAATCGTCTCCCATGCCATCAGTATGAGCGCCTATCTGCGAGA ACAGAGAAGGGAGCTCTATAGTCGAGTGGAGAACTGCAAGGGGGTCTGTAGACAAC TTAATTGAAGGTGGAGGAACAAAATTTGTCTGCAAACTGGAGCCAGAAACATTACCG TCATATTCACCCATTACTAAGATTATTACAGGAGATTGAGCATGCTCTGGGTCTTGG CCAGCCAAACAGTGTCTCTTTCGAGAGTTTCTCACCGTGTACATCAAAAACATCTTT CTCAATCAAGTCTTGCTGAGATCAACAAGGAGATTGAAGGAGTCACTAAAACATCTG	

	ACCCTTTGAAGATTCTGGCCAACGCAGACACCATGAAGGTGCTGGGAGTGCAGCGGCC TCTCCTACAGAGCAATCATTGTGGAGAAGACAGTTCAAGACCTCTGAACCTGATG CATGACTTGAGTGCATATTAGATCAATTCTCAACATGGTGTGGGTGAAGCTCCAGG AGTACAAGGACACCTGCACTGCAGCTTACAGGGGTATTGTCCAGTCAGAGAAAACT TGTATCAGTGCATCCTGGGCAAAAGATGATGATATCAGCAGACTCTTGAAATCTCTA CCAAACTGGATGAATATGGCTCAACCCAAACAGCTGAGGCCAAAAGAGAGGAGGAAG AAGATTTTATAAGGCGAGCTTTTGGCAAGGAGTCTGAAGTTCTTATTGGGAACCTGGG TGATAAATTAATCCCTCCACAAGACATCCTTCGTGACGTGAGTCAAGCCTCAAAGCCTTG GCCAACATGCATGAAGCCTGGAATGGTTGGCAAGTCAACAAAGTCAGCTTTCTCCA ATCTTTCTACATCCAGATGCTTTCTCTGCTCAAGACAGCCACGAAACACGGATCT CCCCCAGTGTGAGCAGATCATGCAGACTCTCAGTGAACCTGCCAAATCGTTCCAG GATATGGCTGACCGCTGCTTGCTTGTCTTACATCTGGAAGTGAGGGTCTACTGTTTCC ACTATCTTATCCCTTTGCAAGGAGGGGAACATATGCCATGTGGCTAATGTGGAAG TATGGATTATGACCCCTGGTGGTCAAGCTCAACAAAGATATCAGCGCATTTGAAGAG GCCATGAGCGCCAGCCTTCAGCAGCAAGTCCAGTATATCTTGAAGGCCTGGGCC ACCTGATCTCTGCATCCTCATTAAATGGTGGCCAGTACTTCAGGCGCATCAGTGAGTC TGGCATCAAGAAAATGTGTAGGAACATTTTGTCTTCAGCAGAAATTTGACCAACATC ACCATGTGCGGGAGGCAGACCTGGACTTTGCAAGGCAGTACTACGAGATGCTTTACA ACACAGCTGACGAGCTCTGAACCTGGTGGTGGACAGGGTGTGAAGTACACGAGCT GGAGTACATCCAGCTCTGACCTGCTGCACCGCAGCCAGACTGGGGTGGGGGAAGT ACCACCCAGAACACGAGCTGAGAGGAGGCTCAAAGAGATCATCTGCGAGCAGGCTGC CATCAAGCAAGCCCAAGGACAAGAAGATAA <u>ACTACCGTTTAGCAGGGCGTACTGCGG</u> <u>TTGGTGACGGGGTCCCTCAGTCACACTCACTTTTTC</u>		
	ORF Start: ATG at 75 ORF Stop: TAA at 2988		
	SEQ ID NO: 160	971 aa	MW at 109984.9kD
NOV53a, CG59553-01 Protein Sequence	MAAEAAGGKYRSTVSKSDPSGLLISVIRTLSTSDVDRENEKRLEEAYEKCDRL DELIVQHYTELTTAIRTYQSITERITNSRNKIKQVKENLLSCKMLLHCKRDELRLKI EGIEHKHVLNLLDEIENIKQVPQKLEQCMASKHYLSATDMLVSAVESLEGPLQVEGL SDLRLLEHLSKMMNLHLVLIDELHRHLYIKSTSRVQRNKEKGKISSLVKDASVPLIDV TNLPTPRKFLDTSYSTAGSSSVREINLQDIKEDLELDPEENSTLFMGILIKGLAKLK KIPETVKAIIERLEQELKQIVKRSTQVADSGYQRGENVTVENPRLLLELLELFDK FNAVAAAHSVVLGVLQDTVVTPLTQQEDIKLYDMADVVKIQDVLQMLLLEYLDMKNT RTASEPSAQLSYASTGREFAAFFAKKKQRPKNLSLKFESSSHAISMSAYLRQRREL YSRSGELQGGPDDNLEGGGTFKVPCKPGARNITVIFHPLLRFIQIEHALGLGPAKQC PLREFLTIVYIKNIFLNQVLAIEINKETEGVTKTSPLKILANADTMKVLGVQRPLQST IIVEKTVQDLLNLMHDLAYSQDQFLNMVCVKLQEKDTCTAAYRGIVQSEKLVISAS WAKDDDISRLKSLPNWMMNAQPKQLRPKREEEDFIRAFGKESEVLIGNLGDKLIP PQDILRDVSDLKALANMHESLEWLASRTKSAFNSNLSTSQMLSPAQDSHTNTDLPVSE QIMQTLSELAKSFQDMADRCLLVLHLEVRVHCFHYLIPLAKEGNYAIVANVESMDYDP LVVKNLKDISAIEAMSASLQHKFYIFEGLGHLISCILINGAQYFRRISESGIKKM CRNIFVLQQLNTNITMSREADLDFARQYYEMLYNTADELLNLVVDQGVKYTELEYIHA LTLHRSQTGVGELTTQNTSCRGGSKRSSASRLPSSKPPRTR		

Further analysis of the NOV53a protein yielded the following properties shown in Table 53B.

Table 53B. Protein Sequence Properties NOV53a	
PSort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.1900 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV53a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 53C.

Table 53C. Geneseq Results for NOV53a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV53a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB93175	Human protein sequence SEQ ID NO:12114 - Homo sapiens, 974 aa. [EP1074617-A2, 07-FEB-2001]	1..947 1..947	947/947 (100%) 947/947 (100%)	0.0
AAW69801	Amino acid sequence of rsec8, a protein present in SA-17S complex - Rattus sp, 975 aa. [WO9828419-A2, 02-JUL-1998]	1..947 1..948	902/948 (95%) 925/948 (97%)	0.0
AAB95143	Human protein sequence SEQ ID NO:17163 - Homo sapiens, 572 aa. [EP1074617-A2, 07-FEB-2001]	403..947 1..545	545/545 (100%) 545/545 (100%)	0.0
AAB58175	Lung cancer associated polypeptide sequence SEQ ID 513 - Homo sapiens, 418 aa. [WO200055180-A2, 21-SEP-2000]	571..947 15..391	369/377 (97%) 369/377 (97%)	0.0
AAG00950	Human secreted protein, SEQ ID NO: 5031 - Homo sapiens, 100 aa. [EP1033401-A2, 06-SEP-2000]	451..544 7..100	76/94 (80%) 79/94 (83%)	3e-36

In a BLAST search of public sequence databases, the NOV53a protein was found to have homology to the proteins shown in the BLASTP data in Table 53D.

Table 53D. Public BLASTP Results for NOV53a				
Protein Accession Number	Protein/Organism/Length	NOV53a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96A65	CDNA FLJ14782 FIS, CLONE NT2RP4000524, HIGHLY SIMILAR TO MUS MUSCULUS SEC8 MRNA (SECRETORY PROTEIN SEC8) - Homo sapiens (Human), 974 aa.	1..947 1..947	947/947 (100%) 947/947 (100%)	0.0
Q9C0G4	KIAA1699 PROTEIN - Homo sapiens (Human), 966 aa (fragment).	9..947 1..939	939/939 (100%) 939/939 (100%)	0.0
O35382	SEC8 - Mus musculus (Mouse), 971 aa.	1..971 1..971	923/972 (94%) 946/972 (96%)	0.0
Q62824	RSEC8 - Rattus norvegicus (Rat), 975 aa (fragment).	1..947 1..948	902/948 (95%) 925/948 (97%)	0.0

Q9P102	REC8 - Homo sapiens (Human), 637 aa (fragment).	339..947 2..610	609/609 (100%) 609/609 (100%)	0.0
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Pfam analysis predicts that the NOV53a protein contains the domains shown in the Table 53E.

Table 53E. Domain Analysis of NOV53a			
Pfam Domain	NOV53a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 54.

The NOV54 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 54A.

Table 54A. NOV54 Sequence Analysis			
	SEQ ID NO: 161	501 bp	
NOV54a, CG59545-01 DNA Sequence	CAACACGAGGAACAATGTCTTCTTTACCCGTGCCATACAACTGCCTGTGTCTTTGTG TGTTGGTTCCTGCGTGATAATCAAAGGGACACTGATCGACTCTTCTATCAACGAACCA CAGCTGCAGGTGGATTTCTACACTGAGATGAATGAGGACTCAGAAATTGCCTTCCATT TGCGAGTGCACTTAGGCCGTGCTGTGGTCATGAACAGTCGTGAGTTTGGGATATGGAT GTTGGAGGAGAATTTACACTATGTGCCCTTTGAGGATGGCAAACCATTTGACTTGCGC ATCTACGTGTGTCTCAATGAGTATGAGGTAAGGTAAATGGTGAATACATTTATGCCCT TTGTCCATCGAATCCGCCCATCATATGTGAAGATGATTCAAGTGTGGAGAGATGTCTC CCTGGACTCAGTGCTTGTCAACAATGGACGGAGATGATCACACTCCTCATTGTTGAGG AAACCTCTTTCTACCTGACCATGGGATTCTTAGAGC		
	ORF Start: ATG at 15	ORF Stop: TGA at 441	
	SEQ ID NO: 162	142 aa	MW at 16511.9kD
NOV54a, CG59545-01 Protein Sequence	MSSLVPYKLPVSLSVGSCVILKGTLLDSSINPQLQVDFYTEMNEDSEIAFHLRVHL GRRVVMNSREFGIWMLEENLHYVPFEDGKPFDLRIYVCLNEYEVKVNVEYIYAFVHRI PPSYVKMIQVWRDVSLSVLVNNRR		

Further analysis of the NOV54a protein yielded the following properties shown in Table 54B.

Table 54B. Protein Sequence Properties NOV54a	
PSort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.1900 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV54a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 54C.

Table 54C. Geneseq Results for NOV54a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV54a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG66741	Human Charcot-Leyden crystal protein 5A (CLC5A) - Homo sapiens, 142 aa. [CN1302875-A, 11-JUL-2001]	1..142 1..142	139/142 (97%) 139/142 (97%)	2e-77
AAG66742	Human Charcot-Leyden crystal protein 5B (CLC5B) - Homo sapiens, 170 aa. [CN1302875-A, 11-JUL-2001]	6..142 34..170	136/137 (99%) 136/137 (99%)	3e-76
AAM79041	Human protein SEQ ID NO 1703 - Homo sapiens, 139 aa. [WO200157190-A2, 09-AUG-2001]	1..139 1..139	107/139 (76%) 116/139 (82%)	2e-56
AAY28350	Full Placental Protein 13 amino acid sequence - Homo sapiens, 139 aa. [WO9938970-A1, 05-AUG-1999]	1..139 1..139	107/139 (76%) 116/139 (82%)	2e-56
AAG78627	Human Charcot-Leyden crystal 4 CLC4 protein #2 - Homo sapiens, 167 aa. [CN1302876-A, 11-JUL-2001]	6..139 34..167	102/134 (76%) 111/134 (82%)	2e-53

In a BLAST search of public sequence databases, the NOV54a protein was found to have homology to the proteins shown in the BLASTP data in Table 54D.

Table 54D. Public BLASTP Results for NOV54a				
Protein Accession Number	Protein/Organism/Length	NOV54a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UHV8	PLACENTAL PROTEIN 13 (PLACENTA PROTEIN 13) - Homo sapiens (Human), 139 aa.	1..139 1..139	107/139 (76%) 116/139 (82%)	9e-56
Q9NR03				9e-45

	PROTEIN - Homo sapiens (Human), 139 aa.	1..139	107/139 (76%)	
A46523	Charcot-Leyden crystal protein - human, 142 aa.	1..142 1..142	76/142 (53%) 96/142 (67%)	7e-36
Q05315	Eosinophil lysophospholipase (EC 3.1.1.5) (Charcot-Leyden crystal protein) (Lysolecithin acylhydrolase) (CLC) (Galactin-10) - Homo sapiens (Human), 141 aa.	2..142 1..141	75/141 (53%) 95/141 (67%)	3e-35
Q96KD6	PLACENTAL PROTEIN 13-LIKE - Homo sapiens (Human), 104 aa (fragment).	1..104 1..104	66/104 (63%) 79/104 (75%)	1e-31

Pfam analysis predicts that the NOV54a protein contains the domains shown in the Table 54E.

Table 54E. Domain Analysis of NOV54a			
Pfam Domain	NOV54a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Gal-bind_lectin: domain 1 of 1	5..137	37/142 (26%) 106/142 (75%)	3.1e-28

Example 55.

The NOV55 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 55A.

Table 55A. NOV55 Sequence Analysis		
	SEQ ID NO: 163	2071 bp
NOV55a, CG59435-01 DNA Sequence	AAACTATTGTAGGCGCAGTCATGCAGGAAAACCTCAGATTGTGCTTCATCAGGAGATG ATATTTAAATATGGGATGCTTCATCTATGACATTGGTGGATAAATTCAACCCACACAC ATCACCACATGGAATCAGCTCAATATGTTGGAGCAGCAATAGTAACCTTTTAGTAACA GCATCTTCCAGTGGCGACAAAATAGTTGTCTCAAGTTGCAAAATGTAACCTGTTCCAC TTTGTAGAGCTTGCTGAAGGCAAAAGCAGACATGTGTCAATTAAATTTACATCTAT GTATTTGGTAAGCGGAGGCCTAAATAACACTGTAAATATTTGGGATTTAAATCAAAA AGAGTTCATCGATCTCTTAAGGATCATAAAGATCAAGTAACCTGTGTAAACATACAATT GGAATGATTGCTACATTGCTTCTGGATCTCTTAGTGGTGAAATTATTTTACACAGTGT AACCCTAAATTTATCTAGTACTCCTTTTGGCCATGGTAGTAACCAAGTTCCGGCACTTG AAGTACTCCTTGTTTAAGAAATCACTACTGGGCAGTGTTCGGATAATGGAATAGTAA CTCTCTGGGATGAAATAGTCAGAGTCCATACCATAACTTTGACAGTGTAACAACAGC TCCAGCGTCAGGCATCTGTTTTCTCCTGTCAATGAATTGCTCTTTGTAACCATAGGC TTGGATAAAAGAATCATCCTCTATGACACTTCAAGTAAGAAGCTAGTGAAACCTTAG TGGCTGACACTCCTCTAACTGCGGTAGATTTTCATGCCTGATGGAGCCACTTTGGCTAT TGGATCTTCCCGGGGAAAATATATCAATATGATTTAAGAAATGTTGAAATCACCAGTT AAGACCATCAGTGTCTACAAGACATCTGTGCAGTGTATAGCATTTCAGTACTCCAAGT TTCTTACTAAGTCAAGTTTAAATAAAGGCTGTTCAAATAAGCCACAAACAGTGAACAA ACGAAGTGTTAATGTGAATGCTGCTAGTGGAGGAGTTGAGAAATCCGGAATGTGAGA GAAGCACCTGCCAGTCCATTGCCACAGTTCTACCACAACCTATGACATCAGCTATGG GGAAAGGAACAGTTGCTGTTCAAGAAAAAGCAGGTTTGCCTCGAAGCATAAACACAGA CACTTTATCTAAGGAACAGACAGTGGAAAAATCAGGATTTCTCCAGCTTTGATGAT	

	ACTGGGAAAAGTAGTTTAGGTGACATGTTCTCACCTATCAGAGATGATGCTGTAGTTA ACAAGGGAAGTGATGAGTCCATAGGCAAAGGAGATGGCTTTGACTTTCTACCCGAGTT GAACCTCAGTGTTCCTCCAAGAAAAAATCCAGTAACCTTCAAGTACTTCAGTATTGCAT TCTAGTCTCTTAATGTTTTATGGGATCTCCAGGGAAGAGGAAAAATGAAACCGTG ATCTAACAGCTGAGTCTAAGAAAAATATATATGGGAAAAACAGGAATCTAAAGACTCCTT CAAAACAGTTAGCAAAGTTGGTCACATCTGGTGTGAAAGTGGAATCTAAATACCTCT CCATCATCTAACCAAAACAAGAAATTTCTGAGAAATTTGAAAAGCCAGAGAAATGAAATTG AAGCCCAAGTTGATATGTGAACCCCAATCAATGGATCCTCAACTCCAAATCCAAAGAT AGCATCTTCTGTCACTGCTGGAGTTGCCAGTTCACTCTCAGAAAAAATAGCCGACAGC ATTGGAATAAACCGGCAAAATGCACCATTGACTTCCATTCAAATTCGTTTTATTTCAGA ACATGATACAGGAAACGTTGGATGACTTTAGAGAAGCATGCCATAGGGACATTGTGAA TTTGCAAGTGGAGATGATTAACAGTTTTCATATGCAACTGAATGAAATGCATTCTTTG CTGGAAAGATACTCAGTGAATGAAGGTTTAGTGGCTGAAATTTGAAAGACTACGAGAAG AAAACAAAAGATTACGGGCCCACTTTTGAAATTTCAAGTGAATACCTTAATGTTCTGTA ATTTGGGAAGTTTCTGGCAACACAGAACTACATAGAATCAT		
	ORF Start: ATG at 22	ORF Stop: TGA at 1999	
	SEQ ID NO: 164	659 aa	MW at 71851.2kD
NOV55a, CG59435-01 Protein Sequence	MQENLRFASSGDDIKIWDASSMTLVDFKNPHTSPHGISSICWSSNSNFLTASSSGDK IVVSSCKCKPVPLLELAEGQKQTCVNLNSTSMYLVSGGLNNTVNIWDLKSKRVHRSLK DHKDQVTCVTYNWDCYIASGSLSGEIIILHSVTTNLSSTPFGHGSNQVRHLKYSLFKK SLGVSVDNGIVTLWDVNSQSPYHNFDSVHKAPASGICFSPVNELEFVTIGLDKRIIL YDTSSKKLVKTLVADTPLTAVDFMPDGATLAIGSSRGKIYQYDLRLMKSPVKTISAHK TSVQCIAPQYSTVLTKSSLNKGCSNKPVTVNKRSVNVNAASGGVQNSGIVREAPATSI ATVLPQPMTSAMGKGTVAVQEKAGLPRSINTDTLSKETDSGNKQDFSSFDOTGKSSLD DMFSPIRDDAVVNKGSDESIGKGDGDFLPLQLNSVFPFRKNPVTSSSVLHSSPLNVF MGSPGKEENENRDLTAESKKIYMGKQESKDSFKQLAKLVTSGAESGNLNTSPSSNQTR NSEKFEKPENIEAQLICEPPINGSSTPNPKIASSVTAGVASSLSEKIADSIGNNRQN APLTSIQIRFIQNMIQETLDDFREACHRDIVNLQVEMIKQFHMQLNEMHSLLEYSVN EGLVAETIERLREENKRLRAHF		
	SEQ ID NO: 165	2009 bp	
NOV55b, CG59435-02 DNA Sequence	AAACATTTTGTAGGCGCAGTCATGCAGGAAAACCTCAGATTTGCTTCATCAGGAGATG ATATTAAAAATATGGGATGCTTCATCTATGACATTGGTGATAAAATCAACCCACACAC ATCACCACATGGAATCAGCTCAATATGTTGGAGCAGCAATAATAACTTTTTAGTAACA GCATCTTCCAGTGGCGACAAAATAGTTGTCTCAAGTTGCAAAATGTAAACCTGTTCCAC TTTTAGAGCTTGCTGAAGGGCAAAAGCAGACATGTGTCAATTTAAATTTCTACATCTAT GTATTTGGTAAGCGGAGGCCCTAAATAACACTGTTAATATTGGGATTTAAATCAAAA AGAGTTCATCGATCTCTTAAGGATCATAAAGATCAAGTAACTTGTGTAACATACAATT GGAATGATTGCTACATTGCTTCTGGATCTCTTAGTGGTGAATTTATTTACACAGTGT AACCACTAATTTATCTAGTACTCCTTTTGGCCATGGTAGTAACCACTGTTTCCGGCAC TTGAAGTACTCCTTGTTTAAAGAAATCACTACTGGGCAGTGTTCGGATAATGGAATAG TAACTCTCTGGGATGTAAATAGTCAGAGTCCATACCATAACTTTGACAGTGTACACAA AGCTCCAGCGTCAGGCATCTGTTTTTCTCCTGTCAATGAATTGCTCTTTGTAACCATA GGCTTGGATAAAAGAATCATCCTCTATGACACTTCAAGTAAGAAGCTAGTGAAGAACTT TAGTGGCTGACACTCCTCTAACTGCGGTAGATTTTCATGCCGTGATGGAGCCACTTTGGC TATTGGATCTTCCCGGGGAAAAATATATCAATATGATTTAAGAAATGTTGAAATCACCA GTTAAGACCATCAGTGCTCACAAGACATCTGTGCAGTGTATAGCATTTTCAGTACTCCA CTGTTCTTACTAAGTCAAGTTTAAATAAAGGCTGTTCAAATAAGCCCAACACAGTGAA CAAACGAAGTGTTAATGTGAATGCTGCTAGTGGAGGAGTTCAGAAATTCGGGAATTGTC AGAGAAGCACCTGCCACGTCCTATTGCCACAGTTCTACCACAACCTATGACATCAGCTA TGGGGAAGGAACAGTTGCTGTTCAAGAAAAAGCAGGTTTGCCCTCGAAGCATAAACAC AGACACTTTATCTAAGGAAACAGACAGTGGAAAAAATCAGGATTTCTCCAGCTTTGAT GATACTGGGAAAAGTAGTTTAGGTGACATGTTCTCACCTATCAGAGATGATGCTGTAG TTAACAAGGGAAGTGATGAGTCCATAGGCAAAGGAGATGGCTTTGACTTTCTACCGCA GTTGAACTCAGTGTTCCTCCAAGAAAAAATCCAGTAACCTCAAGTACTTCAGTATTG CATTCTAGTCTCTTTAATGTTTTTATGGGATCTCCAGGGAAGAGGAAAAATGAAACC GTGATCTAACAGCTGAGTCTAAGAAAAATATATATGGGAAAAACAGGAATCTAAAGACTC CTTCAAACAGTTAGCAAAGTTGGTCACATCTGGTGTGAAAGTGGAATCTAAATACC TCTCCATCATCTAACCAAAACAAGAAATTTCTGAGAAATTTGAAAAGCCAGAGAATGAAA TTGAAGCCCAAGTTGATATGTGAACCCCAATCAATGGATCCTCAACTCCAAATCCAAA GATAGCATCTTCTGTCACTGCTGGAGTTGCCAGTTCACTCTCAGAAAAAATAGCCGAC AGCATTTGAAATAACCGGCAAAATGCACCATTGACTTCCATTCAAATTCGTTTTATTTC AGAACATGATACAGGAAACGTTGGATGACTTTAGAGAAGCATGCCATAGGGACATTGT GAATTTGCAAGTGGAGATGATTAAACAGTTTCATATGCAACTGAAATGAAATGCATTCT TTGCTGGAAGATACTCAGTGAATGAAGGTTTAGTGGCTGAAATTTGAAAGACTACGAG AAGAAAACAAAAGATTACGGGCCCACTTTTGAAATTT		
	ORF Start: ATG at 22	ORF Stop: TGA at 2002	
	SEQ ID NO: 166	660 aa	MW at 71965.3kD
NOV55b, CG59435-02 Protein Sequence	MQENLRFASSGDDIKIWDASSMTLVDFKNPHTSPHGISSICWSSNNNFLTASSSGDK IVVSSCKCKPVPLLELAEGQKQTCVNLNSTSMYLVSGGLNNTVNIWDLKSKRVHRSLK DHKDQVTCVTYNWDCYIASGSLSGEIIILHSVTTNLSSTPFGHGSNQSVRHLKYSLFK		

	KSLGVSVDNGIVTLWDVNSQSPYHNFDSVHKAPASGICFSPVNELLFVTIGLDKRII LYDTSSKKLVKTLVADTPLTAVDFMPDGATLAIGSSRGKIYQYDLRMLKSPVKTI SAH KTSVQCIAFQYSTVLTKSSLNKGCSNKPTTVNKRSVNVNAASGGVQNSGIVREAPATS IATVLPQPMTSAMGKGTAVQEKAGLPRSINTDTLSKETDSGKNQDFSSFDDTGKSSL GDMFSPIRDDAVVNKGSDSIGKGDGDFLPQLNSVFPFRKNPVTSTSVLHSSPLNV FMGSPGKEENENRDLTAESKKIYMGKQESKDSFKQLAKLVTSGAESGNLNTSPSSNQ RNSEKFEKPENEIEAQLICEPPINGSSTPNPKIASSVTAGVASSLSEKIADSIGNNRQ NAPLTSIQIRFIQNMIQETLDDFREACHRDIVNLQVEMIKQFHMQLNEMHSLLEYSV NEGLVAEIERLREENKRLRAHF
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Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 55B.

Table 55B. Comparison of NOV55a against NOV55b.		
Protein Sequence	NOV55a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV55b	1..659	658/660 (99%)
	1..660	659/660 (99%)

Further analysis of the NOV55a protein yielded the following properties shown in Table 55C.

Table 55C. Protein Sequence Properties NOV55a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV55a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 55D.

Table 55D. Geneseq Results for NOV55a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV55a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG74568	Human colon cancer antigen protein SEQ ID NO:5332 - Homo sapiens, 404 aa. [WO200122920-A2, 05-APR-2001]	256..659 1..404	399/404 (98%) 399/404 (98%)	0.0
AAE10677				4e-75

	Homo sapiens, 208 aa. [WO200172955-A2, 04-OCT-2001]	2..159	149/159 (93%)	
AAM70774	Human bone marrow expressed probe encoded protein SEQ ID NO: 31080 - Homo sapiens, 67 aa. [WO200157276-A2, 09-AUG-2001]	240..306 1..67	67/67 (100%) 67/67 (100%)	9e-31
AAM06190	Peptide #4872 encoded by probe for measuring breast gene expression - Homo sapiens, 67 aa. [WO200157270-A2, 09-AUG-2001]	240..306 1..67	67/67 (100%) 67/67 (100%)	9e-31
ABB23122	Protein #5121 encoded by probe for measuring heart cell gene expression - Homo sapiens, 65 aa. [WO200157274-A2, 09-AUG-2001]	307..371 1..65	65/65 (100%) 65/65 (100%)	3e-29

In a BLAST search of public sequence databases, the NOV55a protein was found to have homology to the proteins shown in the BLASTP data in Table 55E.

Table 55E. Public BLASTP Results for NOV55a				
Protein Accession Number	Protein/Organism/Length	NOV55a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
I60167	regulatory protein Nedd1 - mouse, 660 aa.	1..659 1..660	564/660 (85%) 607/660 (91%)	0.0
P33215	NEDD1 protein - Mus musculus (Mouse), 675 aa (fragment).	1..659 16..675	564/660 (85%) 607/660 (91%)	0.0
Q9CWK2	NEURAL PRECURSOR CELL EXPRESSED, DEVELOPMENTALLY DOWN-REGULATED GENE 1 - Mus musculus (Mouse), 660 aa.	1..659 1..660	563/660 (85%) 606/660 (91%)	0.0
Q9FI89	SIMILARITY TO REGULATORY PROTEIN NEDD1 - Arabidopsis thaliana (Mouse-ear cress), 787 aa.	8..533 15..532	145/550 (26%) 246/550 (44%)	4e-40
BAB75165	WD-40 REPEAT PROTEIN - Anabaena sp. (strain PCC 7120), 1526 aa.	2..298 916..1208	92/307 (29%) 147/307 (46%)	2e-18

PFam analysis predicts that the NOV55a protein contains the domains shown in the Table 55F.

Table 55F. Domain Analysis of NOV55a			
Pfam Domain	NOV55a Match Region	Identities/ Similarities for the Matched Region	Expect Value
WD40: domain 1 of 7	28..61	6/37 (16%) 27/37 (73%)	57
WD40: domain 2 of 7	70..105	10/37 (27%) 27/37 (73%)	0.062
WD40: domain 3 of 7	111..147	9/37 (24%) 28/37 (76%)	20
WD40: domain 4 of 7	153..190	10/38 (26%) 29/38 (76%)	3.4
WD40: domain 5 of 7	197..234	7/38 (18%) 25/38 (66%)	19
WD40: domain 6 of 7	240..275	14/37 (38%) 28/37 (76%)	3.1
WD40: domain 7 of 7	282..316	8/37 (22%) 26/37 (70%)	1.3e+03

Example 56.

The NOV56 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 56A.

Table 56A. NOV56 Sequence Analysis		
	SEQ ID NO: 167	1771 bp
NOV56a, CG59439-01 DNA Sequence	GACTGTTTCACCATGCAGTGGCTAATGAGGTTCCGGACCCTCTGGGGCATCCACAAAT CCTTCCACAACATCCACCCTGCCCTTCACAGCTGCGCTGCCGGTCTTTATCAGAATT TGGAGCCCCAAGATGGAATGACTATGAAGTACCGGAGGAATTTAACTTTGCAAGTTAT GTACTGGACTACTGGGCTCAAAAGGAGAAGGAGGGCAAGAGAGGTCCTAAATCCAGCTT TTTGGTGGGTGAATGGCCAAAGGGATGAAGTAAAGTGGAGCTTCAGAGAGATGGGAGA CCTAACC CGCGTGTAGCCAACGTCTTCACACAGACCTGTGGCCTACAACAGGGAGAC CATCTGGCCTTGATGCTGCCTCGAGTTCCTGAGTGGTGGCTGGTGGCTGGGGCTGCA TGCGAACAGGGATCATCTTCATTCTGCGACCATCCTGTTGAAGGCCAAAGACATTCT CTATCGACTACAGTTGTCTAAAGCCAAGGGCATGTGACCATAGATGCCCTTGCCCTCA GAGGTGGACTCCATAGCTTCTCAGTGCCCTCTCTGAAAACCAAGCTCCTGGTGTCTG ATCACAGCCGTGAAGGGTGGCTGGACTTCCGATCGCTGGTTAAATCAGCATCCCCAGA ACACACCTGTGTTAAGTCAAAGACCTTGGACCCAATGGTCATCTTCTCACCAGTGGG ACCACAGGCTTCCCCAAGATGGCAAAACACTCCCATGGGTGGCCTTACAACCCCTCCT TCCCAGGAAGTAGGAAATTACGGAGCCTGAAGACATCTGATGTCTCCTGGTGCCTGTC GGACTCAGGATGGATTGTGGCTACCAATTGGACCCCTGGTGAACCATGGACAGCGGGT TGACAGTCTTTATCCACCATCTGCCACAGTTTGACACCAAGGTATCATACAGACAT TGTTGAAATACCCCATTAACCACTTTTGGGGGGTATCATCTATATATCGAATGATTCT GCAGCAGGATTTACACAGCATCAGGTTCCCTGCCCTGGAGCACTGCTATATCTAGCGGG GAGGTGCTGTGCCCCAAGGATCAGGAGGAGTGAAAAGACGGACGGGCCTTCTGCTCT ACGAGAACTATGGGCAGTCGGAACGGGACTAATTTGTGCCACCTACTGGGGAATGAA GATCAAGCCGGGTTTCATGGGGAAGGCCACTCCACCCTACGACGTCAGGTCATTGAT GACAAGGGCAGCATCCTGCCACCTAACACAGAAGGAAACATTGGCATCAGAATCAAAC CTGTCAGGCCTGTGAGCCTTTCATGTGCTATGAGGGTGACCCAGAGAAGACAGCTAA AGTGGAAATGTGGGACTTCTACAACACTGGGGACAGAGGTAAAGATGGATGAAGAGGG TACATTTGTTTCTGGGGAGGAGTGATGACATCATTAAATGCCTCTGGGTATCGCATCG GGCTGCGAGAGGTGAAGCGCTTTGGTGGAGCACCCAGCGGTGGCGGAGTCAGCCGT GGTGGGCAGCCAGACCCGATTTCGAGGGGAGGTGGTGAAGGCCTTTATTGTCCTGACC	

	CCACAGTTCCTGTCCTATGACAAGGATCAGCTGACCAAGGAAGTGCAGCAGCATGTCA AGTCAGTGACAGCCCCATACAAGTACCCAAGGAAGGTGGAGTTTGTCTCAGAGCTGCC AAAAACCATCACTGGCAAGATTGAACGGAAGGAAGTTCGGAAGAAAGGAGACTGGTCAG ATGTAATCGGCAGTGAAGTCAAGACGCACTG		
	ORF Start: ATG at 13	ORF Stop: TAA at 1744	
	SEQ ID NO: 168	577 aa	MW at 65272.6kD
NOV56a, CG59439-01 Protein Sequence	MQWLMRFRTLWGIHKSFHNHPAPSQLRCRSLSEFGAPRWNDYEVPEEFNFASYVLDY WAQKEKEGKRGPNPAFWVWNGQGDEVKWSFREMGDLTRRVANVFTQTCCGLQQGDHLAL MLPRVPEWWLVAVGCMRTGIIIFIPATILLKAKDILYRLQLSKAKGIVTIDALASEVDS IASQCPSLTKLLVSDHSREGWLDFRSLVKSASPEHTCVKSKTLDPMVIFFTSGTTGF PKMAKSHSHGLALQPSFPGSRKRLSLKTSVSWCLSDSGWIVATIWTLPVPTAGCTVF IHHLPPQFDTKVI IQTLKYPINHFVWGVSSIYRMILQQDFTSIRFPALEHCHYTGGEVVL PKDQBEWKRRRTGLLLYENYQSQSETGLICATYWGMKIKPGFMGKATPPYDVQVIDDKGS ILPNTTEGNIGIRIKPVRPVSLFMCYEGDPEKTAKECGDFYNTGDRGKMDDEGYICF LGRSDDIINASGYRIGPAEVESALVEHPAESA VVGSPPDIRGEVVKAFIVLTPQFL SHDKDQLTKELQQHVKSVTAPYKYPRKVEFVSELPKTITGKIERKELRKKETGQM		
	SEQ ID NO: 169	1659 bp	
NOV56b, CG59439-02 DNA Sequence	GTTTCACCATGCAGTGGCTAATGAGGTTCCGGACCCTCTGGGGCATCCACAAATCCTT CCACAAATCCACCTGCCCTTTCACAGCTGCGCTGCCGGTCTTTATCAGAATTTGGA GCCCCAAGATGGAATGACTATGAAGTACCGGAGGAATTTAACTTTGCAAGTTATGTAC TGGACTACTGGGCTCAAAGGAGAAGGAGGGCAAGAGAGGTCCAAATCCAGCTTTTGTG GTGGGTGAATGGCCAAGGGGATGAAGTAAAGTGGAGCTTCAGAGAGATGGGAGACCTA ACCCGCGGTGTAGCCAACGTCTTCACACAGACCTGTGGCCTACAAAGGAGAGACCATC TGGCCTTGATGCTGCCTCGAGTTCCTGAGTGGTGGCTGGTGGCTGTGGGCTGCATGCG AACAGGGATCATCTTCATTCTCGCGACCATCCTGTTGAAGGCCAAAGACATTCCTCTAT CGACTACAGTTGTCTAAAGCCAAGGGCATTGTGACCATAGATGCCCTTGCCCTCAGAGG TGGACTCCATAGCTTCTCAGTGGCCCTCTCTGAAAACCAAGCTCCTGGTGTCTGATCA CAGCCGTGAAGGGTGGCTGGACTTCCGATCGCTGGTTAAATCAGCATCCCCAGAACAC ACCTGTGTTAAGTCAAAGACCTTGGACCCAATGGTCATCTTCTCACCAGTGGGACCA CAGGCTTCCCCAAGATGGCAAAACACTCCCATGGGTGGCCTTACAACCTCTGCTTCCC AGGAAGTAGGAAATTACGGAGCCTGAAGACATCTGATGTCTCTCTGGTGCCTGTCCGAC TCAGGATGGATTGTGGCTACCATTTGGACCTGGTAGAACCATGGACAGCGGGTTGTA CAGTCTTTATCCACCATCTGCCACAGTTTGACACCAAGGTATCATACAGACATTGTT GAAATACCCCATTAACCACTTTTGGGGGTATCATCTATATATCGAATGATTCTGCAG CAGGATTTACACAGCATCAGGTTCCCTGCCCTGGAGCACTGCTATACTGGCGGGGAGG TCGTGTTGCCCAAGGATCAGGAGGAGTGGAAAAGACGGACGGGCCTTCTGCTCTACGA GAACTATGGGCAGTCGGAACGGGACTAATTTGTGCCACCTACTGGGGAATGAAGATC AAGCCGGGTTTCATGGGGAAGGCCACTCCACCTACGACGTCAGGGTGACCCAGAGA AGACAGCTAAAGTGAATGTGGGGACTTCTACAACACTGGGGACAGAGGAAAGATGGA TGAAGAGGGCTACATTTGTTTCTGGGGAGGAGTGATGACATCATTAATGCCTCTGGG TATCGCATCGGGCTGCAGAGGTTGAAAGTGCTTTGGTGGAGCACCAGCGGTGGCGG AGTCAGCCGTGGTGGGCAGCCAGACCCGATTTCGAGGGGAGGTGGTGAAGGCCTTTAT TGTCTGACCCACAGTTCCTGTCCCATGACAAGGATCAGTGCACCAAGGAAGTGTGCT CAGAGCTGCCAAAACCATCACTGGCAAGATTGAACGGAAGGAAGTTCGGAAGAAAGGA GACTGGTCAGATGTAATCGGCAGTGAAGTCAAGAAC		
	ORF Start: ATG at 9	ORF Stop: TAA at 1638	
	SEQ ID NO: 170	543 aa	MW at 61518.2kD
NOV56b, CG59439-02 Protein Sequence	MQWLMRFRTLWGIHKSFHNHPAPSQLRCRSLSEFGAPRWNDYEVPEEFNFASYVLDY WAQKEKEGKRGPNPAFWVWNGQGDEVKWSFREMGDLTRRVANVFTQTCCGLQQGDHLAL MLPRVPEWWLVAVGCMRTGIIIFIPATILLKAKDILYRLQLSKAKGIVTIDALASEVDS IASQCPSLTKLLVSDHSREGWLDFRSLVKSASPEHTCVKSKTLDPMVIFFTSGTTGF PKMAKSHSHGLALQPSFPGSRKRLSLKTSVSWCLSDSGWIVATIWTLPVPTAGCTVF IHHLPPQFDTKVI IQTLKYPINHFVWGVSSIYRMILQQDFTSIRFPALEHCHYTGGEVVL PKDQBEWKRRRTGLLLYENYQSQSETGLICATYWGMKIKPGFMGKATPPYDVQGDPEKTA KVECGDFYNTGDRGKMDDEGYICFLGRSDDIINASGYRIGPAEVESALVEHPAESA VVGSPPDIRGEVVKAFIVLTPQFLSHDKDQLTKELQQHVKSVTAPYKYPRKVEFVSEL PKTITGKIERKELRKKETGQM		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 56B.

Table 56B. Comparison of NOV56a against NOV56b.		
Protein Sequence	NOV56a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV56b	1..577	543/577 (94%)
	1..543	543/577 (94%)

Further analysis of the NOV56a protein yielded the following properties shown in Table 56C.

Table 56C. Protein Sequence Properties NOV56a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.4712 probability located in mitochondrial matrix space; 0.1737 probability located in mitochondrial inner membrane; 0.1737 probability located in mitochondrial intermembrane space
SignalP analysis:	Likely cleavage site between residues 23 and 24

A search of the NOV56a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 56D.

Table 56D. Geneseq Results for NOV56a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV56a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB43245	Human ORFX ORF3009 polypeptide sequence SEQ ID NO:6018 - Homo sapiens, 537 aa. [WO200058473-A2, 05-OCT-2000]	46..573 1..527	309/529 (58%) 402/529 (75%)	0.0
AAM80008	Human protein SEQ ID NO 3654 - Homo sapiens, 302 aa. [WO200157190-A2, 09-AUG-2001]	331..577 24..302	247/279 (88%) 247/279 (88%)	e-140
AAM80007	Human protein SEQ ID NO 3653 - Homo sapiens, 302 aa. [WO200157190-A2, 09-AUG-2001]	331..577 24..302	247/279 (88%) 247/279 (88%)	e-140
AAM41894	Human polypeptide SEQ ID NO 6825 - Homo sapiens, 390 aa. [WO200153312-A1, 26-JUL-2001]	257..573 7..323	193/317 (60%) 246/317 (76%)	e-116
AAM79024				e-112

	Homo sapiens, 196 aa. [WO200157190-A2, 09-AUG-2001]	1..196	196/196 (100%)	
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In a BLAST search of public sequence databases, the NOV56a protein was found to have homology to the proteins shown in the BLASTP data in Table 56E.

Table 56E. Public BLASTP Results for NOV56a				
Protein Accession Number	Protein/Organism/Length	NOV56a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96A20	MIDDLE-CHAIN ACYL-COA SYNTHETASE1 (MEDIUM-CHAIN ACYL-COA SYNTHETASE) - Homo sapiens (Human), 577 aa.	1..577 1..577	576/577 (99%) 576/577 (99%)	0.0
Q9TVB5	XENOBIOTIC/MEDIUM-CHAIN FATTY ACID:COA LIGASE FORM XL-III PRECURSOR - Bos taurus (Bovine), 577 aa.	1..576 1..576	439/576 (76%) 486/576 (84%)	0.0
Q9BEA2	LIPOATE-ACTIVATING ENZYME PRECURSOR - Bos taurus (Bovine), 577 aa.	1..576 1..576	438/576 (76%) 485/576 (84%)	0.0
Q91VA0	MEDIUM-CHAIN ACYL-COA SYNTHETASE (EC 6.2.1.2) (HYPOTHETICAL 64.8 KDA PROTEIN) - Mus musculus (Mouse), 573 aa.	1..577 1..573	406/577 (70%) 472/577 (81%)	0.0
O70490	KIDNEY-SPECIFIC PROTEIN - Rattus norvegicus (Rat), 572 aa.	1..573 1..567	315/580 (54%) 417/580 (71%)	0.0

Pfam analysis predicts that the NOV56a protein contains the domains shown in the Table 56F.

Table 56F. Domain Analysis of NOV56a			
Pfam Domain	NOV56a Match Region	Identities/ Similarities	Expect Value

		Region	
AMP-binding: domain 1 of 1	87..499	106/425 (25%) 299/425 (70%)	2.5e-96

Example 57.

The NOV57 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 57A.

Table 57A. NOV57 Sequence Analysis			
	SEQ ID NO: 171	2501 bp	
NOV57a, CG59354-01 DNA Sequence	ACACCATGACCACCCTTGATGATAAGTTGCTGGGGGAGAACTGCAGTACTACTATAG CAGCAGTGAGGATGAGGACAGTGACCACGAGGACAAGGACCGAGGCAGATGTGCCCA GCCAGCAGTTCTGTGCTGCAGAGGCTGAGCTGGCAGGCGAAGGCATCTCAGTTAAACA CAATGACTCTGAAGGAGTTTGCCATAATGAATGAGGACCAAGATGATGAAGAGTTTCT GCAGCAGTACCGGAAGCAGCGAATGGAAGAGATGCGGCAGCAGCTTCACAAGGGGCC CAATTCAAGCAGGTTTTTGAGATCTCCAGTGGAGAAGGGTTTTAGACATGATTGATA AAGAACAGAAAAGCATTGTCATCATGGTTTATTTATGAGGATGGCATTCCAGGGGA CGAAGCCATGAATGGTTGCATGATCTGCCTTGCCGACAGATACCCAGCTGTCAAGTTT TGCAAGGTGAAGAGCTCAGTTATTGGCGCCAGCAGTCAGTTACCAGGAATGCCCTTC CTGCCCTGCTGATCTATAAGGGGGGTGAATTGATCGGCAATTTTGTTCGTGTTACTGA CCAGCTGGGGGATGATTTCTTGCTGTGGACCTTGAAGCTTTTCTCCAGGAATTGGA TTACTCCAGAAAAGGAAGTCTTGGTGTGACATCTGTGCGTAACCTGCCACGTGTC ACAGTGAGGATAGCGACCTGGAATAAGATTGAAGTGAATGATGATGATGATGATGAT TCATTGTTTGGGTTGGAATACACGTCATTGTTTATTTTTGTTCCTTTGCTCTTGGCT TTTCAGCTGTTCTTTGTAGTCCCTTTTATTATGCATAAAATAAGAAATCTTAGATT AAATCAGAATGCTGAATAACCTTGTAGCTAGCAATAAGGTGACTTACAATTGTATAAA CAGGAAGCCAGGCTTTTGAAGCTGTTTACTTAAGATTCTGTGGTGTGACATCTCTGTTA TTGTTTCCAGTCAATATTTACAAAGCATCCTAAAGACAGGGTCTTGGAATTTGCTTCC AGATGATCTTAGAGGTCTCTGCCAAGTCTGAGAGTATAAATCTGTAGTATTGTGTTA TTTGCAACGTAAATAGTGCATTTTCTTAATCAAATGATTGTAAATTATATTTACTTGT AATCAGTTCCATAGCTTTAGACGGTGGTTAGATTTTTTTTTCCCAACAGGGGTCTTG TTTAAAGGGGTGAGCCACCGCACCCAGTCTGAGGGGTGGCCTCTGCTGCTGGATTTTC ATGCTCTCTCCAGCATGACTAAGTCTGGAACAGCAGGAAGGGTTGATGCTTACTGAC CTGGTGATGTTAGAAGACAAGTAGTTTATGGATTAAACATTAGAGCTGGAGTGGGGC TGGAAATCTTTGTAAAGGAAGTTCTTTCAGTAAGATGCCCTGCTTGTCTTTGTCTCT TTTTTGTTTAAACAAGGTAACCTTTTTGTTTAAACAAGGTAACCTTTTGTTTAACTAGAT TTTTTTTAAACTTTTTTTTTTTTCATATTGGAAGTAATTCATATTAGTAGAGG AAAATCTGACCAAAACAGAAGCAAAATAAGAAAATTAATAATCTCTAATCTACTA CCTAGAATAAAACACTATTAATATTTTGGTCTGTTTCTGCCAAGGTGTTTCTGTGT ATACATGGATATTTGTTTGTTTTAAACAAACGATGGGATCATCTGAACATCTG TTCTATAGTATGGTCAGCTAATAATATATCAGACCTTTTTTTTATATTATTAATATT CTACAACTTTTTAAAAATGTCTATTAATATTTCCATCGTATAGATGTGATATAAATTTGC TTGATGGTTGTCTCTTAAAAAGAAAGATAGCAAAATCTTTTTTAAATTACAAAAGTG ATAGATGTTCAATTGTAGAAAATGTAATAAACACTGTTAAGACTTAAAGCCATATAAT TCCACCAACCAAAATTAATCCCTTTTGTCAATATTCTAGTCATTTTATAGCCTTTTT TTTCTATGTATTTATAATAATTATCATTTCGCTTTTTTTCCTTTTTTAACTTTAAAA ATGTATATTCTAGGGTCAGGGGAAATGTAATCTGGAATTAAATATAGCCTTAAAAAT CACAAATTTTGATTTTCTGGCTTTTTCAGGAATTGACTAAGTGTAAAGAGTCTTGAAA GTATTTAGTCAACAAACAGAGTGCAATTTTTTTTTTTTGTACTAAGAAAGCTCGTTGTA GTAGAAAGGGTGAATGTATTGAAAATTATTAGAAGCAGGGAAGTATTGTTAGTCTAG CTTATTTCTTTTCAGTCTTTTTTCAATATTTTATAAACATTGAGTACTTACTGAATT TAGTTCTGTGCTCTTCTTATTTAGTGTGTATCATAAATACTTTGATGTTTCAACA TTCTAAATAAATAATTTTCAGTGGCTTCTAATAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAA		
	ORF Start: ATG at 6	ORF Stop: TGA at 726	
	SEQ ID NO: 172	240 aa	MW at 26866.9kD
NOV57a, CG59354-01 Protein Sequence	MTTLDKLLGEKLQYYSSSEDESDHEDKDRGRCAPASSVPAEELAGEGIVNTM TLKEFAIMNEDQDDEEFLQYRQRMEEMRQQLHKGPFKQVFEISSGEGFLDMIDKE QKSIVIMVHIYEDGIPGTEAMNGCMICLAAEYPAVKFKVKSSVIGASSQFTRNALPA LLIYKGGEIIGNFVRVTDQLGDDFFAVDLEAFLOEFGLLPEKEVLVLTSVRNSATCHS EDSDLEID		
	SEQ ID NO: 173	893 bp	
NOV57b,	CACCATGACCACCCTGTATGATAAGTTGCTGGGGGAGAACTGCAGTACTACTATAGC		

CG59354-02 DNA Sequence	AGCAGTGAAGATGAGGACAGTGACCACGAGGACAAGGACCGAGGCATCTCAGTTAAACA CAGGCCCAAAAGGTGTGATCAATGACTGGCGCGCTTCAAGCAGTTGGAGACAGAGCA GAGGGAGGAGCAGTGCCGGGAGATGGAAGGCTGATCAAGAAGCTGTCAATGACTTGC AGGTCCCATCTGGATGAAGAGGAGGAGCAACAGAAAACAGAAAGACCTCCAGGAGAAGA TCAGTGGGAAGATGACTCTGAAGGAGTTTGCCATAATGAATGAGGACCAAGATGATGA AGAGTTTCTGCAGCAGTACCGGAAGCAGCGAATGGAAGAGATGCGGCAGCAGCTTCAC AAGGGGCCCCAATTCAAGCAGGTTTTTGAGATCTCCAGTGGAGAAGGGTTTTAGACA TGATTGATAAAGAACAGAAAAGCATTGTTCATCATGGTTCATATTTATGAGGATGGCAT CAGGGACCGAAGCCATGAATGGTTGCATGATCCGCCTTGCAAGGGGGGTGAATTGATC GGCAATTTTGTTCGTGTTACTGACCAGCTGGGGGATGATTCTTTGCTGTGGACCTTG AAGCTTTTCTCCAGGAATTTGGATTACTCCAGAAAAGGAAGTCTTGGTGTGACATC TGTGCGTAACTCTGCCACGTGTCAAGTGAGGATAGCGACCTGGAATAGATTGAACT GATAGTCTAGTTGCATATAGATTTCTCATTGTTTGGGTTGGAATACACCATTGTTTAT TTTTGTTCTTTGTCTTCTGCTTTTCAGCTGTTCTTTGTAGTCCCTTTTATTATGCA TAAATAAAGAAATTCTTAGATT		
	ORF Start: ATG at 5		ORF Stop: TGA at 749
	SEQ ID NO: 174	248 aa	MW at 29227.4kD
NOV57b, CG59354-02 Protein Sequence	MTTLYDKLLGEKLQYYYSSSEDESDHEDKDRGISVNTGPKGVIINDWRRFKQLETEQR EEQCREMERLIKLSMTCRSHLDEEEQQKQKDLQEKISGKMTLKEFAIMNEDQDDEE FLQYQRKQRMEEMRQLHKGPFQKQVFEISSGEGFLDMIDKEQKSIVIMVHIYEDGIR DRSHEWLHDPCKGEGELIGNFVRVTDQLGDDFFAVDLEAFLQEFGLLPEKEVLVLT SVRNSATCHSEDSLEID		
	SEQ ID NO: 175	891 bp	
NOV57c, CG59354-03 DNA Sequence	CACCATGACCACCTGTATGATAAGTTGCTGGGGAGAACTGCAGTACTACTATAGC AGCAGTGAAGATGAGGACAGTGACCACGAGGACAAGGACCGAGGCATCTCAGTTAAACA CAGGCCCAAAAGGTGTGATCAATGACTGGCGCGCTTCAAGCAGTTGGAGACAGAGCA GAGGGAGGAGCAGTGCCGGGAGATGGAAGGCTGATCAAGAAGCTGTCAATGACTTGC AGGTCCCATCTGGATGAAGAGGAGGAGCAACAGAAAACAGAAAGACCTCCAGGAGAAGA TCAGTGGGAAGATGACTCTGAAGGAGTTTGCCATAATGAATGAGGACCAAGATGATGA AGAGTTTCTGCAGCAGTACCGGAAGCAGCGAATGGAAGAGATGCGGCAGCAGCTTCAC AAGGGGCCCCAATTCAAGCAGGTTTTTGAGATCTCCAGTGGAGAAGGGTTTTAGACA TGATTGATAAAGAACAGAAAAGCATTGTTCATCATGGTTCATATTTATGAGGATGGCAT TCCAGGGACCGAAGCCATGAATGGTTGCATGATCCGCCTTGCCGACAGTACCCAGCT GTCAAGTTCTGCAAGGTGAAGAGCTCAGTTATTGGCGCCAGCAGTCAGTTACCCAGGA ATGCCCTTCTGCCCTGCTGATCTATAAGGGGGGTGAATTGATCGGCAATTTTGTTCG TGTTACTGACCAGCTGGGGGATGATTCTTTGCTGTGGACCTTGAAGCTTTTCTCCAG GAATTTGGATTACTCCAGAAAAGGAAGTCTTGGTGTGCTGACATCTGTGCGTAACTCTG CCACGTGTCAAGTGAGGATAGCGACCTGGAATAGATTGAACTGATAGTCTAGTTGC ATAGATTTCTCATTGTTTGGG		
	ORF Start: ATG at 5		ORF Stop: TGA at 851
	SEQ ID NO: 176	282 aa	MW at 32598.5kD
NOV57c, CG59354-03 Protein Sequence	MTTLYDKLLGEKLQYYYSSSEDESDHEDKDRGISVNTGPKGVIINDWRRFKQLETEQR EEQCREMERLIKLSMTCRSHLDEEEQQKQKDLQEKISGKMTLKEFAIMNEDQDDEE FLQYQRKQRMEEMRQLHKGPFQKQVFEISSGEGFLDMIDKEQKSIVIMVHIYEDGIP GTEAMNGCMIRLAAEYPAVKFCKVKSSVIGASSQFTRNALPALLIYKGGELIGNFVRV TDQLGDDFFAVDLEAFLQEFGLLPEKEVLVLT SVRNSATCHSEDSLEID		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 57B.

Table 57B. Comparison of NOV57a against NOV57b through NOV57c.		
Protein Sequence	NOV57a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV57b	58..240	138/183 (75%)
	100..248	140/183 (76%)
NOV57c	58..240	182/183 (99%)
	100..282	182/183 (99%)

Further analysis of the NOV57a protein yielded the following properties shown in Table 57C.

Table 57C. Protein Sequence Properties NOV57a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV57a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 57D.

Table 57D. Geneseq Results for NOV57a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV57a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE03537	Human secreted protein variant, SEQ ID NO: 228 - Homo sapiens, 301 aa. [WO200132675-A1, 10-MAY-2001]	1..240 1..301	226/301 (75%) 230/301 (76%)	e-117
AAE099657	Human GTPase associated protein-8 - Homo sapiens, 301 aa. [WO200031263-A2, 02-JUN-2000]	1..240 1..301	226/301 (75%) 230/301 (76%)	e-117
AAE02004	Fruitfly viral IAP-associated factor (VIAF) - Drosophila melanogaster, 240 aa. [WO200134798-A1, 17-MAY-2001]	55..214 59..213	52/161 (32%) 86/161 (53%)	3e-14
AAE02003				5e-13

	(VIAF) - Brachydanio rerio, 239 aa. [WO200134798-A1, 17-MAY-2001]	2..237	117/241 (47%)	
AAE02002	Mouse viral IAP-associated factor (VIAF) - Mus musculus, 240 aa. [WO200134798-A1, 17-MAY-2001]	58..240 52..240	59/195 (30%) 99/195 (50%)	4e-12

In a BLAST search of public sequence databases, the NOV57a protein was found to have homology to the proteins shown in the BLASTP data in Table 57E.

Table 57E. Public BLASTP Results for NOV57a				
Protein Accession Number	Protein/Organism/Length	NOV57a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96AF1	HYPOTHETICAL 34.3 KDA PROTEIN - Homo sapiens (Human), 301 aa.	1..240 1..301	226/301 (75%) 230/301 (76%)	e-117
Q13371	Phosducin-like protein (PHLP) - Homo sapiens (Human), 301 aa.	1..240 1..301	225/301 (74%) 230/301 (75%)	e-116
T17321	hypothetical protein DKFZp564M1863.1 - human, 301 aa.	1..240 1..301	225/301 (74%) 230/301 (75%)	e-116
Q923E8	RIKEN CDNA 1200011E13 GENE - Mus musculus (Mouse), 301 aa.	1..240 1..301	210/301 (69%) 223/301 (73%)	e-109
Q63737	Phosducin-like protein (PHLP) - Rattus norvegicus (Rat), 301 aa.	1..240 1..301	210/301 (69%) 223/301 (73%)	e-108

PFam analysis predicts that the NOV57a protein contains the domains shown in the Table 57F.

Table 57F. Domain Analysis of NOV57a

Pfam Domain	NOV57a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Phosducin: domain 1 of 2	35..57	14/23 (61%) 21/23 (91%)	8.7e-08
Phosducin: domain 2 of 2	58..240	133/183 (73%) 174/183 (95%)	9.7e-148

Example 58.

The NOV58 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 58A.

Table 58A. NOV58 Sequence Analysis

	SEQ ID NO: 177	756 bp
NOV58a, CG59319-01 DNA Sequence	GGATCCCAATGAAGATACAGAATGGAATGACATTTTAAGAGATTTGGGCATTCTTCCT CCTAAAGAAGAGTCAAAAGATGAAATTGAAGAAATGGTTTACGTTTACAGAAAGAAG CAATGGTGAACCAATTGAAAAGATGACTCTTGACAGCTAAAGGAAGCTGAAGATGA ATTCGATGAAGAAGATATCAGGCTGTTGAAACATATAGAAAGAAGCGGTTACAGGAA TGGAAAGCTCTTAAGAAAAACAAAAATTTGGAGAATTAAGAGAAATTTCTGGAATC AGTATGTGAATGAAGTCACAAATGCAGAAGAAGATGTGTGGTTATAATTCATCTATA CAGATCAAGCATCCCAATGTGTTTGGTTAACCAGCATCTTAGTCTTCTAGCAAGA AAGTTTCCAGAACTAAATTTGTTAAAGCCATCGTGAATAGCTGTATTCAACACTACC ATGACAAATTGTTTACCAACAATTTTGTGTATAAAAAATGGTCAGATAGAAGCCAAAT CATTGGAATTATAGAATGTGGAGGGATAAATCTCAAGCTGGAAGAACTGAATGGAAG CTAGCAGAAGTTGGAGCAATACAGACTGATTTGGAAGAAAAACCCAGAAAAGACATGG TAGATATGATGGTATCTTCAATTAGAAACACTTCTATTATCATGATGACAGTGATAGCTC CAACAGTGATAATGATACCAATAGAGAGAAATATTCAATAAATAGCTTTTAGTAAAA AA	
	ORF Start: GAT at 2	ORF Stop: TAG at 719
	SEQ ID NO: 178	239 aa MW at 27811.3kD
NOV58a, CG59319-01 Protein Sequence	DPNEDTEWNDILRDPGILPPKEESKDEIEEMVLRLQKEAMVKPFKMTLAQLKEADE FDEEDMQAVETRYKKRLQEWKALKKKQKFGELREISGNQYVNEVTNAEEDVWVI IHL RSSIPMCLLVNQHLSSLARKFPETKFVKAIVNSCIQHYHDNCLPTIFVYKNGQIEAKF IGLIECGGINLKLLELEWKLAEVGAIQTDLEENPRKDMVDMVSSIRNTSIHDDSDSS NSDNDTK	
	SEQ ID NO: 179	745 bp
NOV58b, CG59319-02 DNA Sequence	GGATCCCAATGAAGATACAGAATGGATCCCAATGAAGATACAGAATGGAATGACATTT TAAGAGATTTCCGGCATTCTTCCTCCTAAAGAAGAGTCAAAAGATGAAATTGAAGAAAT GGTTTACGTTTACAGAAAGAAGCAATGGTGAACCAATTGAAAAGATGACTCTTGCA CAGCTAAAGGAAGCTGAAGATGAATTTGATGAAGAAGATATCAGGCTGTTGAAACAT ATAGAAAGAAGCGGTTACAGGAATGGAAGCTCTTAAGAAAAACAAAAATTTGGAGA ATTAAAGAGAAATTTCTGGAATCAGTATGTGAATGAAGTCACAAATGCAGAAGAAGAT GTGTGGGTTATAATTCATCTATACAGATCAAGCATCCCAATGTGTTTGTGGTTAACC AGCATCTTAGTCTTCTAGCAAGAAAGTTTCCAGAACTAAATTTGTTAAAGCCATCGT GAATAGCTGTATTCAACACTACCATGACAATTGTTTACCAACAATTTTGTGTATAAA AATGGTCAGATAGAAGCCAAATTCATTGGAATTATAGAATGTGGAGGGATAAATCTCA AGCTGGAAGAACTTGAATGGAAGCTAGCAGAAGTTGGAGCAATACAGACTGATTTGGA AGAAAACCCAGAAAAGACATGGTAGATATGATGGTATCTTCAATTAGAAACACTTCT ATCCATGATGACAGTGATAGCTCCCAACAGTGATAATGATACCAATAGA	
	ORF Start: ATG at 22	ORF Stop: TAG at 742
	SEQ ID NO: 180	240 aa MW at 27942.5kD

NOV58b, CG59319-02 Protein Sequence	MDPNEDTEWNDILRDFGILPPKEESKDEIEEMVLRLQKEAMVKPFKMTLAQLKEAED EFDEEDMQAVETYRKKRLQEWKALKKKQKFGELREISGNQYVNEVTNAEEDVWVIIHL YRSSIPMCLLVNQHLSLLARKFPETKFKVKAIVNSCIQHYHDNCLPTIFVYKNGQIEAK FIGIIECGGINLKLLELEWKLAEVGAIQTDLEENPRKDMVDMVSSIRNTSIHDDSDS SNSDNDTK
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Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 58B.

Table 58B. Comparison of NOV58a against NOV58b.		
Protein Sequence	NOV58a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV58b	1..239	216/239 (90%)
	2..240	216/239 (90%)

Further analysis of the NOV58a protein yielded the following properties shown in Table 58C.

Table 58C. Protein Sequence Properties NOV58a	
PSort analysis:	0.8800 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV58a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 58D.

Table 58D. Geneseq Results for NOV58a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV58a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE02003	Zebrafish viral IAP-associated factor (VIAF) - Brachydanio rerio, 239 aa. [WO200134798-A1, 17-MAY-2001]	1..237 3..239	133/238 (55%) 181/238 (75%)	3e-75
AAU27979	Mouse contig polypeptide sequence #132 - Mus musculus, 243 aa. [WO200164834-A2, 07-SEP-2001]	1..231 7..240	137/234 (58%) 176/234 (74%)	2e-74

AAU27807	Human full-length polypeptide sequence #132 - Mus musculus, 239 aa. [WO200164834-A2, 07-SEP-2001]	1..231 3..236	137/234 (58%) 176/234 (74%)	2e-74
AAE02001	Human viral IAP-associated factor (VIAF) - Homo sapiens, 239 aa. [WO200134798-A1, 17-MAY-2001]	1..231 3..236	137/234 (58%) 176/234 (74%)	2e-74
AAB68507	Human GTP-binding associated protein #7 - Homo sapiens, 239 aa. [WO200105970-A2, 25-JAN-2001]	1..231 3..236	137/234 (58%) 176/234 (74%)	2e-74

In a BLAST search of public sequence databases, the NOV58a protein was found to have homology to the proteins shown in the BLASTP data in Table 58E.

Table 58E. Public BLASTP Results for NOV58a				
Protein Accession Number	Protein/Organism/Length	NOV58a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9CQU4	1700010B22RIK PROTEIN - Mus musculus (Mouse), 240 aa.	1..239 3..240	208/239 (87%) 229/239 (95%)	e-121
Q9WUP3	PDCL2 - Mus musculus (Mouse), 238 aa (fragment).	1..239 1..238	207/239 (86%) 228/239 (94%)	e-121
Q9DA99	1700016K07RIK PROTEIN - Mus musculus (Mouse), 192 aa.	47..239 1..192	165/193 (85%) 183/193 (94%)	3e-94
CAC40345	SEQUENCE 5 FROM PATENT WO0134798 - Brachydanio rerio (Zebrafish) (Zebra danio), 239 aa.	1..237 3..239	133/238 (55%) 181/238 (75%)	1e-74
Q9H2J4	HTPHLP (UNKNOWN) (PROTEIN FOR MGC:3062) - Homo sapiens (Human), 239 aa.	1..231 3..236	137/234 (58%) 176/234 (74%)	8e-74

PFam analysis predicts that the NOV58a protein contains the domains shown in the Table 58F.

Table 58F. Domain Analysis of NOV58a			
Pfam Domain	NOV58a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Phosducin: domain 1 of 1	60..175	32/120 (27%) 55/120 (46%)	5.8

Example 59.

The NOV59 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 59A.

Table 59A. NOV59 Sequence Analysis			
	SEQ ID NO: 181	981 bp	
NOV59a, CG59576-01 DNA Sequence	GCCACCGCGCCAGCTGGCTTTTGTGTTTTATCCTTCTGCTCCTCATTACCTATTCA CCATCATTGGTAGTCTTATGGTGTCTTTGCCATCAAACCTGGATTCTGCCTGCACAG CTCCTTCTATTCTTCATCAGTGTCTCTCCTTCCTAGAGATCTGGTATACCACCATC ACCATCCCCAAGATGTTCTTCAACCTAGCCAGTGAGCAGAAGACCACCTCCCTGGATG GTTGCCTATTGCAGATGTATTTCTTTTACTCCCTCGGCATCACTGAGGTTTGTCTGCT CACCACCAGGGCTATGGACAGATACCTGGCCATCTGTAATCACCTTTGCTACCCCA GTCACGACACCTCAGCTCTACACTCAGGTGATTCTAGGTTGTTGCATCTGTGGCTTCT TCACGCTGCTCCCTGAGATTGCTTGGATATCCACACTGCCATTTTGTGGTCCAAATCA AATCCACAACATTTTCTGTGACCTTGATCCTATCCTGAATCTAGCATGTGTAGACACT GGCCCAGTTGTTTTAATCAAGGTTGTGGACATTGTACATGCTGTGGAGATCATCACAG CTATAATGCTTGTGACTTTGGCTTACGTCCAAATTATTGCAGTGATCCTAAGAAACTG CTCTGCTGATGGATGCCAAAAGGCATTTTCTACCTATGCTTTCCACCTTGCTATTTTC TTAATCTTTTTTGAAGGTGATGACCTGATGTACCTGCTCTTCTCTGCCAAGTACTCCT TTTTCTGGGACACAACCATCAGCCTAATGTTTGCAGTGCTGTACCGACAACAATCAT CTGTAGTCTGAGGAATAAAGAGATAAAGGAAGCAATAAAAAAGCACATGTGCCAATCA ATGATATGCACACATCATGTCAAATAAGACCAATACACACCTCTTAATTACCAAGA ATATTTATACAAATATTTACATTAATACGTTTCAAGTGTGTTTGTGCTGCTGTG		
	ORF Start: GCC at 1	ORF Stop: TAA at 895	
	SEQ ID NO: 182	298 aa	MW at 33780.0kD
NOV59a, CG59576-01 Protein Sequence	ATAPSWLLFFILLLLIYLFITIGSLMVFFAIKLDLHSSFFYFFISVLSFLEIWTYTI TIPKMFNLLASEQKTTSLDGCLLQMYFFYSLGITEVCLLTTRAMDRYLAICNHLCPYT VTPQLYTVQVILGCCICGFFTLPEIAWISTLPFCGPNQIHNI FCDLDPILNLACVDIT GPVVLIKVVDIVHAVEIITAIMLVTLAYVQIIAIVILRNCSADGCQKAFSTYAFHLAIF LIFFGSVALMYLLFSKYSFFWDTTISLMFAVLSPPTTIICSLRNKEIKEAIKHMCS MICTHHVK		

Further analysis of the NOV59a protein yielded the following properties shown in Table 59B.

Table 59B. Protein Sequence Properties NOV59a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 25 and 26

A search of the NOV59a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 59C.

Table 59C. Geneseq Results for NOV59a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV59a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72586	Human OR-like polypeptide query sequence, SEQ ID NO: 2267 - Homo sapiens, 289 aa. [WO200127158-A2, 19-APR-2001]	7..295 1..289	286/289 (98%) 286/289 (98%)	e-167
AAG71784	Human olfactory receptor polypeptide, SEQ ID NO: 1465 - Homo sapiens, 289 aa. [WO200127158-A2, 19-APR-2001]	7..295 1..289	286/289 (98%) 286/289 (98%)	e-167
AAG71785	Human olfactory receptor polypeptide, SEQ ID NO: 1466 - Homo sapiens, 318 aa. [WO200127158-A2, 19-APR-2001]	5..292 20..311	175/293 (59%) 217/293 (73%)	6e-95
AAU24721	Human olfactory receptor AOLFR220 - Homo sapiens, 343 aa. [WO200168805-A2, 20-SEP-2001]	7..283 53..328	170/279 (60%) 212/279 (75%)	4e-94
AAG71808	Human olfactory receptor polypeptide, SEQ ID NO: 1489 - Homo sapiens, 317 aa. [WO200127158-A2, 19-APR-2001]	7..283 29..304	170/279 (60%) 212/279 (75%)	4e-94

In a BLAST search of public sequence databases, the NOV59a protein was found to have homology to the proteins shown in the BLASTP data in Table 59D.

Table 59D. Public BLASTP Results for NOV59a				
Protein Accession Number	Protein/Organism/Length	NOV59a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96R35	OLFACTORY RECEPTOR - Homo sapiens (Human), 216 aa (fragment).	50..267 1..216	107/218 (49%) 146/218 (66%)	7e-55
Q9EPG2				2e-52

	Mus musculus (Mouse), 314 aa.	19..303	172/289 (58%)	
O95007	Olfactory receptor 6B1 (Olfactory receptor 7-3) (OR7-3) - Homo sapiens (Human), 311 aa.	10..285 28..301	109/279 (39%) 170/279 (60%)	1e-51
Q9QWU6	OLFACTORY RECEPTOR I7 - Mus musculus (Mouse), 327 aa.	1..289 20..314	111/298 (37%) 171/298 (57%)	2e-50
P23270	Olfactory receptor-like protein I7 - Rattus norvegicus (Rat), 327 aa.	1..289 20..314	111/298 (37%) 171/298 (57%)	2e-50

PFam analysis predicts that the NOV59a protein contains the domains shown in the Table 59E.

Table 59E. Domain Analysis of NOV59a			
Pfam Domain	NOV59a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	37..164	30/134 (22%) 90/134 (67%)	5.4e-13

Example 60.

The NOV60 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 60A.

Table 60A. NOV60 Sequence Analysis			
	SEQ ID NO: 183	1201 bp	
NOV60a, CG59557-01 DNA Sequence	AGGATAACTTTATATGTTGCAAAATGACTCACATAGTATATTTATTTAACCAGCCTA ATTTCAGGCTGTTTAGTTGCTTGAAAAGAAGGTTTTTATTGTTCTTTGCATGTACT TAGAATGCTGACTGTGTTTTATGAGCCACAAGTGAAACCGCTGAAAATATGGATCCA GAGAATCAGACAATGGTGACTGAGTTTTATTTCTCTGATTTTCTCAATCTAAGAATG GCAGCCTCTTATCTTCATTCCCTATGCTCTTTATTTATATATTATTCTTGTGGAAA TTTCATGATTTTCTTTGCTGTCCGACCGGACCCCATCTCCATAATCCTATGTACAGT TTTATCAGTGTCTTCTCCTTCTCGGAGATTGGTACACCACCGTGACTATCCCCAAGA TGCTCTCAACCTTCTCAGTGAACAGAAAACCATCTCTTTCATAGTGTGCCTCCTGCA GATGTACTTCTTCCACTCACTCGGGGTACAGAAGCCCTAGTCTTCACAGTGATGGCC ATTGACAGGTGTGTAGCCATCTGCAACCCCTTCGCTATGCAATCACTATGTCCCTTA GACTGTGCATCCAGCTCTCCACTGGCTCTTGCAATTTTGGCTTCCTCATGTTACTGCC AGAGATTGTGTGCAATTTCCACTCTTCCATTCTGTGGCGCCAACCAATTATCAACTC TTTTGTGACTTTGAACCTGTGCTGCAGTTAGCCTGCACAGATACGTACATAATTCTGG TTGAAGATGTGATCCGTGCTATTTCCATTCTGACCTCTGTCTCTGTGCATCACCCTTT CTATTTAAGAATCATCAGGTGATCCTGAGGATTCCCTCTGGTGAGAGTCGTGAGAAG GCTTTCTTCACATGTGCAGCCACATTGCTATTTTCTGTCTGTTTTTGGCAGTGTGT CACTCATGTATCTGCGCTTCTCTGTGCACATTCCCACCATTACTGGACAAGGCCATTGC ACTGATGTTTGTCTGTCTTGGCCCTACTTTTCAACCCAGTAATCTATAGTCTGAGGAAC AAAGATATGAAAACGCCACCAAGAAAATCCTCTGTTCTCAAAGATGTTCAATGCCT CTGGGAGCTAATGGAGTTCACACACCTCTTCAAAGAAATCTCATCATCTCCTTAAG TTTAAATGCTAACAAATCAGTTTTTTAAATTACCATGCA		
	ORF Start: ATG at 121	ORF Stop: TAA at 1111	
	SEQ ID NO: 184	330 aa	MW at 37439.1kD
NOV60a, CG59557-01 Protein Sequence	MLTVFYEPTSETAENMDPENQTMVTEFYFSDFPQSKNGSLFFIPMLFIYIFILVGNF MIFFAVRDPDPLHNPMSYFISVFSFLEIWTYTTIIPKMLSNLLSEQKTISFIGCLLMQ YFFHSLGVTEALVLTVMADRCVAICNPLRYAITMSPLRCIQLSTGSCIFGLMLLPE		

	IVCISTLPFCGANQIHQLFCDFEPVLQLACTDTYIILVEDVIRAIISILTSVSVITLFY LRIITVILRIPSGESRQKAFFTCAAHIAIFLLFPGSVSLMYLRFVTFPPLDKAIAL MFAVLALLFNPIYSLRNKDMKNATKKILCSQKMFNASGS
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Further analysis of the NOV60a protein yielded the following properties shown in Table 60B.

Table 60B. Protein Sequence Properties NOV60a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.0300 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 67 and 68

A search of the NOV60a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 60C.

Table 60C. Geneseq Results for NOV60a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV60a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG71807	Human olfactory receptor polypeptide, SEQ ID NO: 1488 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	16..330 1..315	313/315 (99%) 314/315 (99%)	e-180
AAG71803	Human olfactory receptor polypeptide, SEQ ID NO: 1484 - Homo sapiens, 315 aa. [WO200127158-A2, 19-APR-2001]	16..329 1..314	219/314 (69%) 259/314 (81%)	e-129
AAU24658	Human olfactory receptor AOLFR156 - Homo sapiens, 331 aa. [WO200168805-A2, 20-SEP-2001]	9..329 10..330	218/321 (67%) 259/321 (79%)	e-128
AAU24721	Human olfactory receptor AOLFR220 - Homo sapiens, 343 aa. [WO200168805-A2, 20-SEP-2001]	20..329 33..342	196/310 (63%) 234/310 (75%)	e-111
AAG71808	Human olfactory receptor polypeptide, SEQ ID NO: 1489 - Homo sapiens, 317 aa. [WO200127158-A2, 19-APR-2001]	20..323 9..312	195/304 (64%) 232/304 (76%)	e-111

In a BLAST search of public sequence databases, the NOV60a protein was found to have homology to the proteins shown in the BLASTP data in Table 60D.

Table 60D. Public BLASTP Results for NOV60a				
Protein Accession Number	Protein/Organism/Length	NOV60a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9WU86	ODORANT RECEPTOR S1 - Mus musculus (Mouse), 324 aa.	15..324 8..320	135/315 (42%) 188/315 (58%)	4e-67
Q9EPG2	M51 OLFACTORY RECEPTOR - Mus musculus (Mouse), 314 aa.	20..325 5..311	129/307 (42%) 189/307 (61%)	4e-65
P23270	Olfactory receptor-like protein I7 - Rattus norvegicus (Rat), 327 aa.	24..319 10..310	126/301 (41%) 182/301 (59%)	8e-65
Q9QWU6	OLFACTORY RECEPTOR I7 - Mus musculus (Mouse), 327 aa.	16..319 1..310	128/310 (41%) 184/310 (59%)	9e-64
O13036	CHICK OLFACTORY RECEPTOR 7 - Gallus gallus (Chicken), 323 aa.	16..319 1..305	122/305 (40%) 187/305 (61%)	1e-63

PFam analysis predicts that the NOV60a protein contains the domains shown in the Table 60E.

Table 60E. Domain Analysis of NOV60a			
Pfam Domain	NOV60a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	56..304	45/270 (17%) 172/270 (64%)	2.4e-21

Example 61.

The NOV61 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 61A.

Table 61A. NOV61 Sequence Analysis

	SEQ ID NO: 185	1061 bp
NOV61a, CG59555-01 DNA Sequence	CAATCTGGTCCTAAGTGATCTTTTCTTTTTCACAGGGAAATGGGGGAAAATCAGACA ATGGTCAAGAGTTCTCTCTACTGGGATTCTCTCTGGGCCCAAGGATTCAGATGCTCC TCTTTGGGCTCTTCTCCCTGTTCTATATCTTCAACCCTGCTGGGGAACGGGGCCATCCT GGGGCTCATCTCACTGGACTCCAGACTCCACACCCCATGTACTTCTTCTCTCACAC CTGGCTGTCGTGACATCGCCTACACCCGCAACACGGTGCCCCAGATGCTGGCGAACC TCCTGCATCCAGCCAAGCCCATCTCCTTTGCTGGCTGCATGACGCAGACCTTTCTCTG TTTGAGTTTGGACACAGCGAATGTCTCTGCTGGTGCTGATGCTCCTACGATCGTTAC GTGGCCATCTGCCACCTCTCCGATACTCCGTCATCATGACCTGGAGAGTCTGCATCA CCCTGGCCGTCACTTCTGGACGTGTGGCTCCCTCTGGCTCTGGCCCATGTGGTTCT CATCCTAAGACTGCCCTTCTCTGGCCCTCATGAAATCAACCACTTCTTCTGTGAAATC CTGTCTGTCCTCAGGCTGGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCATCTTTG CAGCCTCGGTGTTCTTCTGGTGGGGCCACCCAGCCTGGTGCTTGTCTCTACTCGCA CATCCTGGCGGCATCCTGAGGATCCAGTCTGGGGAGGGCCGCAGAAAGGCCTTCTCC ACCTGCTCCTCCACCTCTGCGTGGTGGGACTCTTCTTTGGCAGTGCCATCATCATGT ACATGGCCCCAAGTCCGCCATCCTGAGGAGCAGCAAAAGGTCTTTTCTATTTTA CAGTTTTTTCAACCAACACTTAACCCCTGATTACAGCCTGAGGAACGGAGAGGTC AAGGGTGCCCTGAGGAGAGCACTGGGCAAGGAAAGTCATTCTAACTGGTGTGACATT TGACTCTCCCTCTCAGTCATCTCTGGAATCTTGGTACCAAAATACCACCTAAGTTCA CTACTCTCTTTATATCA	
	ORF Start: ATG at 41	ORF Stop: TAA at 971
	SEQ ID NO: 186	310 aa MW at 34713.8kD
NOV61a, CG59555-01 Protein Sequence	MGENTMVFTEFLLGLLPRIQMLLFGFLSLFYIFTLLGNAILGLISLDSRLHTPM YFFLSHLAVVDIAYTRNTVPQMLANLLHPAKPISFAGCMTQTFLCLSPGHSECLLLVL MSYDRYVAICHPLRYSVIMTWRCITLAVTSWTCGSLALAHVVLILRLPFGSPHEIN HFFCEILSVLRACADTWNQVVFIAACVFFLVGPPSLVLVSYSYLAILRIQSGEG RRKAFSTCSSHLGVGLFFGSAIIMYMAKSRHPBEEQKVFFLFYSFFNPFLNPLIYS LRNGEVKGALRRALGKESHS	

Further analysis of the NOV61a protein yielded the following properties shown in Table 61B.

Table 61B. Protein Sequence Properties NOV61a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 43 and 44

A search of the NOV61a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 61C.

Table 61C. Geneseq Results for NOV61a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV61a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM29935	Peptide #3972 encoded by probe for measuring placental gene expression - Homo sapiens, 311 aa. [WO200157272-A2, 09-AUG-2001]	1..310 2..311	310/310 (100%) 310/310 (100%)	0.0
AAM17409	Peptide #3843 encoded by probe for measuring cervical gene expression - Homo sapiens, 311 aa. [WO200157278-A2, 09-AUG-2001]	1..310 2..311	310/310 (100%) 310/310 (100%)	0.0
AAG72949	Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2631 - Homo sapiens, 314 aa. [WO200127158-A2, 19-APR-2001]	1..310 2..311	310/310 (100%) 310/310 (100%)	0.0
AAG72187	Human olfactory receptor polypeptide, SEQ ID NO: 1868 - Homo sapiens, 310 aa. [WO200127158-A2, 19-APR-2001]	1..310 1..310	310/310 (100%) 310/310 (100%)	0.0
AAU04577	Human G-protein coupled receptor like protein, GPCR #11 - Homo sapiens, 308 aa. [WO200153454-A2, 26-JUL-2001]	1..310 1..308	288/310 (92%) 294/310 (93%)	e-165

In a BLAST search of public sequence databases, the NOV61a protein was found to have homology to the proteins shown in the BLASTP data in Table 61D.

Table 61D. Public BLASTP Results for NOV61a				
Protein Accession Number	Protein/Organism/Length	NOV61a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96R46	OLFACTORY RECEPTOR - Homo sapiens (Human), 217 aa (fragment).	67..283 1..217	217/217 (100%) 217/217 (100%)	e-125
O95047	Olfactory receptor 2A4 - Homo sapiens (Human), 310 aa.	1..307 1..307	217/307 (70%) 250/307 (80%)	e-122
Q9NQNO	DJ1005H11.1 (7 TRANSMEMBRANE RECEPTOR	39..307 1..269	187/269 (69%) 216/269 (79%)	e-103

	(OLFACTORY RECEPTOR LIKE PROTEIN)) - Homo sapiens (Human), 272 aa (fragment).			
Q9Z1V2	OLFACTORY RECEPTOR B12 - Mus musculus (Mouse), 223 aa (fragment).	63..285 1..223	172/223 (77%) 190/223 (85%)	9e-98
O43888	OLFACTORY RECEPTOR - Homo sapiens (Human), 217 aa (fragment).	67..282 1..217	173/217 (79%) 188/217 (85%)	1e-97

Pfam analysis predicts that the NOV61a protein contains the domains shown in the Table 61E.

Table 61E. Domain Analysis of NOV61a			
Pfam Domain	NOV61a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	40..289	65/269 (24%) 188/269 (70%)	1.1e-45

Example 62.

The NOV62 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 62A.

Table 62A. NOV62 Sequence Analysis			
	SEQ ID NO: 187	1201 bp	
NOV62a, CG59551-01 DNA Sequence	AGTGGTTGTAAATAATTCTGCTTATATTACCTACAGAGTAAACATTATAGCATTATC ACTCCAGAATCCTTTGTTTCTATGGTTTCCAGATGTTTCCAATGTCTAGATGTTCCAG CTGCCCATCTCTGAGAAATCCAGCTGTGTCTCACAATGGATGCCACAGCCTGTAATGA ATCAGTGGATGGCTCACCCGTCTTCTATCTATTGGGCATCCCTCTCTGCCAGAGACC TTCTTCTCCTCCTGTGTTTTTTATTTTCTCCTCTTCTACCTTCTCATCCTGATGGGTA ATGCCCTGATCCTGGTGGCGTGGTGGCAGAGCCCAGCCTCCACAAGCCCATGTACTT CTTCTGATCAATCTCTCCACCTTGGACATCCTTTTACCACAACCACTGTCCCAAAG ATGCTGTCTTATTCTTGCTTGGGGACCGCTTCTCAGCTTTTCTTCTGCTTACTGC AGATGTACCTCTTCCAAAGTTTACATGTTTCAAGCCTTCATCCTGGTGGTCAATGGC CTATGACCGCTATGTGGCTATCTGCCACCCACTGCACTACCTGTCTCATGAACCCA CAGACCAATGCTACCTTGGCAGCCAGTGCCTGGCTAACTGCCCTCTCTGCCCATCC CAGCAGTAGTAAGGACCTCCAGATGGCATATAACAGCATTGCCTACATCTACCACTG CTTCTGTGATCATCTGGCTGTGGTCCAGGCCTCTGCTCTGACACCACCCCCAGACC CTCATGGGCTTCTGCATCGCCATGGTGGTGTCTTCTCTCCCCCTTCTCTGGTGTCTT TCTCTATGTCCACATCCTGGCCTCAGTGCTTCGCATCAGTTCCCTAGAAAGGACGGGC AAAAGCCTTCTCCACCTGCAGCTCCACCTTCTGGTGTGGGCACCTACTACTCATCT ATTGCCATAGCCTACGTGGCTACAGGGCTGACCTGCCCTTGACTTCCATATCATGG GCAATGTGGTATATGCCATTCTCACACCAATTCTCAACCCCTCATTTACACGCTGAG AAACAGGGATGTAAAGGCAGCCATACCAAAATCATGTCTCAAGACCCAGGCTGTGAC AGGAGCATTTGACCTTTAAATGCAGCTAACTCTGCTTCCAGGACACCAATAACAGTG CTTAGCACAGAGAAAGGACTCAATACATGATAATGAAATAA		
	ORF Start: ATG at 152	ORF Stop: TGA at 1112	
	SEQ ID NO: 188	320 aa	MW at 35502.6kD
NOV62a, CG59551-01 Protein Sequence	MDATACNESVDGSPVYLLGIPSLPETFFLPVFFIFLLFYLLILMGNALILVAVVAEP SLHKPMYFFLINLSTLDILFTTTTVPKMLSLFLGDRFLSFSSCLLQMYLFQSFTCSE AFILVVMAYDRYVAICHPLHYPLMNPQTNAATLAASAWLTALLLPPIPAVVRTSQMAYN SIAYIYHCFCDHLAVVQASCDTTPQTLMGFCIAMVVSFLPLLVLVLSYVHILASVLR ISSLEGRAKAFSTCSSHLLVVGTYSSIAIYVAYRADLPDFHIMGNVVYAILTPIL		

NPLIYTLRNRDVKAAITKIMSQDPGCDRSI

Further analysis of the NOV62a protein yielded the following properties shown in Table 62B.

Table 62B. Protein Sequence Properties NOV62a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.3000 probability located in microbody (peroxisome)
SignalP analysis:	Likely cleavage site between residues 57 and 58

A search of the NOV62a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 62C.

Table 62C. Geneseq Results for NOV62a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV62a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72119	Human olfactory receptor polypeptide, SEQ ID NO: 1800 - Homo sapiens, 295 aa. [WO200127158-A2, 19-APR-2001]	35..290 2..257	213/256 (83%) 228/256 (88%)	e-119
AAU24639	Human olfactory receptor AOLFR134 - Homo sapiens, 325 aa. [WO200168805-A2, 20-SEP-2001]	16..308 17..308	129/293 (44%) 186/293 (63%)	6e-67
AAG72479	Human OR-like polypeptide query sequence, SEQ ID NO: 2160 - Homo sapiens, 324 aa. [WO200127158-A2, 19-APR-2001]	16..308 17..308	129/293 (44%) 186/293 (63%)	6e-67
AAG71590	Human olfactory receptor polypeptide, SEQ ID NO: 1271 - Homo sapiens, 324 aa. [WO200127158-A2, 19-APR-2001]	16..308 17..308	129/293 (44%) 186/293 (63%)	6e-67
AAG71632	Human olfactory receptor polypeptide, SEQ ID NO: 1313 - Homo sapiens, 316 aa. [WO200127158-A2, 19-APR-2001]	16..315 13..312	126/300 (42%) 179/300 (59%)	3e-64

In a BLAST search of public sequence databases, the NOV62a protein was found to have homology to the proteins shown in the BLASTP data in Table 62D.

Table 62D. Public BLASTP Results for NOV62a				
Protein Accession Number	Protein/Organism/Length	NOV62a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9Z236	OLFACTORY RECEPTOR - Rattus norvegicus (Rat), 221 aa (fragment).	70..289 2..221	187/220 (85%) 202/220 (91%)	e-104
CAB43131	OLFACTORY RECEPTOR - Stenella coeruleoalba (Striped dolphin), 172 aa (fragment).	69..240 1..172	136/172 (79%) 148/172 (85%)	1e-73
Q9EPG2	M51 OLFACTORY RECEPTOR - Mus musculus (Mouse), 314 aa.	16..310 12..305	131/295 (44%) 191/295 (64%)	2e-67
Q9H208	HP4 OLFACTORY RECEPTOR - Homo sapiens (Human), 317 aa (fragment).	16..312 12..308	127/297 (42%) 180/297 (59%)	3e-65
Q920G5	OLFACTORY RECEPTOR P3 - Mus musculus (Mouse), 324 aa.	16..308 19..311	126/295 (42%) 180/295 (60%)	1e-62

Pfam analysis predicts that the NOV62a protein contains the domains shown in the Table 62E.

Table 62E. Domain Analysis of NOV62a			
Pfam Domain	NOV62a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	46..295	58/268 (22%) 179/268 (67%)	4.6e-38

Example 63.

The NOV63 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 63A.

Table 63A. NOV63 Sequence Analysis		
	SEQ ID NO: 189	1042 bp

NOV63a, CG59540-01 DNA Sequence	GACCTTTTCATCACACTCTGGTCATTACAACTGTTATTAAGGAATGGGGACAAGCA GCCCTGGGTCACAGAAATTCATCCTGGTTGGATTCCAGCTCAGTCAGAGATGGAGATC TTTCTCTCTTGCATCTTCTCCCTGTATATCTCTTCAGTCTACTGAGGAATGGCATGA ACATGGGACTCATCTGTCTGGATCCAGACTACACACCCCATATACTTCTTCCTGTC ACACTTGGCCGTCATTGACATATACTATGCTTCCAACAATTTGCTCAACATGCTGGAA AACCTAGTGAAACACAAAAAACTATCTCGTTTCATCTCTTGCAATATGCAGATGGCTT TGTATTTGACTTTTGTGCTGCAGTGTGCATGATTTTGGTGGTGATGCTCTATGACAG ATTGTGGCGATCTGCCATCCCTGCATTACACTGTTCATCATGAACCTGGAGAGTGTGC ACAGTACTGGCTATTACTTCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAA TTCTCCTTCTAAGGCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTTCGGTGA AATTCTGTCTGCTCAAACCTGGCCTGTGCAGACACCTGGATTAATGAAATTTTGTGTC TTTGCTGGTGGTGTGTTGTCTTAGTCGGGCCCCCTTTCCTTGATGCTGATCTCCTACA TGCGCATCCTCTTGGCCATCCTGAAGATCCAGTCAGGCGAGGGCCACAGAAAGGACTT CTCTACCTGCTCCTCCACCTCTGTGTGGTGGGTTCTTCTTGGCAACGCCATTGTGTC ATGTACATGGCCCCCAAGTCCGCCATCCCGAGGAGCAGCAGAAGGTCCTTTCCTGTG TTTGACAGCTTTGGAATCAGGTGCTGAACCCCTCTGATCTACAGCTTGAGGAATGC AGAGGTCAAGAGTGCCCCACAAGAGGGCCACTGAAGAAGGAGAGGCTGATGTTACAAT CTCAAAGGCACACAGGAGAGGGCTGCTCCGACAAATGGGAAGTGGCTTTT		
	ORF Start: ATG at 45	ORF Stop: TGA at 960	
	SEQ ID NO: 190	305 aa	MW at 34554.8kD
NOV63a, CG59540-01 Protein Sequence	MGDKQPWVTEFILVGFQLSAEMEIFLSCIFSLLYLFSLLRNGMNMGLICLDPRLHTPI YFFLSHLAVIDIYYASNLLNMLENLVKHKKTISFISCIQMALYLTFAAAVCMILVV MSYDRFVAICHPLHYTVIMNWRVCTVLAITSWACGFSALINLILLRLPFCGPQEVN HFFGEILSVLKLACADTWINEIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSGEG HRKDFSTCSSHLCVVGFFFANAIVMYMAPKSRHPPEEQKVLSLFCSLWNQVLNPLIY SLRNAEVKSAPQEGH		

Further analysis of the NOV63a protein yielded the following properties shown in Table 63B.

Table 63B. Protein Sequence Properties NOV63a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.3000 probability located in microbody (peroxisome)
SignalP analysis:	Likely cleavage site between residues 43 and 44

A search of the NOV63a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 63C.

Table 63C. Geneseq Results for NOV63a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV63a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU24758	Human olfactory receptor AOLFR259 - Homo sapiens, 310 aa. [WO200168805-A2, 20-SEP-2001]	1..300 1..299	258/300 (86%) 275/300 (91%)	e-146
AAG72952				e-144

	exploratorium sequence, SEQ ID NO: 2634 - Homo sapiens, 310 aa. [WO200127158-A2, 19-APR-2001]	1..299	272/300 (90%)	
AAG72377	Human OR-like polypeptide query sequence, SEQ ID NO: 2058 - Homo sapiens, 312 aa. [WO200127158-A2, 19-APR-2001]	1..300 1..299	255/300 (85%) 272/300 (90%)	e-144
AAG72169	Human olfactory receptor polypeptide, SEQ ID NO: 1850 - Homo sapiens, 312 aa. [WO200127158-A2, 19-APR-2001]	1..300 1..299	255/300 (85%) 272/300 (90%)	e-144
AAG71994	Human olfactory receptor polypeptide, SEQ ID NO: 1675 - Homo sapiens, 314 aa. [WO200127158-A2, 19-APR-2001]	1..300 1..299	225/300 (75%) 256/300 (85%)	e-129

In a BLAST search of public sequence databases, the NOV63a protein was found to have homology to the proteins shown in the BLASTP data in Table 63D.

Table 63D. Public BLASTP Results for NOV63a				
Protein Accession Number	Protein/Organism/Length	NOV63a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O95047	Olfactory receptor 2A4 - Homo sapiens (Human), 310 aa.	1..299 1..298	173/299 (57%) 217/299 (71%)	2e-92
O43885	OLFACTORY RECEPTOR - Homo sapiens (Human), 217 aa (fragment).	67..281 1..216	154/216 (71%) 182/216 (83%)	5e-88
O43888	OLFACTORY RECEPTOR - Homo sapiens (Human), 217 aa (fragment).	67..281 1..216	153/216 (70%) 182/216 (83%)	8e-88
Q96R48	OLFACTORY RECEPTOR - Homo sapiens (Human), 217 aa (fragment).	67..281 1..216	153/216 (70%) 181/216 (82%)	2e-87
Q96R47	OLFACTORY RECEPTOR - Homo sapiens (Human), 215 aa (fragment).	67..281 1..214	149/215 (69%) 175/215 (81%)	3e-84

PFam analysis predicts that the NOV63a protein contains the domains shown in the Table 63E.

Table 63E. Domain Analysis of NOV63a			
Pfam Domain	NOV63a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	47..290	55/270 (20%) 174/270 (64%)	9.7e-25

Example 64.

The NOV64 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 64A.

Table 64A. NOV64 Sequence Analysis			
	SEQ ID NO: 191	973 bp	
NOV64a, CG59280-01 DNA Sequence	AGGCACTAAATGAATATCTGTTTAATTCTATAAAGTAACAGAGTTTCTCTTCTCTGGAT TCCCACAGTTTGAAGATGGTAGCCTCCTCTTCTTCATTCCATTGTTTGTATCTACAT ATTCAATTGTCATTGGGAATCTTATTGTATTTTTCAGTCAGGGTGGATACCCGCTCTC CACAACCCCATGTATAATTTTATCAGCATTTTCTCATTTCGGAGATCTGGTACACAA CTGCCACAAATCCCAAGATGCTCTCCATCCTCATCAGCAGGCAGAGGACCATCTCCAT GGTTGGTTGCCTCTTGCAGATGTACTTCTTCCATTCACTGGGAAATTAGAGGGGATT TTGTTGACCACCATGGCCATTGATAGGTACGTTGCCATCTGTAACCTCTCCGCTACC CAACCATCATGACCCCGGGCTCTGTGTTCACTCTCTGTGGGTCCTGCATCTTTGG CTTCTTGTGTTGCTCCAGAGATTGCATGGATTTCACACTGCCCTTCTGTGGACCC AACCAAATCCACAGATCTTCTGTGATTTTGAACCTGTGCTGCGCTTGGCCTGTACAG ACACGTCATGATTCTGATTGAGGATGTGATCCATGCTGTGGCCATTGTATTCTCTGT CCTGATTATTGCCTTTTCTTATATCAGAATCATCACTGTAATCCTGAGGATTCCTCT GTTGAAGGCCCGCAGAAGGCCCTTTTCTACCTGTGCGGCCATCTTAGTGTCTTTCTGA TGTTCTATGGCAGTGTATCCCTCATGTACCTGCGTTTCTCTGCCACTTTCCACCGAT TTTGGACACAGCTGTTGCACTGATGTTTGCAGTTCTTGCTCCCTTTTCAAGCCATC ATCTATAGCTTTAGAAATAAGGACATGAAGATTGCAATTAAAAAGCTTTTCTGCCCTC AGAAGATGGTTAATTTATCTGTAGATTAATGCTAGCTCATAGGCA		
	ORF Start: ATG at 10	ORF Stop: TAA at 955	
	SEQ ID NO: 192	315 aa	MW at 35741.4kD
NOV64a, CG59280-01 Protein Sequence	MNICLIHKVTEFLFSGFPQFEDGSLFFIPLFVIYIFIVIGNLIVFFAVRVDTRLHNP MYNFISIFSFLEIWTYTTATIPKMLSILISRQRTISMVGCLLQMYFFHSLGNSEGILLT TMAIDRYVAICNPLRYPTIMTPGLCVQLSVGSCIFGLVLLPEIAWISTLFFCPGNQI HQIFCDFEPVRLACTDTSMILIEDVIHAVAIVFSVLIIAFSYIRIITVILRIPSVEG RQKAFSTCAHLSVFLMFYGSVSLMYLRFSAFPFILDVAALMFVAFLPFFNPPIYS FRNKDMKIAIKLFCPQKMNLSVD		
	SEQ ID NO: 193	929 bp	
NOV64b, CG59280-02 DNA Sequence	TCTTCTTCATTCCATTGTTTGTATCTACATATTCATTGTCTATTGGGAATCTTATTGT ATTTTTTGCAGTCAGGGTGGATACCCGCTCTCCACAACCCCATGTATAATTTATCAGC ATTTTCTCATTCTCGAGATCTGGTACACAACCTGCCACAATCCCAAGATGCTCTCCA TCCTCATCAGCAGGCAGAGGACCATCTCCATGGTTGGTTGCCTCTTGCAGATGTACTT CTTCCATTCACTGGGAAATTCAGAGGGGATTTGTTGACCACCATGGCCATTGATAGG TACGTTGCCATCTGTAACCTCTCCGCTACCCAACCATCATGACCCCGGGCTCTGTG TTCAGCTCTCTGTGGGGTCTGCATCTTTGGCTTTCTTGTGTTGCTCCAGAGATTGC ATGGATTTCCCACTGCCCTTCTGTGGACCCAACCAAATCCACAGATCTTCTGTGAT TTTGAACCTGTGCTGCGCTTGGCCTGTACAGACAGCTCCATGATTCTGATTGAGGATG TGATCCATGCTGTGGCCATTGTATTCTCTGTCTGATTATTGCTTTTCTTATATCAG AATCATCACTGTAATCCTGAGGATTCCCTCTGTTGAAGGCCGCCAGAAGGCCCTTTTCT ACCTGTGCCGCCCATCTTAGTGCTTTTCTGATGTTCTATGGCAGTGTATCCCTCATGT ACCTGCGTTTCTCTGCCACTTTCCACCGATTTTGGACACAGCTGTTGCACTGATGTT TGCAGTTCTTGCTCCCTTTTCAACCCATCATCTATAGCTTTAGAAATAAGGACATG AAGATTGCAATTAAGAGCTTTTCTGCCCTCAGAAGATGGTTAATTTATCTGTAGATT AATGCTAGCTCATAGGCACCTTTCACTGTGGATGTTACTCTAACACAATAAACCATAT A		
	ORF Start: TTC at 3	ORF Stop: TAA at 870	
	SEQ ID NO: 194	289 aa	MW at 32772.9kD

NOV64b, CG59280-02 Protein Sequence	FFIPLFVIYIFIVIGNLIVFFAVRVDTRLHNPMYNFISIFSFLFIWYTTATIPKMLSI LISRQRTISMVGCLLQMYFFHSLGNSEGILLTTMAIDRYVAICNPLRYPTIMTPGLCV QLSVGSCIFGFLVLLPEIAWISTLPFCGPNQIHQIFCDPEPVLRLACTDTSMILIEDV IHAVAIVFSVLIIAFSYIRIITVILRIPSVGRQKAFSTCAAHLVFLMFYGSVSLMY LRFSAFPPIILDTAVALMFAVLAPFFNPIIYSFRNKDMKIAIKKLFQPKMVLNSVD
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Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 64B.

Table 64B. Comparison of NOV64a against NOV64b.		
Protein Sequence	NOV64a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV64b	27..315 1..289	289/289 (100%) 289/289 (100%)

Further analysis of the NOV64a protein yielded the following properties shown in Table 64C.

Table 64C. Protein Sequence Properties NOV64a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.3000 probability located in microbody (peroxisome)
SignalP analysis:	Likely cleavage site between residues 54 and 55

A search of the NOV64a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 64D.

Table 64D. Geneseq Results for NOV64a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV64a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG71805	Human olfactory receptor polypeptide, SEQ ID NO: 1486 - Homo sapiens, 256 aa. [WO200127158-A2, 19-APR-2001]	59..314 1..256	255/256 (99%) 255/256 (99%)	e-145
AAG71803	Human olfactory receptor polypeptide, SEQ ID NO: 1484 - Homo sapiens, 315 aa. [WO200127158-A2, 19-APR-2001]	9..311 9..311	243/303 (80%) 267/303 (87%)	e-143

AAU24658	Human olfactory receptor AOLFR156 - Homo sapiens, 331 aa. [WO200168805-A2, 20-SEP-2001]	9..311 25..327	240/303 (79%) 264/303 (86%)	e-140
AAG71807	Human olfactory receptor polypeptide, SEQ ID NO: 1488 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	9..313 9..313	222/305 (72%) 259/305 (84%)	e-131
AAU24721	Human olfactory receptor AOLFR220 - Homo sapiens, 343 aa. [WO200168805-A2, 20-SEP-2001]	9..308 37..336	209/300 (69%) 242/300 (80%)	e-119

In a BLAST search of public sequence databases, the NOV64a protein was found to have homology to the proteins shown in the BLASTP data in Table 64E.

Table 64E. Public BLASTP Results for NOV64a				
Protein Accession Number	Protein/Organism/Length	NOV64a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9EPG2	M51 OLFACTORY RECEPTOR - Mus musculus (Mouse), 314 aa.	1..302 4..303	137/303 (45%) 194/303 (63%)	2e-71
Q9EPV0	M50 OLFACTORY RECEPTOR (OLFACTORY RECEPTOR M50) - Mus musculus (Mouse), 316 aa.	6..302 4..301	132/298 (44%) 191/298 (63%)	3e-71
Q9EPG1	M50 OLFACTORY RECEPTOR - Mus musculus (Mouse), 316 aa.	6..302 4..301	130/298 (43%) 190/298 (63%)	2e-70
Q9WU86	ODORANT RECEPTOR S1 - Mus musculus (Mouse), 324 aa.	1..310 12..321	133/313 (42%) 190/313 (60%)	4e-69
Q96KK4	DJ994E9.5 (OLFACTORY RECEPTOR, FAMILY 10, SUBFAMILY C, MEMBER 1 (HS6M1-17)) - Homo sapiens (Human), 306 aa.	9..314 2..306	137/307 (44%) 189/307 (60%)	9e-68

Pfam analysis predicts that the NOV64a protein contains the domains shown in the Table 64F.

Table 64F. Domain Analysis of NOV64a			
Pfam Domain	NOV64a Match Region	Identities/ Similarities for the Matched Region	Expect Value

7tm_1: domain 1 of 1	41..289	51/269 (19%) 179/269 (67%)	2.2e-33
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Example 65.

The NOV65 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 65A.

Table 65A. NOV65 Sequence Analysis			
	SEQ ID NO: 195	972 bp	
NOV65a, CG59568-01 DNA Sequence	GCATGGTGATCCTGTCTCTGGGAAAACCAAACGATGAGAGTGAATTCGTGCTTCAAGG ATTCTCTTCCATCAGACAGTTAAATATTTTCTCTTTATGATAATTTTAGTTTTCTAC ATCTTAACTGTTTCTGGAACATCCTCATTGTCTCTTAGTTTTAGTCAGACATCATC TCCACACCCCTATGTACTTCTCCTGGTGAACCTGTCTGTCTGGAGATCTGGTATAC CTCTAACATCATCCCCAAATGTTGCTGATTATCATAGCTGAAGAGAAGACTATCTCT GTGGCTGGCTGGCTGGCACAATTCTACTTCTTCGGATCCCTGGCTGCCACGGAGTGC TCTTGCTCACTGTGATGTCCTATGATCGCTACCTAGCCATCTGCCAGCCTCTTTGCTA CCGTGTCTCATGACTGGCCCCCTTTGCATCAGGCTAGCTGTGGCTCTTGGTTCTGC TGCTTCTCCTTACAGCAATCACCATGGTCTTGCTATGTAGACTAACCTTCTGTGGAG CCTATGAAACTGATCACTTCTTTGTGACTTCACCCCTCTGGTTCATCTCTCTGCA GGATACCTCAGTGACTGAGACATTGCCTTTGCCACCTCTTCTGCAGTAACCTGTATC CCATTTCTCTCATTGTAGCCTCCTACTCCTGCGTCCTTTCTGCTATCCTAAGAAATC CATCTTGACAGGCCAGAAAAAGGCCTTCTCCACCTGCTCTTCCCACCTCACTGTGGT CATAGTGTTTTATGGGACACTGATTGCCACATACCTTGTGCCCTCAGCCAACTCATC CAACTCTGTGCAAGGGTCTCTCTGCTCTACATCATCTGACACCCATGTTTAAAC CCATCATTTATAGCCTGAGAAATAGAGACATCCATGAAGCTCTGAAGAAGTGCTTGAG GAAGAAGTCAGGTGTTTGCCTTAGATAATACGAAAAGGAAAAAA		
	ORF Start: ATG at 3	ORF Stop: TAA at 954	
	SEQ ID NO: 196	317 aa	MW at 35713.4kD
NOV65a, CG59568-01 Protein Sequence	MVLISWENQTMREVFVLQGFSSIRQLNIFLPMIILVFYILTVSGNILIVLLVLRHHL HTPMYFLLVNLSCLEIWYTSNII PKMLLI IIAEBKTSVAGWLAQFYFFGSLAATECL LLTVMSYDRYLAICQPLCYRVLMTGPLCIRLAAGSWFCCFLITAITMVLRLTFCGP YETDHFPCDFPLVHLSMDTSVTETIAFATSSAVTLIPFLILIVASYSCVLSAILRI SCTGQKAFSTCSSHLTVVIVFYGTLLIATYLVPSANSSQLLCKGSSLLYIILTPMFNP IIYSLRNRDIHEALKKCLRKKSGVCLR		

Further analysis of the NOV65a protein yielded the following properties shown in Table 65B.

Table 65B. Protein Sequence Properties NOV65a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3888 probability located in mitochondrial inner membrane; 0.3030 probability located in mitochondrial intermembrane space
SignalP analysis:	Likely cleavage site between residues 45 and 46

A search of the NOV65a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 65C.

Table 65C. Geneseq Results for NOV65a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV65a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72527	Human OR-like polypeptide query sequence, SEQ ID NO: 2208 - Homo sapiens, 316 aa. [WO200127158-A2, 19-APR-2001]	1..316 1..316	315/316 (99%) 315/316 (99%)	0.0
AAG72231	Human olfactory receptor polypeptide, SEQ ID NO: 1912 - Homo sapiens, 316 aa. [WO200127158-A2, 19-APR-2001]	1..316 1..316	315/316 (99%) 315/316 (99%)	0.0
AAG72084	Human olfactory receptor polypeptide, SEQ ID NO: 1765 - Homo sapiens, 316 aa. [WO200127158-A2, 19-APR-2001]	1..316 1..316	315/316 (99%) 315/316 (99%)	0.0
AAG72700	Murine OR-like polypeptide query sequence, SEQ ID NO: 2382 - Mus musculus, 314 aa. [WO200127158-A2, 19-APR-2001]	1..308 3..308	154/308 (50%) 208/308 (67%)	2e-83
AAG71814	Human olfactory receptor polypeptide, SEQ ID NO: 1495 - Homo sapiens, 317 aa. [WO200127158-A2, 19-APR-2001]	8..311 5..308	142/304 (46%) 208/304 (67%)	7e-79

In a BLAST search of public sequence databases, the NOV65a protein was found to have homology to the proteins shown in the BLASTP data in Table 65D.

Table 65D. Public BLASTP Results for NOV65a				
Protein Accession Number	Protein/Organism/Length	NOV65a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9GZK7	Olfactory receptor 11A1 (Hs6M1-18) - Homo sapiens (Human), 315 aa.	1..308 1..306	147/308 (47%) 202/308 (64%)	4e-77
O13036	CHICK OLFACTORY RECEPTOR 7 - Gallus gallus (Chicken), 323 aa.	7..311 4..308	139/305 (45%) 198/305 (64%)	1e-76
Q9JKA6	OLFACTORY RECEPTOR P2 - Mus musculus (Mouse), 315 aa.	4..313 1..311	143/311 (45%) 194/311 (61%)	1e-75

Q9WU86	ODORANT RECEPTOR S1 - Mus musculus (Mouse), 324 aa.	14..308 21..315	144/295 (48%) 189/295 (63%)	2e-75
Q9UGF6	Olfactory receptor 5V1 (Hs6M1-21) - Homo sapiens (Human), 321 aa.	7..305 4..302	138/299 (46%) 199/299 (66%)	5e-75

PFam analysis predicts that the NOV65a protein contains the domains shown in the Table 65E.

Table 65E. Domain Analysis of NOV65a			
Pfam Domain	NOV65a Match Region	Identities/ Similarities for the Matched Region	Expect Value
granulin: domain 1 of 1	144..155	7/13 (54%) 11/13 (85%)	1.7
Trypan_glycop: domain 1 of 1	218..241	6/24 (25%) 21/24 (88%)	7.9
7tm_1: domain 1 of 1	44..293	53/268 (20%) 172/268 (64%)	1.5e-31

Example 66.

The NOV66 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 66A.

Table 66A. NOV66 Sequence Analysis			
	SEQ ID NO: 197	987 bp	
NOV66a, CG59224-01 DNA Sequence	CATCTTCCTATGTGTCATGTCTCCTCTTAATGACACAAAAATGGAAGTCCTTAGATTC CTCCTTATCGGGATCACTGGACTGGAGAAAAGTCGCACCTGGATATCCATTCTTTCT TATCTGTGTACCTTCTTTCTTGGATGGGTAATTTTACCGTCCTCTTTTATCAAGAC AGAGCAAAGCCTCCATGAACCTATGTATTATTGCTTTCCATGCTCTCCATCTCTGAC CTAGGGCTGTCTCTGTCTTCTTACCCATCACTTTGGGACTATTTCCTATTTTGATGTCC ATGAAATTCATGCAGCTCCATGCTTTGCCAGGAATTTTTTATCCATCTGTTTACAGT CAGTGAAGCCTCTGTACTGTCTGTAATGGCATTTGACTGGTATGTGGCAATCCACAGT CCTTTGAGATACAGCACTATCTTAAGTAGTCCAGAGCCATCAAAACAGGGGTTCTTC TGACTTCCAAGAAATGTTCTTTTGATCCTTCCACTGCCCTTTCTCTTGCAAAGGCTGAG ATATTGTCAATAAACCTGCTCTCCACTCCTATTGTCTCCACCAGGATGTCATGAAG CTGATGTGTTCTGACAACACAGTCAATGTTGTCTACGGACTCTGTGCAGGACTTTCTA CTATGCTGGACTTGGTGTATTATTACCTTCTCCTATATGATTTTAAAGGCTGTAAGG AATTGCTACCCCGAGACAGCAGTTCAAGGCCCTCAACACGTGCATCTCTCACATCTGT GCTGTGCTTATCTTCTATGTGCCACGCTGAGTGCTGCCATGCTCCACAGCTTTTGCCA GGGATGTGTCTCCTATGATCCACGTCCTCATGGCTGATATTTTCTGCTGGTGCCACC CCTGTGTAATCCCATCGTGTACTGTGTGAAGACCCACCAATCCGAGAAAAGGTTGTG GGGAAACTTTGTCCAAAAGTAAGTTGATCAAAGGAATGAGAAAGGGAATGAATGTATA A		
	ORF Start: ATG at 17	ORF Stop: TGA at 953	
	SEQ ID NO: 198	312 aa	MW at 35250.7kD
NOV66a, CG59224-01 Protein Sequence	MSPLNDTKMEVLRFLLLIGITGLEKSRTWISIPFLSVYLLSWMGNFTVLFPIKTEQSLH EPMYYLLSMLSISDLGLSLSSLPITLGLFLFDVHEIHAAPCFQAEFFIHLFTVSEASV LSVMAFDWYVAIHSPLRYSTILTSPIRAIKTGVLTSKNVLLILPLPFLQLRLRYCHQN		

LLSHSYCLHQDVMKLMCSNTNVVYGLCAGLSTMLDLVFITFSYMLRAVLGIATPR QQFKALNTCISHICAVLIFYVPTLSAAMLHQFARDVSPMIHVLMAIDFLLVPPLLNPI VYCVKTHQIREKVVGKLCPKVS

Further analysis of the NOV66a protein yielded the following properties shown in Table 66B.

Table 66B. Protein Sequence Properties NOV66a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.2007 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 50 and 51

A search of the NOV66a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 66C.

Table 66C. Geneseq Results for NOV66a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV66a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72488	Human OR-like polypeptide query sequence, SEQ ID NO: 2169 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	1..312 1..313	309/313 (98%) 309/313 (98%)	e-176
AAG71557	Human olfactory receptor polypeptide, SEQ ID NO: 1238 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	1..312 1..313	309/313 (98%) 309/313 (98%)	e-176
AAU24573	Human olfactory receptor AOLFR63 - Homo sapiens, 313 aa. [WO200168805-A2, 20-SEP-2001]	1..310 1..311	186/311 (59%) 246/311 (78%)	e-109
AAG71558	Human olfactory receptor polypeptide, SEQ ID NO: 1239 - Homo sapiens, 313 aa. [WO200127158-A2, 19-APR-2001]	1..310 1..311	185/311 (59%) 245/311 (78%)	e-108
AAU24682	Human olfactory receptor AOLFR181 - Homo sapiens, 312 aa. [WO200168805-A2, 20-SEP-2001]	1..307 1..306	188/308 (61%) 237/308 (76%)	e-106

In a BLAST search of public sequence databases, the NOV66a protein was found to have homology to the proteins shown in the BLASTP data in Table 66D.

Table 66D. Public BLASTP Results for NOV66a				
Protein Accession Number	Protein/Organism/Length	NOV66a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL35109	PROSTATE-SPECIFIC G PROTEIN-COUPLED RECEPTOR RA1C - Mus musculus (Mouse), 320 aa.	14..304 11..303	141/293 (48%) 199/293 (67%)	2e-77
O88628	Olfactory receptor 51E2 (G-protein coupled receptor RA1c) - Rattus norvegicus (Rat), 320 aa.	14..304 11..303	141/293 (48%) 200/293 (68%)	2e-77
CAC38935	SEQUENCE 9 FROM PATENT WO0131014 - Homo sapiens (Human), 318 aa.	5..304 6..306	145/302 (48%) 206/302 (68%)	2e-77
CAC37756	SEQUENCE 1 FROM PATENT WO0125434 - Homo sapiens (Human), 317 aa.	5..304 5..305	145/302 (48%) 206/302 (68%)	3e-77
Q9H255	Olfactory receptor 51E2 (Prostate specific G-protein coupled receptor) (HPRAJ) - Homo sapiens (Human), 320 aa.	14..304 11..303	139/293 (47%) 198/293 (67%)	2e-76

PFam analysis predicts that the NOV66a protein contains the domains shown in the Table 66E.

Table 66E. Domain Analysis of NOV66a			
Pfam Domain	NOV66a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 2	43..151	30/111 (27%) 73/111 (66%)	6.3e-14
7tm_1: domain 2 of 2	212..292	16/92 (17%) 52/92 (57%)	0.052

Example 67.

The NOV67 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 67A.

Table 67A. NOV67 Sequence Analysis			
	SEQ ID NO: 199	994 bp	
NOV67a, CG59222-01 DNA Sequence	<p>CACAATGTCTGTCTTCAATAGTTCTGCCTTATACCCTCGTTCTCCTCTAACGGGCTCTCAGGCCTTGAAAGCAGATATGACTTGATTTCCCTGCCATCTTCTTGGTTTATGCCCTCTCAATTGCCGGGAACATTAGCATCCTCTTCATTATCAGAACTGAGTCTTCCCTCCCAACCGATGTATTACTTTCTGTCAATGCTGGCATTCACTGACCTGGGCTATCTAAACTACCTTACCTACCATGTTCACTGTCTTCTGGTTCCATGCCCGGGAGATCTCCTTCTATGCTTGTCTGGTCCAAATGTACTTCATTTCATGTTTTCTCGATTATTGAGTCAGCTGTACTCTGGCTATGGCCTTTGACTGCTTTATAGCAATCTGTGAACCTTGGCCTATGCCATCCTAACCAATGATGTAATCATTGGGATTGGGTGGCAATTGCTGGAAGGCCCTGGCTCTGGTCTTTCAGCTTCTTTCCTCTTGAAGAGGCTTCAATATCATGATGTCAATATTCTGTCTACCTCTTCTGCTGCACACGAGACCTCATAAAGACGACTGTATCCAATGTGTCGAGTCAGCAGCATCTATGGCCTCATGGTGGTCATCTGTTCCATGGGACTTGATCAGTGCTTCTCCTCTCTCTATGTCTCATCCTGGGCACAGTGTGAGTATAGCCTCAAGGCAGAGAGAGTGAGAGCCCTCAATACTTGCATCTCCCACATCTGTGCTGTACTACCTTCTATACACCAATGATTGGGCTATCTATGATCCATCGCTATGGACAGAATGCTCCTCAATTGTCCATGTGCTGATGGCCAATGTCTACTTGCTGGTTCCACCTCTCATGAACCCGTTGTCTACAGTGTTAAGACCAAGCAGATTTCGTGACAGAATCTTCAATAAATTCAAGAAACATGAAGTGTAGATGACAGAGATTCTGAACATAACTTTCCTCCATTCCCTATATATT</p>		
	ORF Start: ATG at 5	ORF Stop: TAG at 944	
	SEQ ID NO: 200	313 aa	MW at 35044.2kD
NOV67a, CG59222-01 Protein Sequence	<p>MSVFNSSALYPRFLLTGLSGLESRYDLISLPFLVYATSIAGNISILFIIRTESSLHQPMPYYFLSMLAFTDLGLSNTTLPTMFSVFWFHAREISFNACLVQMYFIHVFSIIESAVLLAMAFDFCIAICEPLRYAAILTNDVVIIGIGLAAGRALALVFPASFLKRLQYHDVNLISYLFCLHQDLIKTTVSNCRVSSIYGLMVVICSMGLDSVLLLLSVYLILGTVLSIASIAAERVRLNTCISHICAVLTFYTPMIGLSMIHRYGQNASSIVHVLNANVYLLVPLMNPVVYSVKTKQIRDRIFNKFKKHEV</p>		

Further analysis of the NOV67a protein yielded the following properties shown in Table 67B.

Table 67B. Protein Sequence Properties NOV67a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4047 probability located in mitochondrial inner membrane; 0.4000 probability located in Golgi body; 0.3480 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV67a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 67C.

Table 67C. Geneseq Results for NOV67a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV67a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72605	Human OR-like polypeptide query sequence, SEQ ID NO: 2286 - Homo sapiens, 318 aa. [WO200127158-A2, 19-APR-2001]	1..309 4..313	295/310 (95%) 298/310 (95%)	e-163
AAG71519	Human olfactory receptor polypeptide, SEQ ID NO: 1200 - Homo sapiens, 318 aa. [WO200127158-A2, 19-APR-2001]	1..309 4..313	295/310 (95%) 298/310 (95%)	e-163
AAU24683	Human olfactory receptor AOLFR182 - Homo sapiens, 314 aa. [WO200168805-A2, 20-SEP-2001]	5..308 9..312	178/304 (58%) 235/304 (76%)	e-102
AAG71715	Human olfactory receptor polypeptide, SEQ ID NO: 1396 - Homo sapiens, 314 aa. [WO200127158-A2, 19-APR-2001]	5..308 9..312	178/304 (58%) 235/304 (76%)	e-102
ABB44526	Human GPCR4a polypeptide SEQ ID NO 11 - Homo sapiens, 315 aa. [WO200174904-A2, 11-OCT-2001]	5..308 6..309	169/304 (55%) 227/304 (74%)	2e-96

In a BLAST search of public sequence databases, the NOV67a protein was found to have homology to the proteins shown in the BLASTP data in Table 67D.

Table 67D. Public BLASTP Results for NOV67a				
Protein Accession Number	Protein/Organism/Length	NOV67a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9H344	Olfactory receptor 51I2 (HOR5'beta12) - Homo sapiens (Human), 312 aa.	13..308 12..307	154/296 (52%) 221/296 (74%)	2e-91
Q9H2C8	ODORANT RECEPTOR HOR3'BETA1 - Homo sapiens (Human), 321 aa.	2..308 10..316	160/307 (52%) 216/307 (70%)	5e-89
Q9H343	Olfactory receptor 51I1 (HOR5'beta11) - Homo sapiens (Human), 314 aa.	5..312 5..313	156/309 (50%) 223/309 (71%)	9e-89

AAL35109	PROSTATE-SPECIFIC G PROTEIN-COUPLED RECEPTOR RA1C - Mus musculus (Mouse), 320 aa.	13..309 11..307	148/297 (49%) 207/297 (68%)	2e-86
Q924X8	OLFACTORY RECEPTOR S85 - Mus musculus (Mouse), 314 aa.	2..304 3..305	150/303 (49%) 221/303 (72%)	1e-85

Pfam analysis predicts that the NOV67a protein contains the domains shown in the Table 67E.

Table 67E. Domain Analysis of NOV67a			
Pfam Domain	NOV67a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	42..138	24/99 (24%) 67/99 (68%)	7.8e-14

Example 68.

The NOV68 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 68A.

Table 68A. NOV68 Sequence Analysis			
	SEQ ID NO: 201	981 bp	
NOV68a, CG59220-01 DNA Sequence	GCAATGAGAAACCGCAGTGTTCCTCCCTGAGTTGTCTCCTCGGGCTGTCAGCTGGCC CCCAGACCCAGACTCTGCTCTTTGTGCTGTTTCGTGGTGATTGGCTCCTGACTGTGAT GGGAAACCTGCTGCTGCTGGTGGTGATTAAATGCTGATTCTTGCCCTCCACACCCCAT TACTTCTTCTCTGGGACAATTGTCCTTCTTGGATCTCTGCCATTCTCTGTCACTGCAC CTAAGCTGTTGGAGAACCCTCCTGTCTGAGAAGAAAACCATCTCAGTAGAGGGCTGCAT GGCTCAGGTCTTCTTTGTGTTTGCCACTGGGGGCACTGAATCCTCCCTGCTTGCTGTG ATGGCCTATGACCGCTATGTTGCCATCAGCTCTCCTTTGCTCTATGGCCAAGTGATGA ACAGACAGCTGTGTTCAAGGCTGGTGGGGGCTCATGGGGCTTGGCTTTTCTGGATGC CCTCATCAATATCCTTGTAGCTCTCAATTTAGACTTCTGTGAGGCTCAAAATATCCAC CACTTCAGCTGTGAGCTGCCCTCTCTCTATCCTTTGTCTTGCTCTGATGTGTGAGCAA GTTTTACCACCTGCTCTGCTCCAGCTTCTGCAATTCTTTGGAATTTTCTCATGAT ATTCTTGTCTTATATTGCAATTTGTGCCACCATCCTGAGGATCAGCTCCACTACAGGC AGAAGCAAAGCCTTCTCCACCTGCTCCTCCACCTCACTGCAGTGATTTTCTTTTATG GCTCCGATTACTCCGCTATCTCATGCCAAATTCAGGATCCATTCAAGAGCTGATCTT CTCCTTGCAGTACAGCGTGATCACTCCCATGCTGAATCTCCTCATTTACAGCCTGAAG AACAGGGAGGTGAAGGCAGCTGTGAGAAGAACATTGAGAAATATTTCTAGTGTTTCA ATAGACTTATGAAATCAGAATGATGAGGGAAGTGGATAGAACTGCAACAAGCA		
	ORF Start: ATG at 4	ORF Stop: TAG at 919	
	SEQ ID NO: 202	305 aa	MW at 33732.3kD
NOV68a, CG59220-01 Protein Sequence	MRNRSVVEFVLLGLSAGPQTQTLFVLFVVICLLTVMGNLLLLLVINADSLHTPMY FFLGQLSFLDLCHSSVTAPKLENNLSEKKTISVEGCMAQVFFVFATGGTESSLLAVM AYDRYVAISSPLLYGQVMNRQLCSGLVGGSWGLAFLDALINILVALNLDCEAQNIHH FSCELPISLYPLSCSDVSASFSTLLCSSLPHFFGNFLMIFLSYICILSTILRISSTTGR SKAFSTCSSHLTAVIFFYGSGLRLYMPNSGSIQELIFSLQYSVITPMLNLLIYSLKN REVKA AVRRTLRLKYF		

Further analysis of the NOV68a protein yielded the following properties shown in Table 68B.

Table 68B. Protein Sequence Properties NOV68a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 50 and 51

A search of the NOV68a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 68C.

Table 68C. Geneseq Results for NOV68a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV68a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU24771	Human olfactory receptor AOLFR328 - Homo sapiens, 312 aa. [WO200168805-A2, 20-SEP-2001]	3..304 5..306	212/302 (70%) 251/302 (82%)	e-120
AAG98585	Mouse olfactory receptor 7 - Mus musculus domesticus, 214 aa. [WO200146262-A2, 28-JUN-2001]	66..279 1..214	144/214 (67%) 169/214 (78%)	1e-78
AAG72680	Murine OR-like polypeptide query sequence, SEQ ID NO: 2362 - Mus musculus, 337 aa. [WO200127158-A2, 19-APR-2001]	3..305 20..324	148/305 (48%) 201/305 (65%)	3e-74
AAG71546	Human olfactory receptor polypeptide, SEQ ID NO: 1227 - Homo sapiens, 315 aa. [WO200127158-A2, 19-APR-2001]	3..301 5..306	143/302 (47%) 201/302 (66%)	2e-73
AAG66701	Human GPCR1 polypeptide - Homo sapiens, 311 aa. [WO200160865-A2, 23-AUG-2001]	3..301 5..306	143/302 (47%) 201/302 (66%)	2e-73

In a BLAST search of public sequence databases, the NOV68a protein was found to have homology to the proteins shown in the BLASTP data in Table 68D.

Table 68D. Public BLASTP Results for NOV68a				
Protein Accession Number	Protein/Organism/Length	NOV68a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JM36	OLFACTORY RECEPTOR - Mus musculus domesticus (western European house mouse), 214 aa (fragment).	66..279 1..214	144/214 (67%) 169/214 (78%)	5e-78
Q9QZ18	OLFACTORY RECEPTOR - Mus musculus (Mouse), 312 aa.	3..299 5..303	142/299 (47%) 193/299 (64%)	2e-72
Q9EPG6	B1 OLFACTORY RECEPTOR - Mus musculus (Mouse), 314 aa.	3..299 5..303	140/299 (46%) 196/299 (64%)	2e-72
P23266	Olfactory receptor-like protein F5 - Rattus norvegicus (Rat), 313 aa.	3..305 5..309	142/305 (46%) 196/305 (63%)	9e-72
Q9EQA3	ODORANT RECEPTOR K30 - Mus musculus (Mouse), 311 aa.	3..305 5..310	143/306 (46%) 202/306 (65%)	2e-71

PFam analysis predicts that the NOV68a protein contains the domains shown in the Table 68E.

Table 68E. Domain Analysis of NOV68a			
Pfam Domain	NOV68a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	39..286	54/268 (20%) 169/268 (63%)	1.7e-29

Example 69.

The NOV69 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 69A.

Table 69A. NOV69 Sequence Analysis		
	SEQ ID NO: 203	957 bp
NOV69a, CG59218-01 DNA Sequence	GTCCACAATGGCCAATCAGACTGTGGTGACTGAGTTCTTCTCCAAGGCCTGACGGAT ACCAAAGAGCTTCAGGTGGCTGTTTTCTGCTCCTGCTGCTTGCCCTACCTTGTGACTG TCTCTGGGAACCTGATCATCATCAGCCTGACCTTGCTGGACACCCGCTGCAGACATC TATGTACTTATTTTCCAGAATCTGTCTGCTTAGAAATTTGGTTCCAGACAGTCATC GTGCCCAAGATGCTCAACATGGCCATGGGGACCAAGACCGTTAGCTTTGCTGGGT GCATTACCCAGGACTTTTCTTTCCACATCTTCTGGGGGCCACAGAGTTCTTCTCCT CACAGCCATGGCCTATGACCAGTATATGCCATCTGCAAGCCCTCCACTACCCCATG CTCATAAGTAGTAGAGTCTGCACACAGCTCATCCTCACCTGCTGGCTACTAGGTTTCT CCTTCATCATCATGCCTGTCTCCTGACCAGTCAGCTTCCATTCTGTGATACCCACAT CAAGCATTTCTTCTGTGACTACACGCTCTAATGGAGGTGGTCTGCAGTGGGCCAAAG GTGCTGGAGATGGTGATTTTACCCTGGCCTTAGTAGCACTGTTTGGCACCTTGGTAC	

	TCATCACCCCTGTCCTATGTCCAGATCATCCAGACAATTGTCAGAAATCCCCGCTGTCCA GGAGAGGAAGAAGGCTTCTCTACCTGTTCTCTCATGTCATTATGGTTACCATGTGT TATGACAGCTGCTTCTTTATGTATGTCAAGCCCTCTCCAGGAAAGTGGGTGATGTCA ACAAGGGAGTGTCTTAATCAATACAATTATTGCCCCACTGTTAAATCCCTTCATCTG TACTCTGAGGAACCAACAAGTTAAGCAGGTAATGAAAGACCTAGTCAGAAAAATGACT TTGTTCCAAATAAATAAGGCCCTAAAA		
	ORF Start: ATG at 8		ORF Stop: TAA at 944
	SEQ ID NO: 204	312 aa	MW at 35358.1kD
NOV69a, CG59218-01 Protein Sequence	MANQTVVTEFFLQGLTDTKELQVAVFLLLLAYLVTVSGNLI IISLTLLDTRLQTSMY LFLQNLSCLEIWFQTVIVPKMLLNIAMGKTVSFAGCITQDFFPHLLGATEFFLLTA MAYDQYIAICKPLHYPLISSRVCTQLILTCWLLGFSFIIMPVILTSQLPFCDTTHKH FFCDYTPLMEVVCSGPKVLEMVDFTLALVALFGLVLITLSYVQIIQITIVRIPAVQER KKAFFSTCSSHVMVTCYDSCFFMYVKPSPGKWVDVNGVSLINTIIAPLLNPFICTL RNQQVKQVMKDLVRKMTLQNK		

Further analysis of the NOV69a protein yielded the following properties shown in Table 69B.

Table 69B. Protein Sequence Properties NOV69a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.0300 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 40 and 41

A search of the NOV69a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 69C.

Table 69C. Geneseq Results for NOV69a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV69a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72538	Human OR-like polypeptide query sequence, SEQ ID NO: 2219 - Homo sapiens, 313 aa. [WO200127158-A2, 19-APR-2001]	1..312 1..313	284/317 (89%) 293/317 (91%)	e-157
AAG72229	Human olfactory receptor polypeptide, SEQ ID NO: 1910 - Homo sapiens, 313 aa. [WO200127158-A2, 19-APR-2001]	1..312 1..313	284/317 (89%) 293/317 (91%)	e-157
AAU24761	Human olfactory receptor AOLFR112B - Homo sapiens, 309 aa. [WO200168805-A2, 20-SEP-2001]	1..306 1..306	173/307 (56%) 227/307 (73%)	2e-96

AAU24765	Human olfactory receptor AOLFR225B - Homo sapiens, 309 aa. [WO200168805-A2, 20-SEP-2001]	1..306 1..306	166/307 (54%) 227/307 (73%)	2e-94
AAG66353	GPCR partial protein sequence - Unidentified, 313 aa. [WO200155179- A2, 02-AUG-2001]	1..309 1..310	160/311 (51%) 209/311 (66%)	4e-87

In a BLAST search of public sequence databases, the NOV69a protein was found to have homology to the proteins shown in the BLASTP data in Table 69D.

Table 69D. Public BLASTP Results for NOV69a				
Protein Accession Number	Protein/Organism/Length	NOV69a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9Z1V0	OLFACTORY RECEPTOR C6 - Mus musculus (Mouse), 313 aa.	1..309 1..310	160/311 (51%) 209/311 (66%)	2e-86
CAC88326	SEQUENCE 18 FROM PATENT WO0164879 - Homo sapiens (Human), 331 aa.	8..306 12..311	142/301 (47%) 200/301 (66%)	4e-78
CAC88328	SEQUENCE 22 FROM PATENT WO0164879 - Homo sapiens (Human), 331 aa.	8..306 12..311	142/301 (47%) 198/301 (65%)	2e-77
CAC88327	SEQUENCE 20 FROM PATENT WO0164879 - Homo sapiens (Human), 331 aa.	8..306 12..311	141/301 (46%) 198/301 (64%)	8e-77
O70270	OLFACTORY RECEPTOR-LIKE PROTEIN - Rattus norvegicus (Rat), 327 aa.	3..308 11..316	136/307 (44%) 208/307 (67%)	4e-76

PFam analysis predicts that the NOV69a protein contains the domains shown in the Table 69E.

Table 69E. Domain Analysis of NOV69a			
Pfam Domain	NOV69a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	39..244	47/214 (22%) 147/214 (69%)	1.9e-25

Example 70.

The NOV70 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 70A.

Table 70A. NOV70 Sequence Analysis			
	SEQ ID NO: 205	962 bp	
NOV70a, CG59216-01 DNA Sequence	CATCTTCCTATGTGTCATGTCTCCTCTTAATGACACAAAAATGGAAGTCCTTAGATTC CTCCTTATCGGGATCACTGGACTGGAGAAAAGTCGCACCTGGATATCCATTCTTTCT TATCTGTGTACCTTCTTTCTTGGATGGGTAATTTTACCGTCCTCTTTTTTATCAAGAC AGAGCAAAGCCTCCATGAACCTATGTATTATTGCTTTCCATGCTCTCCATCTCTGAC CTAGGGCTGTCTGTCTTCTTACCCATCACTTTGGGACTATTCTTATTGTATGTCC ATGAAATTCATGCAGCTCCATGCTTTGCCAGGAATTTTTATCCATCTGTTTACAGT CAGTGAAGCCTCTGTACTGTCTGTAATGGCATTGACTGGTATGTGGCAATCCACAGT CCTTTGAGATACAGCACTATCTTAAGTAGTCCCAGAGCCATCAAAACAGGGGTTCTTC TGACTTCCAAGAATGTTCTTTTGATCCTTCCACTGCCCTTTCTCTTGCAAAGGCTGAG ATATTGTCAAAAACCTGCTCTCCCACTCCTATTGTCTCCACAGGATGTCTATGAAG CTGATGTGTTCTGACAACACAGTCAATGTTGTCTACGGACTCTGTGCAGGACTTTCTA CTATGCTGGACTTGGTGTATTACCTTCTCCTATATTATGATTTTAAGGGCTGTACT GGGAATTGCTACCCACAGACAGCAGTTCAAGGCCCTCAACACGTGCATCTCTCACATC TGTGCTGTGCTTATCTTCTATGTGCCACGCTGAGTGTGCCATGCTCCACCAAGTTG CCAGGGATGTGTCTCCTATGATCCACGTCTCATGGCTGATATTTTCTGCTGGTGCC ACCCCTGTTGAATCCCATCGTGTACTGTGTGAAGACCCACCAATCCGAGAAAAGGTT GTGGGGAACCTTTGTCCAAAAGTAAGTTGATCAA		
	ORF Start: ATG at 17	ORF Stop: TGA at 956	
	SEQ ID NO: 206	313 aa	MW at 35363.9kD
NOV70a, CG59216-01 Protein Sequence	MSPLNDTKMEVLRFLLLIGITGLEKSRTWISIPFLSVYLLSWMGNFTVLFFIKTEQSLH EPMYLLSMLSISDLGLSLSSLPITLGLFLFDVHEIHAAPCPAQEFFIHLFTVSEASV LSVMAFDWYVAIHSPLRYSTILTSPIRAIKTGVLITSKNVLLILPLPFLQLRLRYCHQN LLSHSYCLHQDVMKLMCSDNTNVVYGLCAGLSTMLDLVFTFSYIMILRAVLGIATP RQQFKALNTCISHICAVLIFYVPTLSAAMLHQFARDVSPMIHVLMAIDIFLLVPPLLNP IVYCVKTHQIREKVVGKLCPKVS		

Further analysis of the NOV70a protein yielded the following properties shown in Table 70B.

Table 70B. Protein Sequence Properties NOV70a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.2007 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 50 and 51

A search of the NOV70a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 70C.

Table 70C. Geneseq Results for NOV70a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV70a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72488	Human OR-like polypeptide query sequence, SEQ ID NO: 2169 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	1..313 1..313	310/313 (99%) 310/313 (99%)	e-178
AAG71557	Human olfactory receptor polypeptide, SEQ ID NO: 1238 - Homo sapiens, 319 aa. [WO200127158-A2, 19-APR-2001]	1..313 1..313	310/313 (99%) 310/313 (99%)	e-178
AAU24573	Human olfactory receptor AOLFR63 - Homo sapiens, 313 aa. [WO200168805-A2, 20-SEP-2001]	1..311 1..311	186/311 (59%) 246/311 (78%)	e-110
AAG71558	Human olfactory receptor polypeptide, SEQ ID NO: 1239 - Homo sapiens, 313 aa. [WO200127158-A2, 19-APR-2001]	1..311 1..311	185/311 (59%) 245/311 (78%)	e-109
AAU24682	Human olfactory receptor AOLFR181 - Homo sapiens, 312 aa. [WO200168805-A2, 20-SEP-2001]	1..308 1..306	188/308 (61%) 238/308 (77%)	e-107

In a BLAST search of public sequence databases, the NOV70a protein was found to have homology to the proteins shown in the BLASTP data in Table 70D.

Table 70D. Public BLASTP Results for NOV70a				
Protein Accession Number	Protein/Organism/Length	NOV70a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC38935	SEQUENCE 9 FROM PATENT WO0131014 - Homo sapiens (Human), 318 aa.	5..305 6..306	145/302 (48%) 207/302 (68%)	5e-79

AAL35109	PROSTATE-SPECIFIC G PROTEIN-COUPLED RECEPTOR RA1C - Mus musculus (Mouse), 320 aa.	14..305 11..303	141/293 (48%) 199/293 (67%)	7e-79
CAC37756	SEQUENCE 1 FROM PATENT WO0125434 - Homo sapiens (Human), 317 aa.	5..305 5..305	145/302 (48%) 207/302 (68%)	7e-79
O88628	Olfactory receptor 51E2 (G-protein coupled receptor RA1c) - Rattus norvegicus (Rat), 320 aa.	14..305 11..303	141/293 (48%) 200/293 (68%)	7e-79
Q9H255	Olfactory receptor 51E2 (Prostate specific G-protein coupled receptor) (HPRAJ) - Homo sapiens (Human), 320 aa.	14..305 11..303	139/293 (47%) 198/293 (67%)	7e-78

Pfam analysis predicts that the NOV70a protein contains the domains shown in the Table 70E.

Table 70E. Domain Analysis of NOV70a			
Pfam Domain	NOV70a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 2	43..151	30/111 (27%) 73/111 (66%)	6.3e-14
YCF9: domain 1 of 1	208..262	10/59 (17%) 31/59 (53%)	7.5
7tm_1: domain 2 of 2	212..293	18/93 (19%) 55/93 (59%)	0.00034

Example 71.

The NOV71 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 71A.

Table 71A. NOV71 Sequence Analysis		
	SEQ ID NO: 207	995 bp
NOV71a, CG59214-01 DNA Sequence	GCACAATGTCTGTCTTCAATAGTTCTGCCTTATACCCTCGCTTCTCTTAACGGGCCT CTCAGGCCTTGAAAGCAGATATGACTTGATTCCCTGCCCATCTTCTTGGTTTATGCC ACCTCAATTGCGGGGAACATTAGCATCCTCTTCATTATCAGAACTGAGTCTTCCCTCC ACCAACCGATGATTACTTTCTGTCAATGCTGGCATTCACTGACCTGGGCCTATCTAA CACTACCTTACCTACCATTGTTCACTGTCTTCTGGTTCCATGCCCGGAGATCTCCTTC AATGCTTGCTGGTCCAAATGTACTTCATTATGTTTCTCGATTATTGAGTCAGCTG TACTCCTGGCTATGGCCTTTGACTGCTTTATAGCAATCTGTGAACCTTGCGCTATGC AGCCATCCTAACCAATGATGTAATCATGGGATTGGGTTGGCAATTGCTGGAAGGGCC TTGGCTCTGGTCTTCCAGCTTCTTCTCTTGAAGAGGCTTCAATATCATGATGTCA ATATTCTGTCTACCTCTTCTGCCTGCACGAGACCTCATAAAGACGACTGTATCCAA CTGTCGAGTCAGCATCTATGGCCTCATGGTGGTCATCTGTTCCATGGGACTTGAT TCAGTGCTTCTCCTCTCTCTATGTCCTCATCCTGGGCACAGTGTGAGTATAGCCT	

	CCAAGGCAGAGAGAGTGAGAGCCCTCAATACTTGCATCTCCACATCTGTGCTGTACT CACCTTCTATACACCAATGATTGGGCTATCTATGATCCATCGCTATGGACAGAATGCT TCCTCAATTGTCCATGTGCTGATGGCCAATGTCTACTTGCTGGTTCCACCTCTCATGA ACCCCGTTGTCTACAGTGTAAAGACCAAGCAGATTCTGTACAGAATCTTCAATAAATT CAAGAAACATGAAGTGTAGATGACAGAGATTCTGAAACATACTTTCCCTCCATTCCC CATATATTT		
	ORF Start: ATG at 6	ORF Stop: TAG at 945	
	SEQ ID NO: 208	313 aa	MW at 35044.2kD
NOV71a, CG59214-01 Protein Sequence	MSVFNSALYPRFLTGLSGLESRYDLISLPFLVYATSIAGNISILFIIRTESSLHQ PMYYFLSMLAFTDLGLSNTTLPTMFSVFWFHAREISFNACLVQMYFIHVFSIIIESAVL LAMAFCFIAICEPLRYAAILTNDVIIIGILAAGRALALVFPASFLKRLQYHDVNI LSYLFCLHQDLIKTTVSNCRVSSIYGLMVVICSMGLDSVLLLLSYVLILGTVLSIASK AERVRLNTCISHICAVLTFYTPMIGLSMIHRYQNASSIVHVLMAVYLLVPLMNP VVYSVKTKQIRDRIFNKFKKHEV		

Further analysis of the NOV71a protein yielded the following properties shown in Table 71B.

Table 71B. Protein Sequence Properties NOV71a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4047 probability located in mitochondrial inner membrane; 0.4000 probability located in Golgi body; 0.3480 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV71a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 71C.

Table 71C. Geneseq Results for NOV71a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV71a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG72605	Human OR-like polypeptide query sequence, SEQ ID NO: 2286 - Homo sapiens, 318 aa. [WO200127158-A2, 19-APR-2001]	1..309 4..313	295/310 (95%) 298/310 (95%)	e-163
AAG71519	Human olfactory receptor polypeptide, SEQ ID NO: 1200 - Homo sapiens, 318 aa. [WO200127158-A2, 19-APR-2001]	1..309 4..313	295/310 (95%) 298/310 (95%)	e-163
AAU24683	Human olfactory receptor	5..308 9..312	178/304 (58%) 235/304 (76%)	e-102

	aa. [WO200168805-A2, 20-SEP-2001]			
AAG71715	Human olfactory receptor polypeptide, SEQ ID NO: 1396 - Homo sapiens, 314 aa. [WO200127158-A2, 19-APR-2001]	5..308 9..312	178/304 (58%) 235/304 (76%)	e-102
ABB44526	Human GPCR4a polypeptide SEQ ID NO 11 - Homo sapiens, 315 aa. [WO200174904-A2, 11-OCT-2001]	5..308 6..309	169/304 (55%) 227/304 (74%)	2e-96

In a BLAST search of public sequence databases, the NOV71a protein was found to have homology to the proteins shown in the BLASTP data in Table 71D.

Table 71D. Public BLASTP Results for NOV71a				
Protein Accession Number	Protein/Organism/Length	NOV71a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9H344	Olfactory receptor 51I2 (HOR5 ^{beta} 12) - Homo sapiens (Human), 312 aa.	13..308 12..307	154/296 (52%) 221/296 (74%)	2e-91
Q9H2C8	ODORANT RECEPTOR HOR3 ^{BETA} 1 - Homo sapiens (Human), 321 aa.	2..308 10..316	160/307 (52%) 216/307 (70%)	5e-89
Q9H343	Olfactory receptor 51I1 (HOR5 ^{beta} 11) - Homo sapiens (Human), 314 aa.	5..312 5..313	156/309 (50%) 223/309 (71%)	9e-89
AAL35109	PROSTATE-SPECIFIC G PROTEIN-COUPLED RECEPTOR RA1C - Mus musculus (Mouse), 320 aa.	13..309 11..307	148/297 (49%) 207/297 (68%)	2e-86
Q924X8	OLFACTORY RECEPTOR S85 - Mus musculus (Mouse), 314 aa.	2..304 3..305	150/303 (49%) 221/303 (72%)	1e-85

PFam analysis predicts that the NOV71a protein contains the domains shown in the Table 71E.

Table 71E. Domain Analysis of NOV71a			
Pfam Domain	NOV71a Match Region	Identities/ Similarities for the Matched Region	Expect Value
7tm_1: domain 1 of 1	42..138	24/99 (24%) 67/99 (68%)	7.8e-14

Example 72.

The NOV72 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 72A.

Table 72A. NOV72 Sequence Analysis			
	SEQ ID NO: 209	1004 bp	
NOV72a, CG59211-01 DNA Sequence	CTTCTCATCTTTTCCCTCAAATACTGGGATGTCCATTCTCAATACCTCTGAAATGGAA ATCTCTATTTTCTACTTGGTTGGGATCCCAGGTTTGGAGCATGCCAATATTTGGATCT CTATCCCCCATATGTCTCATGTACACTGTTGCTATCCTAGGGAATTGTACCATTCGTGT TTTCATAAAACAGAGCCTTCTTGCATGAGCCCATGTACTATTTTCTCTCCATGTTG GCTCTCTCTGACCTGGGACTATCCCTCTCCTCTCTCCCTACCATGTTAAGGATTTTCC TGTTCAATGCTCCAGGAATTTCCCTGATGCCTGTATTGCTCAAGAGTTTTCATCCA TGGATTCTCAGCTATGGAGTCATCTGTACTTCTTATAATGTCCTTTGATCGCTTTATT GCCATCTGCAACCCCTGAGATACACTTCCATCCTCACCAGTGCCAGAGTCATTCAAA TTGGGCTTGCTTTTCTCTCAAAAATGTTTGTGTGATCCTCCCATTTCTTTCACTCT AAAACATCTAAAATATTGTAAGAAGAACCTCCTGTCCCAATCCTACTGCCTCCATCAA GATGTCATGAAACTGGCCTGCACTGACAACAAGGTCAACATCATCTATGGCTTATTTG TGGCTCTCACAGGCATCCTAGACTTGACATTTATTTTCATGTCCTACATGTTGATACT GAAAGCAGTGTGTGAGCATAGCATCAAGAAAGAAAAGGCTCAAGGTCTCAATACATGT GTTTCCACATCTGTGCTGTGCTCATCTTCTATGTGCCATTATCTCCCTAGCTGTCA TCTACCGGTTTGCCAAACACAGTTTCCCAATCACTAGGATCCTCATAGCTGATGCTTT TCTGCTGGTGCCCTCCATTGATGAACCCCATGTATACTGTGTGAAGAGCCAGCAGATA AGAAATCTTGCTTTAGAAAACTGTGCCAGAAGCAAAGCTGAAGCGGATGCTTAACCA <u>CATGATGCTTAACCCAA</u>		
	ORF Start: ATG at 29	ORF Stop: TGA at 968	
	SEQ ID NO: 210	313 aa	MW at 35313.1kD
NOV72a, CG59211-01 Protein Sequence	MSILNTSEMEISIFYLVGIPGLEHANIWISIPICLMTYVAILGNCTILFFIKTEPSLH EPMYFPLSMLALSDLGLSLSLPTMLRIFLFPNAPGISPDACIAQEFFIHGFSAMESSV LLIMSFDRFIAICNPLRYTSILTSARVIQIGLAFSLKNVLLILPFPFTLKHLYCKKN LLSQSYCLHQDVMKLACTDNKVNIIYGLFVALTGILDLTFIFMSYMLILKAVLSIASR KKRLKVLNLCVSHICAVLIFYVPIISLAVIYRFKHSFPITRILIADAFLLVPPLMNP IVYCVKSQQIRNLVLEKLCQKQS		

Further analysis of the NOV72a protein yielded the following properties shown in Table 72B.

Table 72B. Protein Sequence Properties NOV72a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.0300 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 44 and 45

A search of the NOV72a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 72C.

Table 72C. Geneseq Results for NOV72a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV72a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG71564	Human olfactory receptor polypeptide, SEQ ID NO: 1245 - Homo sapiens, 322 aa. [WO200127158-A2, 19-APR-2001]	1..313 5..317	312/313 (99%) 312/313 (99%)	e-177
AAU24573	Human olfactory receptor AOLFR63 - Homo sapiens, 313 aa. [WO200168805-A2, 20-SEP-2001]	1..312 1..312	225/312 (72%) 272/312 (87%)	e-131
AAG71721	Human olfactory receptor polypeptide, SEQ ID NO: 1402 - Homo sapiens, 316 aa. [WO200127158-A2, 19-APR-2001]	1..311 1..311	236/312 (75%) 267/312 (84%)	e-131
AAU24682	Human olfactory receptor AOLFR181 - Homo sapiens, 312 aa. [WO200168805-A2, 20-SEP-2001]	1..308 1..306	224/308 (72%) 265/308 (85%)	e-131
AAG71701	Human olfactory receptor polypeptide, SEQ ID NO: 1382 - Homo sapiens, 312 aa. [WO200127158-A2, 19-APR-2001]	1..308 1..306	224/308 (72%) 265/308 (85%)	e-131

In a BLAST search of public sequence databases, the NOV72a protein was found to have homology to the proteins shown in the BLASTP data in Table 72D.

Table 72D. Public BLASTP Results for NOV72a				
Protein Accession Number	Protein/Organism/Length	NOV72a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9H344	Olfactory receptor 51I2 (HOR5 ^{beta} 12) - Homo sapiens (Human), 312 aa.	12..304 10..303	152/294 (51%) 219/294 (73%)	6e-90
Q9EQQ7				9e-89

	(Mouse), 319 aa.	1..310	219/310 (70%)	
Q9H343	Olfactory receptor 51I1 (HOR5'beta11) - Homo sapiens (Human), 314 aa.	4..313 4..314	154/311 (49%) 226/311 (72%)	9e-89
CAC38935	SEQUENCE 9 FROM PATENT WO0131014 - Homo sapiens (Human), 318 aa.	5..305 6..306	153/302 (50%) 217/302 (71%)	2e-87
CAC37756	SEQUENCE 1 FROM PATENT WO0125434 - Homo sapiens (Human), 317 aa.	5..305 5..305	153/302 (50%) 217/302 (71%)	3e-87

PFam analysis predicts that the NOV72a protein contains the domains shown in the Table 72E.

Table 72E. Domain Analysis of NOV72a			
Pfam Domain	NOV72a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DUF40: domain 1 of 1	109..134	10/26 (38%) 20/26 (77%)	0.38
7tm_1: domain 1 of 2	43..144	27/107 (25%) 71/107 (66%)	1.6e-15
7tm_1: domain 2 of 2	212..293	16/93 (17%) 56/93 (60%)	4.7
Sina: domain 1 of 1	300..311	7/12 (58%) 10/12 (83%)	1

Example 73.

The NOV73 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 73A.

Table 73A. NOV73 Sequence Analysis		
	SEQ ID NO: 211	1581 bp
NOV73a, CG59276-01 DNA Sequence	CTGGTGGGTTGGCGGCTAAGGGGCGGAGACAAGAGGGGCGCCACCATCTCTCCAAT GGAAGGGGAGACAGGGGCGGGCTTAATGACGGAAGGAGCATGGCGTGGAGACACCTGAA AAAGCGGGCCAGGATGCTGTGATCATCTGGGGGAGGAGGACTTCTCTTCGCTCC TACCTGATGGCCACGGGAGATGAGCGTTTCTATGCTGAACACCTGATGCCGACTCTGC AGGGGCTGCTGGACCCGGAGTCAGCCACAGACTGGCTGTTTCGCTTCACTCCCTGGG GCTCCTTCCACGGGCGAGATTTCAAGACTCTGACATGCTGGAAGTGAGAGTTCTGGGC CATAAATTCGAAATCCAGTAGGAATTGCTGCAGGATTTGACAAGCATGGGGAAGCCG TGGACGGACTTTATAAGATGGGCTTTGGTTTGTGAGATAGGAAGTGTGACTCCAAA ACCTCAGGAAGGAAACCTAGACCCAGAGTCTTCCGCCTCCCTGAGGACCAAGCTGTC ATTAACAGGTATGGATTTAACAGTCACGGGCTTTCAGTGGTGAACACAGGTTACGGG CCAGACAGCAGAAGCAGGCCAAGCTCAGAGAAGATGGACTGCCTCTGGGGGTCAACTT GGGGAAGAACAAGACCTCAGTGGACGCCGCGGAGGACTACGCAGAAGGGGTGCGCGTA CTGGGCCCCCTGGCCGACTACCTGGTGGTGAATGTGTCCAGCCCCAACACTGCCGGGC TGGGAGCCTTCAGGGAAGGCCGAGCTGCGCGCCTGCTGACCAAGGTGCTGCAGGA	

	GAGGGATGGCTTGGCGAGAGTGCACAGGCCGGCAGTCTTGGTGAAGATCGCTCCTGAC CTCACCAGCCAGGATAAGGAGGACATTGCCAGTGTGGTCAAAGAGTTGGGCATCGATG GGCTGATTGTTACGAACACCACCGTGAGTCGCCCTGCGGGCTTCAGGGTGCCCTCGG CTCTGAACAGGAGGGGTGAGTGGGAAGCCCTCGGGATTATCAACTCAAAACCATT CGGGAGATGTATGCACTCACCAAGGCAAGGTTTCCCGTCGAGTTCCTCATATTGGGG TTGGTGGTGTGAGCAGCGGGCAGGACGCGCTGGAGAAGATCCGGGCAGGGGCTCCCT GGTGCAGCTGTACACGGCCCTCACCTTCTGGGGGCCACCCGTTGTGGGCAAAGTCAAG CGGGAACCTGGAGGCCCTTCTGAAGGAGCAGGGCTTGGCGGAGTCACAGATGCCATTG GAGCAGATCATCGGAGGATGAGGAAACGGGCAGAGAAGCGGCTGATTGTCCAGTCCCC CTGCGTGGAGGCTGCTTGGCTGGGCTCGAGCCCGCGGTGGTGGGTGAGTTGGGACCT GGTGGTCTGCTGGTGGTCACTTTGGGAATTTCCAGGTACGATTGTTTTAGGCACTGT TCTTTGACTTGGTTGCAGAAAACAGATTTTGCAACACTTTCCAAGGACACAGTGTTA CCACTCCCTCACCTGCCATGGCCTCTTGGTTCTGCTTTAACTTCTGAGCCTCAGGG AGTCCATCTTGTCTG		
	ORF Start: ATG at 97	ORF Stop: TGA at 1555	
	SEQ ID NO: 212	486 aa	MW at 52982.6kD
NOV73a, CG59276-01 Protein Sequence	MAWRHLKKRAQDAVILGGGGLLFASYLMATGDERFYAEHLMPTLQGLLDPESAHRLA VRFTSLGLLPRARFQSDMLEVRVLGHKFRNPVGIAAGFDKHGEAVDGLYKMGFGFVE IGSVTPKPQEGNPRPRVRLPEDQAVINRYGFNSHGLSVVEHRLRARQQKQAKLTEDG LPLGVNLGKNKTSVDAEDYAEGVRLGPLADYLVVNVSSPNTAGLRSLQGKAELRRL LTKVLQERDGLRRVHRPAVLVKIAPDLTSQDKEDIASVVKELGIDGLIVTNTTVSRPA GLQALRSETGGLSGKPLRLDTQTIREMYALTQKVSRRVPIIGVGGVSSGQDALEK IRAGASLVQLYTALTFWGPPVVGKVKRELEALLKEQGGVTDAGADHRRMRKRAEK RLIVQSPCVAANLGGSPAVVQQLGPGGLLVVSLGISRYDCFQALFFDLVAEKQILQH FPRTQCYHSLTLPWPLGSAFNF		

Further analysis of the NOV73a protein yielded the following properties shown in Table 73B.

Table 73B. Protein Sequence Properties NOV73a	
Psort analysis:	0.8110 probability located in plasma membrane; 0.6400 probability located in endoplasmic reticulum (membrane); 0.3700 probability located in Golgi body; 0.1839 probability located in microbody (peroxisome)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV73a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 73C.

Table 73C. Geneseq Results for NOV73a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV73a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB70780	Tobacco dihydro-orotase protein - Nicotiana tabacum, 458 aa. [WO200118190-A2, 15-MAR-2001]	36..398 81..458	199/383 (51%) 257/383 (66%)	e-101
AAG01301	Human secreted protein, SEQ ID NO:	1..144 1..144	143/144 (99%) 144/144 (99%)	3e-79

	[EP1033401-A2, 06-SEP-2000]			
AAG91420	C glutamicum protein fragment SEQ ID NO: 5174 - Corynebacterium glutamicum, 371 aa. [EP1108790-A2, 20-JUN-2001]	76..396 60..366	131/328 (39%) 190/328 (56%)	6e-60
AAB46597	C. glutamicum dihydroorotate dehydrogenase protein - Corynebacterium glutamicum, 321 aa. [DE19929364-A1, 28-DEC-2000]	76..396 10..316	131/328 (39%) 190/328 (56%)	6e-60
AAB80123	Corynebacterium glutamicum MP protein sequence SEQ ID NO:980 - Corynebacterium glutamicum, 334 aa. [WO200100843-A2, 04-JAN-2001]	76..396 23..329	131/328 (39%) 190/328 (56%)	1e-59

In a BLAST search of public sequence databases, the NOV73a protein was found to have homology to the proteins shown in the BLASTP data in Table 73D.

Table 73D. Public BLASTP Results for NOV73a				
Protein Accession Number	Protein/Organism/Length	NOV73a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q02127	Dihydroorotate dehydrogenase, mitochondrial precursor (EC 1.3.3.1) (Dihydroorotate oxidase) (DHODEHASE) - Homo sapiens (Human), 396 aa (fragment).	1..399 2..396	392/399 (98%) 394/399 (98%)	0.0
PC1219	dihydroorotate oxidase (EC 1.3.3.1) precursor - human, 397 aa.	1..399 3..397	388/399 (97%) 393/399 (98%)	0.0
Q63707	Dihydroorotate dehydrogenase, mitochondrial precursor (EC 1.3.3.1) (Dihydroorotate oxidase) (DHODEHASE) - Rattus norvegicus (Rat), 395 aa.	1..399 1..395	350/399 (87%) 369/399 (91%)	0.0
O35435	Dihydroorotate dehydrogenase, mitochondrial precursor (EC 1.3.3.1) (Dihydroorotate oxidase) (DHODEHASE) - Mus musculus (Mouse), 395 aa.	1..399 1..395	346/399 (86%) 366/399 (91%)	0.0
Q9FZM9	DIHYDROOROTATE DEHYDROGENASE - Oryza sativa (Rice), 468 aa.	29..398 79..468	206/394 (52%) 261/394 (65%)	e-101

PFam analysis predicts that the NOV73a protein contains the domains shown in the Table 73E.

Table 73E. Domain Analysis of NOV73a			
Pfam Domain	NOV73a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DHodehase: domain 1 of 1	77..381	183/331 (55%) 282/331 (85%)	1.9e-169

Example 74.

The NOV74 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 74A.

Table 74A. NOV74 Sequence Analysis			
	SEQ ID NO: 213	1875 bp	
NOV74a, CG59268-01 DNA Sequence	ATGGCCGAGCCTCGCCTCTGCGCGACTGCCAGGCCTGGAAGGATGCGAGGCTCCCGC TCTCCACCACAAGCAACGAAGCCTGCAAGCTGTTTCGATGCCACGCTGACCCAGTATGT AAAATGGACCAATGACAAGAGTCTCGGTGGCATCGAGGGCTGCCTGTCAAAGCTCAAA GCAGCAGATCCAACCTTTGTGATGGGCCACGCCATGGCTACTGGCCTTGTGCTGATTG GCATGGGAAGCTCCGTGAAGCTGGACAAAGAGCTGGACCTGGCTGTGAAGACAATGGT GGAGATTTCAAGAACCCAGCCGCTGACAAGGCGGGAGCAGCTGCACGTGTCTGCAGTA GAGACATTTGCCAATGGGAACCTTCCGAAAGCCTGTGAACTATGGGAACAGATTCTCC AGGACCAACCCGACAGACATGTTGGCCCTGAAATTTCCCATGATGCTTATTTTACCT GGGCTATCAGGAACAGATGAGAGATTCTGTTGCTCGAATTTACCCCTTCTGGACACCT GACATCCCCCTAAGCAGCTATGTGAAAGGCATCTACTCTTTTGGCTTGATGGAAACCA ACTTCTACGACCAGGCAGAAAACTCGCCAAAGAGGCACCAACTCTTTGTCTTCAACA CCAGCACCCCAAGACAATACTGGGCAGGAAAGCAGGCTGTGATGGGGCCAGGAGT GGTAACACATGGGCTCTGTGTCTGCAGCCCCAGGCTGACGATGGTGGTGACACCG TCGCTCACATCCAGAGATGAAAGCAGAGATCAAGGATGGGTTGGAATTCATGCAGCA CTCAGAGACCTTCTGGAAGGACTCTGATATGTTGGCTTGTCATAACTATTGGCACTGG GCTTTATATCTGATTGAGAAGGGTTTAATAAGGAGAAGCTTTATCTTCCAGGGCGAAT ATGAGGCGCGCTGACCATCTACGATACCCACATCCTTCCCAGCCTGCAGGCCAACGA TGCAATGCTGGACGTGGTGGACAGCTGCTCCATGCTCTACCGCCTGCAGATGGAAGGA GTGCTCTGTGGGCCAGCGGTGGCAGGATGTCTGCTGTGGCCCGGAAGCAGCCGAG ACCACATCCTGCTGTTCAATGACGCACACTTCTGATGGCATCCCTGGGTGCACACGA CCCCCAGACCACAGGAGCTGCTGACCACCTGCGGGACGCCAGCAGTATGCGAG GGGCCTTCTCGGGGTGGGGTCTCACCCTGCCGAGAGGTGCCAGGCCTTTGCCTGTA TTATCAGCAATCCTGACGGTCTGTTAGATTGGCACTGTTATGCTCTGTTACAGATGA GCAAACTGAGGCTGGAAGATCCCCAGGGGAGAACTGCCAGCACCTCCTGGCCCGAGAC GTGGGGCTGCCCTGTGCCAGGCCCTGGTGGAGGCTGAGGACGGGAACCTGACCCGG TCCTGGAGCTGCTCTGCCCATCCGCTACCGGATCGTCCAGCTCGGTGGGAGCAATGC CCAGAGAGACGCTCTCAACCAAGCTGCTGATTACGCGCGCTTAACTGCACCTCCAGC GTCCATAAGAACGTAGCCCGGAGCCTTCTGATGGAGCGTGATGCTTGAAGCCCAACT CGCCCTGACCGAGCGGCTCATCCGCAAGGCAGCTACCGTCCACCTCATGCAGAAGCC TTCTACCGCCCAACCCCACTGCAGGCTGCTCTCCTCATGGAAGGAGGCGGCGCGC GATGAGCCTTCAAGCTGCCGGGCAGGGACGTGAACATGGATGACCTAAGAAGGAAG GCAAGTCTCTGTGCTGCCGGCCTGTTGTTGTTTCAGGATGTTTCAGTAGAGATGGAGG TGATTTAATGTTTCCCTGA		
	ORF Start: ATG at 1	ORF Stop: TGA at 1873	
	SEQ ID NO: 214	624 aa	MW at 69393.3kD
NOV74a, CG59268-01 Protein Sequence	MAAASPLRDCQAWKDARLPLSTTSNEACKLFDATLTQYVKNWTDKSLGGIEGCLSKLK AADPTFVMGHAMATGLVLIGTGSSVKLDKELDLAVKTMVEISRTQPLTRRQLHVS ETFANGNFPKACELWEQILQDHPDMLALKFSDAYFYLGYEQMRDSVARIYPFWTP DIPLSSYVKGIYSFGLMETNFYDQAEKLAKEAPTLCLQHHPDNYWAGKAGCDGARS GNTWALCLQPQADAWSVHTVAHIHEMKAEIKDGLFQMHSSETFWKSDMLACHNYWHW		

ALVLIKGLIRRTLPFQGEYEAALTIYDTHILPSLQANDAMLDVVDSCSMLYRLQMEG VSVGQRWQDVLPAVKHSRDHILLFNDHFLMASLGAHDPQTTQELLTLRDASEYAE GPSRGGGPHPAERCQAFACII SNPDGSVRLALLCLLTDEQTEAGRSPGENCQHLLARD VGLPLCQALVEAEDGNPDRVLELLLPYRIVQLGGSNAQRDVFNQLLIHAALNCTSS VHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMQKPSTRQPPQAALSMEGGGGR DEPSACRAGDVNMDDPKKEGKSLLLRCCCSGCSVEMEGDLMFP

Further analysis of the NOV74a protein yielded the following properties shown in Table 74B.

Table 74B. Protein Sequence Properties NOV74a	
PSort analysis:	0.4328 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1137 probability located in mitochondrial inner membrane; 0.1137 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV74a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 74C.

Table 74C. Geneseq Results for NOV74a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV74a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41338	Human polypeptide SEQ ID NO 6269 - Homo sapiens, 478 aa. [WO200153312-A1, 26-JUL-2001]	1..559 10..478	463/559 (82%) 466/559 (82%)	0.0
AAM39552	Human polypeptide SEQ ID NO 2697 - Homo sapiens, 453 aa. [WO200153312-A1, 26-JUL-2001]	1..529 1..439	434/529 (82%) 437/529 (82%)	0.0
AAG02871	Human secreted protein, SEQ ID NO: 6952 - Homo sapiens, 104 aa. [EP1033401-A2, 06-SEP-2000]	1..102 1..102	102/102 (100%) 102/102 (100%)	1e-52
AAM40893	Human polypeptide SEQ ID NO 5824 - Homo sapiens, 746 aa. [WO200153312-A1, 26-JUL-2001]	568..604 1..37	32/37 (86%) 32/37 (86%)	2e-10
AAM40892	Human polypeptide SEQ ID NO 5823 - Homo sapiens, 746 aa. [WO200153312-A1, 26-JUL-2001]	568..604 1..37	32/37 (86%) 32/37 (86%)	2e-10

In a BLAST search of public sequence databases, the NOV74a protein was found to have homology to the proteins shown in the BLASTP data in Table 74D.

Table 74D. Public BLASTP Results for NOV74a				
Protein Accession Number	Protein/Organism/Length	NOV74a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAH18918	HYPOTHETICAL 45.7 KDA PROTEIN - Homo sapiens (Human), 404 aa.	66..559 1..404	399/494 (80%) 402/494 (80%)	0.0
Q9NWP8	KAIA2372 PROTEIN - Homo sapiens (Human), 336 aa.	1..352 1..310	305/352 (86%) 308/352 (86%)	e-172
Q9XW02	Y54G11A.4 PROTEIN - Caenorhabditis elegans, 497 aa.	4..556 6..458	165/557 (29%) 256/557 (45%)	3e-61
Q9XW01	Y54G11A.7 PROTEIN - Caenorhabditis elegans, 407 aa.	4..347 6..305	122/347 (35%) 177/347 (50%)	7e-53
Q98CS1	MLR5032 PROTEIN - Rhizobium loti (Mesorhizobium loti), 440 aa.	60..553 46..435	145/496 (29%) 215/496 (43%)	1e-43

Pfam analysis predicts that the NOV74a protein contains the domains shown in the Table 74E.

Table 74E. Domain Analysis of NOV74a			
Pfam Domain	NOV74a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Monooxygenase: domain 1 of 1	225..410	28/238 (12%) 121/238 (51%)	6.4

Example 75.

The NOV75 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 75A.

Table 75A. NOV75 Sequence Analysis		
	SEQ ID NO: 215	1851 bp
NOV75a, CG59549-01 DNA Sequence	CAGCTACAGCAAACATCGTTCGAGATGTCCCAAGAGGGCAGCACAGGTGGCTTAC CAGACTTAGTGACTGAAAGCCTGTTTCAGCAGCCAGAGGAGCAGTCTGGAGTAGCAGC GGTGACGGCGGCCTCCTCAGACATTGAAATGGCAGCCACAGAGCCATCGACCGGAGAT GGTGGTGATACCAGGGATGGTGGTTTCCTGAACGATGCCAGCACAGAAAATCAAAACA CAGACTCAGAAAGTTCAAGTGAAGACGTCGAACTTGAAAGCATGGGTGAAGGTTTATT	

	TGGTTACCCGTTAGTGGGAGAGGAGACAGAAAGGGAGGAGGAAGAAGAGATGGAG GAGGAAGGGGAGGAGGAAGAACAGCCTCGGATGTGTCCACGATGCGGTGGCACCACACC ATGATCAGTGTGTTAGACGAGGATCAGGCGTTGGAGGAGTGGATTTCCTCAGAGAC ATCTGCCCTGCCCGATCTCGCTGGCAAGTCCTTACTGCTCTTCGCCAGCGGCAGCTG GGTTCAGTGCCCGCTTTGTATATGAGGCTGTGGGGCAAGAACCTTTGTGCAGCGTT TCCGCCTGCAGTATCTTCTTGGGAAGCCATGCCGTTCTGTCAGTACCATACACTTTAA CCAGCGTGGCACCAGCTGGCCAGTAGCGGTGATGACTTAAGGGTGATAGTGTGGGAC TGGGTGCCGAGAGCCAGTACTGAACTTTGAGAGTGGTCACGATATTAATGTATCATCC AGGCTAAGTTCTTTCCTAACTGTGGTGATTCCACTCTGGCCATGTGTGGCCATGATGG ACAGGTACGGGTAGCAGAACTAATTAATGCATCATATTGCGAGAATACTAAGCGTGTG GCCAAGCACAGGGGACCTGCCACGAGTTGGCTCTGGAGCCAGACTCTCCTTATAAGT TCCTCACTTCAGGTGAAGATGCCGTTGTGTTACCAATTGACCTCAGGCAAGACCGGCC AGCTTCAAAAGTTGTGGTAACAAGAGAAAATGATAAGAAAGTCGGACTGTATACAATC TCTATGAATCCTGCCAATATTACCAATTGCAGTGGGTGGAGATGATCATTTGTAA GGATTTATGACCAGAGGAGAATTGATAAGAAAGAAAACATGGAGTACTCAAGAAATT CACTCCTCATCATCTGTTTATTGTGATTCCCAACAAACATCACCTGCGTGTGTAC AGCCACGATGGCACAGAGCTCCTGGCCAGCTACAATGATGAAGATATTTACCTCTTCA ACTCCTCTCTCAGTGTGTTCAATATGTTAAGAGATATAAGGGGCACAGCAATAA TGACACAATCAAATGTGTTAATTTCTATGGCCCCGGAGTGAAGTTGTCTGTGAGCGGT AGTGATTGTGGGCACGTCTTCTCTGGGAGAAATCATCTCCAGATCATCCAGTTCA TGGAGGGGACAGAGGAGATATAGTAACTGTCTTGAACCCACCTTACCTACCTGT GTTGGCGACCACTGGCCTAGATCAGCATGTCAGGATCTGGACACCCACAGCTAAAAC GCCACTGAGCTTACTGGGTTAAAAGATGTGATTAAGAAGAACAAGCAGGAGCGAGATG AAGACAACCTTGAACATACGGAAGCTGTTTGACAACCGCATGCTTCGTTCTTCGTGCG TCACCTGTTACAGAGAGCTCATCAACCCGGCTGGAGAGATCATGGAGCTGAGTTCCCA GATGAAGAAGAGTTGGATGAGTCTTCCAGCACCTCAGATACATCCGAGGAGGAGGGCC AAGATCGAGTGCAGTGCATACCCTCTGAAGGCTCATATCCAGTCCAGCTAG		
	ORF Start: ATG at 25 ORF Stop: TGA at 1825		
	SEQ ID NO: 216	600 aa	MW at 67372.4kD
NOV75a, CG59549-01 Protein Sequence	MSHQEGSTGGLPDLVTESLFSSPEEQSGVAAVTAASSDIEMAATEPSTGDGGDTRDGG FLNDASTENQNTDSESSSEDVELESMGEGLPFYPLVGEETEREEEEEMEEGEHEEQ PRMCPRCGGTNHDQCLLDEDQALEEWISSETTSALPRSRWQVLTALRQRLGSSARFVY EACGARTFVQRFRLQYLLGSHAGSVSTIHFNRGTRLASSGDDLRLVWVDWVRQKPV NFESGHDINVIAKFFPNCGDSTLAMCGHDGQVRVAELINASYCENTKRVAKHRGPAH ELALEPDSFYKFLTSGEDAVVFTIDLRQDRPASKVVVTRENDKVGlyTISMNPANIY QFAVGGHDQFVRIYDQRRIDKENNGVLKKFTPHHLVYCDPPTNITCVVYSHDGTLL ASYNDEDIYLFNSSLSDGAQYVKRYKGRNNDTIKCVNFGPRSEFVVSQSDCGHVFF WEKSSSQIIQFMEDRGDIVNCLPFPYLPVLATSGLDQHVRIWTPAKTATELTGLK DVIKKNKQERDEDNLNYTDSFDNRMLRFFVRHLLQRAHQPGWRDHGAEPDEEELDES SSTSDTSEEGQDRVQCIPS		

Further analysis of the NOV75a protein yielded the following properties shown in Table 75B.

Table 75B. Protein Sequence Properties NOV75a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0442 probability located in microbody (peroxisome)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV75a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 75C.

Table 75C. Geneseq Results for NOV75a				

Identifier	#, Date]	Residues/ Match Residues	Similarities for the Matched Region	Value
AAR85870	WD-40 domain-contg. Mus musculus protein - Mus musculus, 816 aa. [WO9521252-A2, 10-AUG-1995]	95..589 333..815	295/495 (59%) 372/495 (74%)	e-179
AAM73935	Human bone marrow expressed probe encoded protein SEQ ID NO: 34241 - Homo sapiens, 164 aa. [WO200157276-A2, 09-AUG-2001]	1..157 8..164	157/157 (100%) 157/157 (100%)	2e-87
AAM61216	Human brain expressed single exon probe encoded protein SEQ ID NO: 33321 - Homo sapiens, 164 aa. [WO200157275-A2, 09-AUG-2001]	1..157 8..164	157/157 (100%) 157/157 (100%)	2e-87
AAM34114	Peptide #8151 encoded by probe for measuring placental gene expression - Homo sapiens, 164 aa. [WO200157272-A2, 09-AUG-2001]	1..157 8..164	157/157 (100%) 157/157 (100%)	2e-87
AAB57007	Human prostate cancer antigen protein sequence SEQ ID NO:1585 - Homo sapiens, 214 aa. [WO200055174-A1, 21-SEP-2000]	408..600 22..214	144/194 (74%) 162/194 (83%)	2e-80

In a BLAST search of public sequence databases, the NOV75a protein was found to have homology to the proteins shown in the BLASTP data in Table 75D.

Table 75D. Public BLASTP Results for NOV75a				
Protein Accession Number	Protein/Organism/Length	NOV75a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q12839	H326 PROTEIN - Homo sapiens (Human), 597 aa.	1..600 1..597	408/604 (67%) 471/604 (77%)	0.0
Q01078	PROTEIN PC326 - Mus musculus (Mouse), 747 aa.	95..589 264..746	295/495 (59%) 372/495 (74%)	e-178
Q9W091	CG8001 PROTEIN - Drosophila melanogaster (Fruit fly), 748 aa.	68..587 209..711	178/533 (33%) 280/533 (52%)	1e-77
Q96E00	UNKNOWN (PROTEIN FOR MGC:9478) - Homo sapiens (Human), 273 aa.	1..246 1..243	141/249 (56%) 173/249 (68%)	8e-66
Q9M1E5	HYPOTHETICAL 54.0 KDA PROTEIN - Arabidopsis thaliana (Mouse-ear cress), 481 aa.	183..536 42..419	136/382 (35%) 209/382 (54%)	2e-62

PFam analysis predicts that the NOV75a protein contains the domains shown in the Table 75E.

Table 75E. Domain Analysis of NOV75a			
Pfam Domain	NOV75a Match Region	Identities/ Similarities for the Matched Region	Expect Value
WD40: domain 1 of 7	188..224	13/37 (35%) 29/37 (78%)	0.0016
WD40: domain 2 of 7	231..269	12/39 (31%) 26/39 (67%)	11
WD40: domain 3 of 7	278..315	9/38 (24%) 24/38 (63%)	2.2e+02
WD40: domain 4 of 7	326..363	8/38 (21%) 27/38 (71%)	8.8
WD40: domain 5 of 7	382..418	5/37 (14%) 27/37 (73%)	12
WD40: domain 6 of 7	429..466	6/38 (16%) 26/38 (68%)	18
WD40: domain 7 of 7	473..509	11/37 (30%) 22/37 (59%)	0.51

Example 76.

The NOV76 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 76A.

Table 76A. NOV76 Sequence Analysis		
	SEQ ID NO: 217	7497 bp
NOV76a, CG59641-01 DNA Sequence	<p>ATGGTCTTGCTTCTTTGCTATCTTGTCTGATTTTCTCCTGTCTGACCTTTTCTCTGGT TAAAAATCTGGGGGAAAATGACGGACTCCAAGCCGATCACCAGAGTAAATCAGAAGC AAACCTCATCCCGAGCCAGGAGCCCTTTCCAGCCTCTGTATACTCAGGGGAGACACCG CAGAGAAATGGGGAGGGCCACACTCTGCCCAAGACACCCAGCCAGGGCCAGCCAGCCT CCCACAAAGGCCCAAGATGCCGGTCGGCGGAGAACTCCCTACACCCCTCCACCA GAAGCCCCCAAGAAACCCCTTTCTTCCAGTGACGCAGCACCCTCCCCAGAGCTTCAA GCCAACGGGACTGGGACACAAGGTCTGGAGGCCACAGATACCAATGGCCTGTCTCTCT CAGCCAGGCCCCAGGGCCAGCAAGCTGGCTCCCTCCAAAGAAGACAAGAAGCAGGC AAACATCAAGAGGCAGCTGATGACCAACTTCATCCTGGGCTCTTTTGATGACTACTCC TCCGACGAGGACTCTGTGCTGGCTCATCTCGTGAGTCTACCCGGAAGGGCAGCCGGG CCAGCTTGGGGGCCCTGTCCCTGGAGGCTTATCTGACCAAGGCCGAGCATGTCCGG ACTCCACCTGGTGAAGAGGGGACGGGAACAACAAGAGCTGGACCTGCAAGAGACTTT ACCGTGGCTTCTCCCGCTGAGTTTGTACACGCTTGGGGGGCTCCGGTCTACGAGA AGGTGCTTATTGCCAACACGGGATTGCCGCCGTGAAGTGCATGCCCTCATCCGAG GTGGGCTTATGAGATGTTCCGCAACGAGCGGGCCATCCGGTTTGTGTGATGGTGACC CCCGAGGACCTTAAGGCCAACGCAGAGTACATCAAGATGGCGGATCATACGTCCTCCG TCCAGGAGGGCCCAATAACAACAATATGCCAACGTGGAGCTGATTGTGGACATTGC CAAGAGAATCCCGGTGAGGCGGTGTGGGCTGGCTGGGGCCATGCTTCAGAAAACCT AACTTCCGGAGCTGCTGTGCAAGAATGGAGTTGCTTTCTTAGGCCCTCCAGTGAGG CCATGTGGGCTTAGGAGATAAGATCGCCTCCACCGTTGTGCGCCGAGCGCTACAGGT CCCAACCTGCGCTGGAGTGGAAGCGGCTGACAGTGGAGTGGACAGAAGATGATCTG CAGCAGGGAAAAGAAATCAGTGTCCAGAAGATGTTTATGACAAGGGTTCGCTGAAG ACGTAGATGAGGGCTTGGAGGCAGCAGAAAAGAAATGGTTTCCATTGATGATCAAGC TTCTGAAGGTGGCGGAGGGAAGGGAATCCGGAAGGCTGAGAGTGGCGAGGACTTCCCG ATCCTTTTCAGACAAGTACAGAGTGAGATCCAGGCTCGCCCATCTTTCTCATGAAGC TGGCCAGCAGCGCCCTCAGCTGGAAGTTAGATCCTCGTGACAGTATGGGAATGC TGTGTCTGTTTGGTCCGACTGCTCCATCCAGCGCGGCATCAGAAGATCGTTGAG GAAGCACCGGCCACCATCGCCCGCTGGCCATATTCGAGTTTATGGAGCAGTGTGCCA TCCGCTGGCCAGACCGTGGGCTATGTGAGTGCAGGGACAGTGAATACCTCTATAG TCAGGATGGCAGCTTCCACTTCTTGGAGCTGAATCCTCGCTTGAGGTGGAACATCCC TGACAGAAATGATTGCTGATGTTAATCTGCGCGCCGCCAGTACAGTCCGCAATGG GCGTGCCACTGCACCGGCTGAAGGATATCCGGCTTCTGTATGGAGAGTACCATGGGG AGTGACTCCCATTTCTTTTGAACCCCTCAAACCTCCCTCGCCCGAGGCCACGTC ATTGCCCGCAGAATCACCAGCGAAAACCCAGACGAGGGTTTAAAGCCAGAGCTCCGGGA CTGTCCAGGAACCTGAATTTCCGGAGCAGCAAGAACGTGTGGGCTTACTTCAGCGTGGC CGTACTGGAGGCTGCACGAGTTTGGGATTCCCAATTGGGCACTGCTTCTCTGG GGAGAGAACCGGGAAGAGGCCATTTCAACATGGTGGTGGCTTGAAGGAATGTGCA TCCAGGCGACTTTAGGACTACCGTGAATACCTCATTAACTCTGGAGACCGAGAG CTTCCAGAACACGACATCGACACCGGGTGGTGGACTACCTCATGTGAGAAAGTG CAGGCGGAGAACCGGATATCATGCTTGGGGTGTATGCGGGGCTTGAACGTGGCCG ATGCGATGTTGAGAAGTGCATGACAGATTCTTACACTCCCTGGAAGGGGCCAGGT CTCCAGCGGATTCTACTGAACTCGTAGATGTGGAATTAATTTACGGAGGTGTT AAGTACATTCTCAAGGTGGCCCGGAGTCTCTGACCATGTTCTGTTCTCATCATGAATG GCTGCCACATCGAGATTGATGCCACCGGCTGAATGATGGGGGCTCTGCTCTCCTA CAATGGGAACAGCTACACCACCTACATGAAGGAAGAGGTTGACAGTTACCGAATTACC ATCGGCAATAAGACGTGTGTGTTTGAGAAGGAGAACGATCCTACAGTCTGAGATCCC CCTCGGCTGGGAAGCTGACACAGTACACAGTGGAGGATGGGGGCCACGTTGAGGCTGG GAGCAGCTACGCTGAGATGGAGGTGATGAAGATGATGACCTGAACGTTACAGGAA AGAGGCCGGGTGAAGTACATCAAGCGTCCAGGTGCCGTGCTGGAAGCAGGCTGCGTGG TGGCCAGGCTGGAGCTGATGACCTTCTAAAGTCCACCGGCTGAACCGTTACAGG AGAACTCCCTGCCAGCAGACACTGCCCATCCTCGGAGAGAACTGCACACAGGTCTTC CACAGCGTCTGGAAAACCTCACAACGTCATGAGTGGCTTTTGTCTGCCAGAGCCCG TTTTTAGCATAAAGCTGAAGGAGTGGGTGCAGAAGCTCATGATGACCTCCGGACCC GTCACTGCCGCTGCTGGAGCTGCAGGAGATCATGACAGCGTGGCAGGCGCATCCCC GCCCTGTGGAGAAGTCTGTCCGAGGGTGTGGCCAGTATGCCAGCAACATCACT CCGTGCTGTGCCAGTTCCTCCAGCCAGCAGATAGCCACCATCTGGACTGCCATGCAGC CACCCTGCAGCGGAAGGCTGATCGAGAGGTCTTCTCATCAACACCCAGAGCATCGTG CAGTTGGTCCAGAGATACCGCAGCGGGATCCGCGGCTATATGAAAACAGTGGTGTGG ATCTCCTGAGAAGATACTTGGTGTGAGAGCAAGGCAAGAGATGCTGATGCCAACAC CAGTGGGATGGTGGGGCGTGAGGAGCCTGAGCTTTACCTCTGTGTGGTGTGTTCTC TCCCCGAATCCCACTACGACAAGTGTGTGATAAACCAGGGAGCAGTTCAAGCCAG ACATGTCCAGGTGCTGGACTGCATCTTCTCCACGCACAGGTGGCCAGAAGAACCA GCTGGTGTATGTTGATGATGAGCTGTGTGGCCAGACCCTTCCCTGTGCGACGAG CTGATCTCATCTCAACGAGCTCACTCAGCTGAGCAAAAGCGAGCACTGCAAAAGTGG</p>	

	<p>CCCTCAGAGCCCGGCAGATCCTGATTGCCTCCACCTCCCCTCCTACGAGCTGCGGCA TAACCAGGTGGAGTCCATTTTCCTGTCTGCCATTGACATGTACGCCACCAGTTCTCTG CCCAGAACTCAAGAAATTAATACTTTCGGAACAACCATCTTCGACGCTCTGCTCTA CTTTCTTCTATACGCAACAAAGTCGTGTGCATGGCGTCTTGGAGGTTTACGTGCG GAGGGGTACATCGCCTATGAGTTAAACAGCCTGCAGCACCGGCAGCTCCCGGACGGC ACCTGCGTGGTAGAATTCCAGTTTCATGCTGCCGTCTCCACCGCAACCGGATGACCG TGCCCATCAGCATCACCAACCTGACCTGCTGAGGCACAGCACAGAGCTCTTCATGGA CAGCGGCTTCTCCCACTGTGCCAGCGCATGGGAGCCATGGTAGCCTTCAGGAGATTTC GAGGACTTCACCAGAAATTTTGATGAAGTCATCTCTTGCTTCGCCAACGTGCCCAAAG ACACCCCTCTTCAGCGAGGCCCGCACCTCCCTATACTCCGAGGATGACTGCAAGAG CCTCAGAGAAGAGCCCATCCACATTCTGAATGTGTCCATCCAGTGTGCAGACCCTG GAGGATGAGGCACTGGTGCCGATTTACGGACATTCGTACAGTCCAAGAAAAATATCC TTGTGGATTATGGACTCCGACGAATCACATTCTTGATTGCCAAGAGTTTGCAAGA TCGCATTTACCGTCACTTGGAACTGCCCTGGCCTTCAGTCTTAACCGGATG CGTAACCTCGATCTGACCGCGTGCCTGTGCCAACCAAGATGCACCTTTACCTGG GTGCTGCCAAGGTGAAGGAAGGTGTGGAAGTGACGGACCATAGGTTCTTCATCCGCGC CATCATCAGGCACTCTGACCTGATCAAAAGGAAGCCTCTTCAATACCTGCAGAAC GAGGGTGAAGCGCTGCTCTGAGGAGCATGGACGAGCTGGAGGTGGCGTTCAATAACA CCAGCGTGCACCGACTGCAACCACATCTCCTCAACTTCGTGCCCACTGTCATCAT GGACCCCTTCAAGATCGAGGAGTCCGTGCGCTACATGGTTATGCGCTACGGCAGCCGG CTGTGGAACCTCCGTGTGCTACAGGCTGAGGTCAAGATCAACATCCGCCAGACCA CCGGCAGTGCCGTTCCCATCCGCTGTTTCATACCAATGAGTCGGGCTACTACCTGGA CATCAGCCTCTACAAAGAAGTGACTGACTCCAGATCTGGAATATCATGTTTCACTCC TTCGGCAACAAGCAAGGGCCCCAGCACGGGATGCTGATCAATACTCCCTACGTCACCA AGGATCTGCTCCAGCCCAAGCGATTCCAGGCCAGACCTGGGAACCATCACTCTA TGACTTCCCGGAAATGTTTCAGGCAGGCAAGTCCGGCGGCTCAGACGCGGTACATGTG CACAATGTGCAGGCTCTCTTAAACTGTGGGGTCCCCAGACAAGTATCCCAAGACA TCCTGACATACACTGAATTAGTGTGGACTCTCAGGCCAGCTGGGAGATGAACCG ACTTCTGGTGGAAATGAGGTGGGCATGGTGGCCTTCAAAATGAGGTTTAAAGACCCAG GAGTACCCGGAAGGACGGGATGTGATCGTCATCGGCAATGACATCAGCTTTTCGATTG GATCCTTTGGCCCTGGAGAGGACCTTCTGTACCTGCGGGCATCCGAGATGGCCCGGGC AGAGGCAATTCCAAATTTACGTGGCAGCCAACAGTGGCGCCGATTGGCATGGCA GAGGAGATCAACACATGTTCCACGTGGCTTGGGTGGACCCAGAAGACCCCAAAAA AAAAAAAACAGTGGCTTTCAGTGCAGGGAACCTGGATTCTGAGCCTCACTAAAGTATT TTTTAAGGGATTTAAATACCTGTACCTGACTCCCAAGACTACACAGAATCAGCTCC CTGACTCCGTCCTGTAACACATCGAGGAAGGAGAGATGTCAGATGATGATGATGAT CGGATATCATCGGAAGGATGATGGCTTGGGCTGGAGAATCTGAGGGCTCAGGCAT GATTGTGGGGAGTCTCTCTGGCTTACGAAGAGATCGTCACCATTAGCTTGGTGACC TGCCGAGCCATTGGGATTGGGGCTACTTGGTGAGGCTGGGCCAGCGAGTATCCAGG TGGAGAATTCACATCATCTCTCAGGAGCAAGTGTCTCAACAAGGCTCTGGGAAG AGAGGTCTACACATCCAACAACAGCTGGGTGGCGTTAGATCATGCATTACAATGGT GTCTCCACATCACCGTGCCAGATGACTTTGAGGGGGTTTATACCATCTGGAGTGGC TGCTCTATATGCCAAGGATAATCACAGCCTGTCCCTATCATCACCACTGACACCC CATTGACAGAGAAATGAATTCCTCCCATCCAGAGCTCCCTACGACCCCGGTGGATG CTTGACAGGAAGGCCTCACCAACTCTGAAGGGAACGTGGCAGAGCGGATTTTGGACC ACGGCAGTTTCAAGGAAATCATGGCACCTGGGCGCAGACCGTGGTGACAGGACGAGC AAGGCTTGGGGGATTCCCGTGGGAGTGATTGCTGTGGAGACACCGACTGTGGAGGTG GCAGTCCCTGCAGACCTGCCAACCTGGATTCTGAGGCCAAGATAATTCAGCAGGCAG GACAGGTGTGGTTCCAGACTCAGCCTACAAAACCGCCAGGCCGTCAAGGACTTCAA CCGGGAAGATTGCCCTGATGATCTTTGCCAACTGGAGGGGGTCTCCGGTGGCATG AAAGACATGTATGACAGGTGCTGAAGTTGGAGCCTACATCGTGAGCGCCTTAGAC AATACAAACAGCCATCCTGATCTATATCCCGCCTATGCGGAGCTCCGGGAGGCTC CTGGGTGGTCATAGATGCCACATCAACCCGCTGTGCATAGAAATGTATGACAGACAA GAGAGCAGGGGTGTGTTCTGGAACAGAGGGGACAGTGGAGATTAAGTTCCGAAGA AAGATCTGATAAAGTCCATGAGAAGGATCGATCCAGCTTACAAGAAGCTCATGGAACA GCTAGGGGAACCTGATCTCTCCGACAAGGACCGAAAGGACCTGGAGGGCCGGCTAAAG GCTCGGAGGACCTGCTGCTCCCATCTACCACAGGTGGCGGTGCAGTTCGCCGACT TCCATGACACACCCCGCGGATGCTGGAGAAGGGCGTCATATCTGACATCTCTGGAGT GAAGACCGCACGACCTTCTGTATTGGCGTCTGCGCCGCTCTCTCTGGAGGACAG GTCAAGCAGGAGATCTGCAGGCCAGCGGGAGCTGAGTCAGTGCATATCCAGTCCA TGCTGCGTCTGCTGTTCTGTGAGACGGAGGGGGCTGTCAAGGCCTACTTGTGGGACA CAACCAGGTGGTTGTGCACTGGCTGGAACAGCACTGGCAGGCGGGGATGGCCCGCGC TCCACCATCCGTGAGAACATCACGTACCTGAAGCACGACTGTGCTCAAGACCATCC GAGGCCCTGGTTGAAGAAAAACCCGAGGTGGCCGTGGACTGTGTGATATACCTGAGCCA GCACATCAGCCAGCTGAGCGGGCGCAGGTGTTCACTGCTGTCTACCATGGACAGC CCGGCTCCACCTGA</p>		
	ORF Start: ATG at 1	ORF Stop: TGA at 7495	
	SEQ ID NO: 218	2498 aa	MW at 280484.4kD
NOV76a, CG59641-01 Protein Sequence	<p>MVLLCLSLIFSLTFSWLKIWKMTDSKPIKSKSEANLIPSQEPFPASDNSGETP QRNGEGHTLPKTPSQAPASHKGPDKDAGRRRLSPSHQKPPRNPPLSSSDAAPSPELQ ANGTGTQGLEATDTNGLSSARPQGGQAGSPSKEDKKQANIKRQLMTNFIILGSFDDYS SDEDSVAGSSRSRTRKGSRLGALSLEAYLTTRPSMSGLHLVVKRGREHKLLDLHRDF TVASPAEFVTRFGDRVIEKVLIANNGIAAVKCMRSIRRWAYEMFRNERAIRFVVMVT PEDLKANAIEYIKMADHYVPVPGGPNNNNYANVELIVDIKRIPVQAVWAGWGHAENP</p>		

KLPELLCKNGVAFGLGPPSEAMWALGDKIASTVVAQTLQVPTLPWSSGSLTVEWTEDDL QQGKRISVPEDVYDKGVKDVDEGLEAAERIGFPLMIKASEGGGKGIRKAESAEDFP ILFRQVQSEIPGSPFIPLMKLAQHARHLEVQILADQYGNVSLFGRDCSIQRRHQKIVE EAPATIAPLAIFEFMEQCAIRLAKTVGVVSAGTVEYLYSQDGSFHFLELNPRQLQVHP CTEMIADVNLPAALQIAMGVPLHRLKDIRLLYGESPWGVTPISEFETPSNPPLARGHV IAARITSENPDDEGFKPSSGTQVELNFRSSKNVWGYFSVAATGGLHEFADSSQGHCFWS GENREEAISNMVVALKELSIRGDFRTTVEYLINLLETESFQNNNDITGWLVDYLIAEKV QAEKPDIMLGVVCGALNVADAMFRTCMDFLHSLERGQVLPADSLNLNVDVELIYGGV KYILKVARQSLTMFVLMNGCHIEIDAHRLNDGGLLSYNGNSYTTYMKEEVDSYRIT IGNKTCVFEKENDPTVLRSPSAGKLTQYTVEDGGHVEAGSSYAEMEVMKMTLNVQE RGRVKYIKRPGAVLEAGCVVARLELDDPSKVHPAEPFTGELPAQOTLPILGEKLHQVF HSVLENLTNMSGFCLPEPVFSIKLKEWVQKLMMLRHPSLPLELQEIIMTSVAGRIP APVEKSVRRVMAQYASNITSVLCQFPSSQIATILDCHAATLQKADREVFVINTQSI QLVQRYRSGIRGYMKTVVLDDLRLRYLRVESKARDADANTSGMVGVRSLSTSVVCFV SPESHYDKCVINLREQFKPDMSQVLDICFSHAQVAKKNQVIMLIDELCGPDPSSLDE LISILNELTQLSKSEHKVALRARQILIASHLPSYELRHNQVESIFLSAIDMYGHQFC PENLKKLILSETTIFDVLPTFFYHANKVVCMALEVVYRRGYIAYELNSLQHRQLPDG TCVVEFQFMLPSSHPNRMTVPISITNPDLRHSTELFMDSGFSPLCQRMGAMVAFRRF EDFTRNFDEVISCFANVPKDTPLFSEARTSLYSEDDCKSLREPIHILNVSIQCADHL EDEALVPILRTFVQSKNINLVDYGLRRITFLIAQEFADRIYRHLEPALAFQLELNR RNFDLTAVPCANHKMHLYLGAARKVKEGVEVTDHRFFIRAIIRHSDLITKEASFELQN EGERLLEAMDELEVAFNNTSVRTDCNHI FLNFVPTVIMDPFKIEESVRYMVMRYGSR LWKLRLVLAQEVKINIRQTTTGSAPVIRLFTNESGYLDISLYKEVTDSDSGNIMFHS FGNKQGPQHGMINTPYVTKDLLQAKRFQAQTLGTTYIYDFPEMFQASPAQAQTRVHV HNQALFKLWGSFDPKYPKDILTYTELVLDSQGLVEMNRLPGNEVMVAFKMRFTQ EYPEGRDVIVIGNDITFRIGSFGPGEDLLYLRASEMARAEIPKIYVAANSGARIGMA EEIKHMFHVAWVDPEDPHKKKTVAFSAGNWRSLTKVFFKGFKYLYLTPQDYTRISS LNSVHCKHIEEGGESRYMITDIIGKDDGLGVENLRGSGMIAGESSLAYEEIVTISLVT CRAIGIGAYLVRIGQRVIVQVENSIIILTGASALNKVLGREVYTSNNQLGGVQIMHYNG VSHITVPDDFEGVYTI LEWLSYMPKDNHSPVPIITPTDPIREIEFLPSRAPYDPRWM LAGRPHPTLKGTVQSGFFDHGSFKEIMAPWAQTVVTGRARLGGIPVGVIIVETRTVEV AVPADPANLDSEAKIIQQAGQVWFSDSAYKTAQAVKDFNREKLPLMIFANWRGFSGGM KDMYDQVLKFGAYIVDGLRQYKQPIIYIPPYAELRGGSWVVIDATINPLCIEMYADK ESRGGVLEPEGTVEIKFRKKDLIKSMRRIDPAYKKLMEQLGEPDLSKDRKDLLEGRLK AREDLLPIYHQVAVQFADFHDTPGRMLEKGVISDILEWKTARTFLYWRLLRLLLEDQ VKQEILQASGELSHVHIQSMRLRRWFVETEGAVKAYLWDDNNQVQVQWLEQHWQAGDGP STIRENITYLKHDSVLKTIIRGLVEENPEVAVDCVIYLSQHSIPAERAQVHLLSTMDS PAST

Further analysis of the NOV76a protein yielded the following properties shown in Table 76B.

Table 76B. Protein Sequence Properties NOV76a	
PSort analysis:	0.6850 probability located in endoplasmic reticulum (membrane); 0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 25 and 26

A search of the NOV76a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 76C.

Table 76C. Geneseq Results for NOV76a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV76a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU32848	Novel human secreted protein #3339 - Homo sapiens, 2486 aa. [WO200179449-A2, 25-OCT-2001]	26..2498 1..2486	2316/2555 (90%) 2339/2555 (90%)	0.0
AAR05707	Acetyl-CoA-carboxylase - Gallus sp, 2324 aa. [JP02057179-A, 26-FEB-1990]	163..2498 17..2324	1728/2375 (72%) 2003/2375 (83%)	0.0
AAB86033	Bovine acetyl-coenzyme A carboxylase-alpha protein fragment - Bos taurus, 2288 aa. [DE19946173-A1, 05-APR-2001]	204..2497 14..2288	1719/2342 (73%) 1969/2342 (83%)	0.0
AAR98811	Erysiphe graminis acetyl coenzyme A carboxylase - Erysiphe graminis f.sp.hordei, 2273 aa. [FR2727129-A1, 24-MAY-1996]	235..2490 42..2271	1045/2326 (44%) 1432/2326 (60%)	0.0
AAY24150	Candida albicans acetyl CoA carboxylase - Candida albicans, 2270 aa. [WO9932635-A1, 01-JUL-1999]	239..2489 88..2269	1015/2300 (44%) 1396/2300 (60%)	0.0

In a BLAST search of public sequence databases, the NOV76a protein was found to have homology to the proteins shown in the BLASTP data in Table 76D.

Table 76D. Public BLASTP Results for NOV76a

Protein Accession Number	Protein/Organism/Length	NOV76a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O00763	Acetyl-CoA carboxylase 2 (EC 6.4.1.2) (ACC-beta) [Includes: Biotin carboxylase (EC 6.3.4.14)] - Homo sapiens (Human), 2483 aa.	1..2498 1..2483	2349/2528 (92%) 2384/2528 (93%)	0.0
O70151	ACETYL-COA CARBOXYLASE - Rattus norvegicus (Rat), 2456 aa.	1..2497 1..2455	2068/2524 (81%) 2224/2524 (87%)	0.0
CAA48770	ACETYL-COA CARBOXYLASE (EC 6.4.1.2) - Homo sapiens (Human), 2339 aa.	163..2498 17..2339	1921/2390 (80%) 2086/2390 (86%)	0.0

P11029	Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Includes: Biotin carboxylase (EC 6.3.4.14)] - Gallus gallus (Chicken), 2324 aa.	163..2498 17..2324	1732/2375 (72%) 2004/2375 (83%)	0.0
P11497	Acetyl-CoA carboxylase 1 (EC 6.4.1.2) (ACC-alpha) [Includes: Biotin carboxylase (EC 6.3.4.14)] - Rattus norvegicus (Rat), 2345 aa.	163..2497 17..2345	1736/2396 (72%) 1993/2396 (82%)	0.0

Pfam analysis predicts that the NOV76a protein contains the domains shown in the Table 76E.

Table 76E. Domain Analysis of NOV76a			
Pfam Domain	NOV76a Match Region	Identities/ Similarities for the Matched Region	Expect Value
CPSase_L_chain: domain 1 of 1	249..372	49/132 (37%) 117/132 (89%)	2.2e-57
CPSase_L_D2: domain 1 of 1	374..619	102/253 (40%) 218/253 (86%)	6.6e-118
Biotin_carb_C: domain 1 of 1	640..747	40/118 (34%) 100/118 (85%)	1.9e-53
biotin_lipoyl: domain 1 of 1	885..951	22/75 (29%) 56/75 (75%)	6.5e-17
Carboxyl_trans: domain 1 of 2	1783..1878	31/100 (31%) 88/100 (88%)	7.4e-34
GTP_cyclohydroI: domain 1 of 1	2287..2304	6/18 (33%) 13/18 (72%)	6.6
Carboxyl_trans: domain 2 of 2	1897..2374	191/504 (38%) 447/504 (89%)	4.1e-258

Example 77.

The NOV77 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 77A.

Table 77A. NOV77 Sequence Analysis		
	SEQ ID NO: 219	1624 bp

NOV77a, CG59630-01 DNA Sequence	CGCGCGCCGGGGATGGAGCCGAGCCCGGCGCGCCCGGAGCTGCCGGCGCGGGGCC CCGGCGGCGCCTGCGAGCTGGGCGGCGCGCGGCGCGCCATGAGCCTCGCCAT CCACAGACACCAGGCAACCGCTACGACCTGGCCGTGCCGCCACGAGACGGTGGAG GGGTGCGCAAGCGGTTGTCCAGCGCCTCAAAGTGCCCAAGGAGCGCCTGGCTCTTC TCCACAAAGACACGCGGCTCAGTTCGGGGAAGCTGCAGGAGTTCGGCGTGGGTGATGG CAGCAAGCTGACCTTGGTACCCACCGTGAAGCGGGCCTCATGTCTCAGGCCTCAAGG CCGGAACAGTCCGTGATGCAAGCTCTCGAGAGTCTACGGAGACGAGCCCCAGCGG CGCCCGGGCGGCGCGGCTGGCGGAGGAGGCTTCGGGAAATACAGATTCAATTTATT TAAGCGTCCGTGGCACCAGCAGGAGCCAGAGCCAGAGAGGGGCGGCGAGAGGCC CAGGTCAGTGAATTCCTGTGGGCGGTTCCGCCACTGACACTGGCCTTCGGTGTGGGCG ACCACATGATGTTCTGTGAGCTGCAGCTCGCGGCCAGCAGCTCCACTGCAACACCG CCATGTGTGGCGGCTCGGCGCGCGCGCTGTGCGCGGGGGGACCCAGCATAGCC TCCCCGTGTCTCGCCCTGCGGCGCGGTGTCCAGTCCGCGCCGAGTCCCCCGGTGC CCACCGGCGGCTCCCTGCACTCTCCCTCGCCATCACAGCGGCTCTCTCCGTCCCA CGCAGCCTCCACCCTGCGCGGAGCAGATGGACTGCTCCCCACGGCCAGCAGCAGT GCCAGTCTCGGTGCCAGCACCAGTCTACCCAGGGGGCAGCCTGCCCGCGCTCCC GAAAACCCGCGCGCTCATCGAGAGCTTTGTGAATCAGCCCCGGGGGTCTTCTCAGG GACCTTCTGTGGCAGCTACACCCAACTGCCAAGACAGCAGCGGGCGGCGCGGCGT GACATCGGCACCATCTGCAGATCCTGAACGACCTCCTGAGCGCCACCGGCACTACC AGGGCATGCCCCCTTCGCTGGCCAGCTCCGCTGCCACGCCAGTGTCTCCCGGCTC ACCGGCGCGGAGCTGCGCCCGAGAACTACCTCCTGCGAGAAGCTCAGGCTGCCCGC TCAGCCTCCCTGTGCGAGGCCAGAGCCAGATCCGATGTGCAAGCCCCGGGTGACC GGCTTCGGCAGACAGAAAACCGCGCCACGCGCTGCAAGGTGGAAACGGTGCAGCTGCT TCTGCAGCAGAAACGGCTCCGTAGAAAGGCCCGCGGACGCGCGGGGTCCGTACCAC TGGTCACCCAGCCGCAAGGCCGCGCGCAGCAGCAGCAGTAGCAGCGGGGCGGCGGCA GCCCCAGCAGGCTCCGGCTTGGGCTCGACTTCGAGGACTCCGTGTGGAAGCCAGA AGTCAACCTGACATCAAGTCAGAGTTCGTGGTGGCTTAGGATCTTCGGATCGGCCAC CCTCGCCCCGCAACCCAGGCCAGGGCGGCGGGGACTCCGAGAGCCCCCGGAGAGAAC
	ORF Start: ATG at 13 ORF Stop: TAG at 1546
	SEQ ID NO: 220 511 aa MW at 53949.3kD
NOV77a, CG59630-01 Protein Sequence	MEPQPGGARSRRGAPGACELGPAAEAPMSLAHSTTGTRYDLAVPPDETVEGLRK RLSQRLLKVPKERLALLHKDTRLSSGKLQEFVGDGSKLTLVPTVEAGLMSQASRPEQS VMQALESLTETQPPAAGPGRAGGGGFRKYRFLFKRPWHRQGPQSPERGGERPQVSD FLSGRSPPLTALRVGDHMMFVQLQLAAQHAPLQHRHVLAAAAAARGDPPIASPV SPCRPVSSAARVPPVPTSPSPASPSPIITAGSFRSHAASTTCPEQMDCSPTASSSASPG ASTTSTPGASPAPRSRKPAGVIESFVNHPGVFSGTFSGLTLPNCQDSSGRPRRDIGT ILQILNDLLSATRHYQMPPSLAQLRCHAQCSPASPADLAPRTTSCSKLTAAPSASL LQGSQIRMKPPGDRLRQENRATRCKVERLQLLLQKRLRRKARRDARGPYHWSPS RKAGRSDSSSSGGGSPSEASGLGLDFEDSVWKPEVNPDIKSEFVVA

Further analysis of the NOV77a protein yielded the following properties shown in Table 77B.

Table 77B. Protein Sequence Properties NOV77a	
PSort analysis:	0.3000 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.1526 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV77a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 77C.

Table 77C. Geneseq Results for NOV77a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV77a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB56832	Human prostate cancer antigen protein sequence SEQ ID NO:1410 - Homo sapiens, 236 aa. [WO200055174-A1, 21-SEP-2000]	267..493 1..227	189/227 (83%) 195/227 (85%)	e-104

In a BLAST search of public sequence databases, the NOV77a protein was found to have homology to the proteins shown in the BLASTP data in Table 77D.

Table 77D. Public BLASTP Results for NOV77a				
Protein Accession Number	Protein/Organism/Length	NOV77a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JJJ6	MIDNOLIN - Mus musculus (Mouse), 508 aa.	1..511 1..508	475/514 (92%) 486/514 (94%)	0.0
Q96BW8	SIMILAR TO MIDNOLIN - Homo sapiens (Human), 177 aa (fragment).	338..511 4..177	174/174 (100%) 174/174 (100%)	2e-97
Q9W2S4	CG9732 PROTEIN - Drosophila melanogaster (Fruit fly), 989 aa.	213..363 524..677	58/155 (37%) 80/155 (51%)	6e-18
AAL40834	BPLF1 - Human herpesvirus 4 (Epstein-Barr virus), 3179 aa.	200..406 320..530	64/223 (28%) 95/223 (41%)	2e-07
Q9BKV7	PPG3 - Leishmania major, 1325 aa.	213..328 984..1104	37/121 (30%) 66/121 (53%)	2e-06

PFam analysis predicts that the NOV77a protein contains the domains shown in the Table 77E.

Table 77E. Domain Analysis of NOV77a

Pfam Domain	NOV77a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ubiquitin: domain 1 of 1	31..99	19/79 (24%) 46/79 (58%)	0.00033
PI3_PI4_kinase: domain 1 of 1	411..427	7/18 (39%) 14/18 (78%)	1.5

Example 78.

The NOV78 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 78A.

Table 78A. NOV78 Sequence Analysis

	SEQ ID NO: 221	1034 bp
NOV78a, CG59561-01 DNA Sequence	CCACCGCCACAGCTGCCAGCATGTCTGGCCCAGACATCAAGACGCCGACCGCCATCCA GATCTGCCGATTATGCGGGACGCTAATGTGGCCCGCAATGTCTACGGCGGGACCATC CTGAAGATGATCAAAGAGGCGGGCGCCATCATCAGCACC CGGCATTGCAATCCGCAGA ACGGGGATCGCTGTGTGGCCGCTCTGGCTCGGGTCGAGTGCACCCACTTCTGTGGCC CATGTGCATCGGTGAGGTGGCCACGTCAGCGCGGAGATCACCTACACCTCCAAGCAC TCTGTGGAGGTGAGGTCAACATGATGTCCGAAAACATCCTCACAGGTGCCAAAAGC TGACCAATAAGGCCACCCTCTGGTATGCGCCCTGTGCTGACGAACGTGGACAAGGT CCTCGAAGAGCCTCCTGTTGTGTATTTCCGGCAGGAGCAGGAGGAGGAGGGCCAGAAG CGGTACAAAACCCAGAAGCTGGAGCGCATGGAGACCAACTGGAGGAACGGGGACATCG TCCAGCCAGTCCTCAACCCAGAGCCGAACACTGTCAGCTACAGCCAGTCCAGCTTGAT CCACCTGGTGGGGCCTTCAGACTGTACCCTGCACAGCTTCGTGTCATGAAGGGGTGACC ATGAAGGTCATGGACGAGGTGCGCGGGATCTTGGCTGCACGCCACTGCAAGACCAACC TCGTCACAGCCTCCATGGAGGCCATTAATTTTGACAACAAGATCAGAAAAGGCTGCAT CAAGACCATCTCCGACGCATGACCTTCACGAGCAATAAGTCCGTAGAGATCGAGGTG TTGGTGGATGCCGACTGTGTGTGGACAGCTCTCAGAAGCGCTACAGGGCCGCCAGTG TCTTCACCTATGTGCTGAGCCAGGAAGGCAGGTGCTGCCCATGCCCCAGCTCGT GCCGGAGACCCAGGACGAGAAGGGCTTTGAGGCCTGGCTCGGTGGCTCACGCCTATAA TCCAGCACTTTAGGATGCTGAGGCAGGCGGATCACTTGACGTCAGGA	
	ORF Start: ATG at 21	ORF Stop: TAA at 984
	SEQ ID NO: 222	321 aa MW at 35738.7kD
NOV78a, CG59561-01 Protein Sequence	MSGPDIKTPTAIQICRIMRDANVARNVYGGTILKMIKEAGAIISTRHCNPQNGDRCVA ALARVECTHFLWPMCI GEVAHVSAEITYTSKHSVEVQVNMSENILTGAKKLTNKATL WYAPLSLTNVDKVL EPPVYFRQEEEGQKRYKTQKLERMETNWRNGDIVQPVLPN EPNTVSYSSQLIHLVGPSDCTLHSFVHEGVMTKVMDEVAGILAA RHCKTNLVTASME AINFDNKIRKGCIKTISGRMTFTSNKSVEIEVLVDADCVVDSQKRYRAASVFTYVSL SQEGRSLPMPQLVPETQDEKGFEAWLGGSRL	

Further analysis of the NOV78a protein yielded the following properties shown in Table 78B.

Table 78B. Protein Sequence Properties NOV78a	
PSort analysis:	0.8000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV78a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 78C.

Table 78C. Geneseq Results for NOV78a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV78a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW74896	Human secreted protein encoded by gene 169 clone HPTTU11 - Homo sapiens, 339 aa. [WO9839448-A2, 11-SEP-1998]	1..310 1..313	273/313 (87%) 292/313 (93%)	e-154
AAY71115	Human Hydrolase protein-13 (HYDRL-13) - Homo sapiens, 375 aa. [WO200028045-A2, 18-MAY-2000]	1..310 33..316	247/313 (78%) 266/313 (84%)	e-133
AAY35275	Chlamydia pneumoniae transmembrane protein sequence - Chlamydia pneumoniae, 155 aa. [WO9927105-A2, 03-JUN-1999]	187..310 16..138	35/124 (28%) 72/124 (57%)	1e-09
AAG92590	C glutamicum protein fragment SEQ ID NO: 6344 - Corynebacterium glutamicum, 339 aa. [EP1108790-A2, 20-JUN-2001]	24..309 35..307	69/296 (23%) 112/296 (37%)	7e-08
AAB76624	Corynebacterium glutamicum MCT protein SEQ ID NO:230 - Corynebacterium glutamicum, 339 aa. [WO200100805-A2, 04-JAN-2001]	24..309 35..307	69/296 (23%) 112/296 (37%)	7e-08

In a BLAST search of public sequence databases, the NOV78a protein was found to have homology to the proteins shown in the BLASTP data in Table 78D.

Table 78D. Public BLASTP Results for NOV78a
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Protein Accession Number	Protein/Organism/Length	NOV78a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O00154	Cytosolic acyl coenzyme A thioester hydrolase (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (CTE-II) (Brain acyl-CoA hydrolase) (BACH) - Homo sapiens (Human), 338 aa.	1..310 1..313	274/313 (87%) 293/313 (93%)	e-154
Q91V12	ACYL-COA HYDROLASE (HYPOTHETICAL 37.6 KDA PROTEIN) - Mus musculus (Mouse), 338 aa.	1..310 1..313	265/313 (84%) 287/313 (91%)	e-150
Q64559	Cytosolic acyl coenzyme A thioester hydrolase (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (CTE-II) (Brain acyl-CoA hydrolase) (BACH) (ACT) (LACH1) (ACH1) - Rattus norvegicus (Rat), 338 aa.	1..310 1..313	263/313 (84%) 286/313 (91%)	e-149
JC5416	palmitoyl-CoA hydrolase (EC 3.1.2.2), hepatic - rat, 343 aa.	12..310 17..318	251/302 (83%) 276/302 (91%)	e-142
Q9Y541	DJ20208.3.1 (HBACH (BRAIN ACYL-COA HYDROLASE (ACYL COENZYME A THIOESTER HYDROLASE, EC 3.1.2.2)) (ISOFORM 1)) - Homo sapiens (Human), 237 aa (fragment).	1..202 33..236	181/204 (88%) 190/204 (92%)	e-100

PFam analysis predicts that the NOV78a protein contains the domains shown in the Table 78E.

Table 78E. Domain Analysis of NOV78a			
Pfam Domain	NOV78a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Acyl-CoA_hydro: domain 1 of 1	165..305	46/147 (31%) 131/147 (89%)	1.1e-47

Example 79.

The NOV79 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 79A.

Table 79A. NOV79 Sequence Analysis

	SEQ ID NO: 223	4203 bp
NOV79a, CG59452-01 DNA Sequence	AATGTGATGGGATCACTAGCATGTCTGCGGAGAGCGGCCCTGGGACGAGATTGAGAAA TCTGCCAGTAATGGGGATGGACTAGAACTTCCCAAATGTCTACAACACAGGCCAG GCCAACCCAGCCAGCCACGACGACCAACCCCGCCCGCCAGAGACCTCCA ACCCTAACAGCCCAAGAGGACAGCAACCAACTGCAATACCTGCTCAGAGTGGTGT CAAGACACTATGGAAACACCACTTTGCATGGCCTTCCAGCAGCCTGTGGATGCCGTC AAGCTGAACCTCCCTGATTACTATAAGATCATTTAAACGCCTATGGATATGGGAACAA TAAAGAAGCGCTTGGAAACAACTATTACTGGAATGCTCAGGAATGTATCCAGGACTT CAACACTATGTTTACAAATTGTTACATCTACAACAAGCCTGGAGATGACATAGTCTTA ATGGCAGAAGCTCTGGAAGAGCTCTTCTTGCAAAAATAAATGAGCTACCCACAGAAG AAACCGAGATCATGATAGTCCAGGCAAAAGGAAGAGGACGTGGGAGGAAAGAAACAGG TACAGCAAAACCTGGCGTTTCCACGGTACCAACACAACCTCAAGCATGCACTCCTCCG CAGACCCAGACCCCTCAGCCGAATCCTCCTCCTGTGACGGCCACGCCTACCCCTTCC CTGCCGTCACCCGGACCTCATCGTCCAGACCCCTGTGATGACAGTGGTGCCTCCCA GCCACTGCAGACCCCGCCAGTGCCTCCCGCCAGCCACAACCCCGCTCCAGCT CCCCAGCCCGTACAGAGCCACCCACCCATCATCGCGGCCACCCACAGCCTGTGAAGA CAAGAAGGGAGTGAAGAGGAAAGCAGACACCCACCCCGCCAGCATTGACCCCAT TCACGAGCCCTCGCTGCCCCCGAGCCCAAGACCCCAAGTGGGAGGAAAGAAACAGG GAGAGCAGCCGCGCTGTGAAACCTCCAAAGAAGGACGTGCCGACTCTCAGCAGCACC CAGCACCAGAGAAGAGCAGCAAGGTCTCGGAGCAGCTCAAGTCTGACGCGCATCCT CAAGGAGATGTTTCCAAAGAAGCAGCCGCGCTACGCTGGCCCTTCTACAAGCCTGTG GACGTGGAGGCACTCGGCTTACACGACTACTGTGACATCATCAAGCACCCATGGACA TGAGCACAATCAAGTCTAACTGGAGGCCGCTGAGTACCGTGTGCTCAGGAGTTTGG TGCTGACGTCCGATTGATGTTCTCCAAGTCTATAAGTACAACCTCCTGACCATGAG GTGGTGGCCATGGCCCGCAAGCTCCAGGATGTGTTTCAAAATGCGCTTTGCCAAGATGC CGGACGAGCTGAGGAGCCAGTGGTGGCGGTGCTCCTCCCGGAGCCTCCCTCCAC CAAGGTTGTGGCCCGCCCTCATCCAGCGACAGCAGCAGCGATAGCTCCTCGGACAGT GACAGTTCGACTGATGACTCTGAGGAGGAGCGAGCCAGCGGTGGCTGAGCTCCAGG AGCAGCTCAAAGCCGTGCACGAGCAGCTTGACGCTCTCTCAGCCCGCAGAGCAAA ACCAAAGAAAAGGAGAAAGACAAGAGGAAAAGAAAAGAAAAGCAGAAAAGGAAA GAGGAAGTGAAGAGAAATAAAAAAGCAAGCCAAAGGAACCTCCTCTAAAAGAGCA AGAAAAATAATAGCAGCAACAGCAATGTGAGCAAGAAGGAGCCAGCGCCATGAAGAG CAAGCCCTCCCAAGTATGAGTCCGAGGAAGAGGACAAGTCAAGCACCCATGGCAT GAGGAGAAGCGGAGCTCAGCTTGGACATCAACAAGCTCCCGGCGAGAAGCTGGGCC GCGTGGTGACATCATCCAGTCACGGGAGCCCTCCCTGAAGAAATCCAACCCCGACGA GATTGAAATCGACTTTGAGACCTGAAGCCGTCCCACTGCGTGGAGTGGAGCGCTAT GTCACTCCTGTTTGGGAAAGAAAAGGAACCTCAAGCTGAGAAAGTGTGATGATTG CCGGCTCCTCAAGATGAAGGCTTCTCGTCTCAGAGTCCGAGAGCTCCAGTGAATC CAGCTCCTCTGACAGCAAGACTCCGAAACAGAGATGGCTCCGAAGTCAAAAAAGAA GGGCAACCCGGGAGGAGCAGAAAGCAGCACCATCATCACCACCATGCGAGC AGGCCCGGCTCCTGTGCCCCAGCAGCCGCCCCGCTCCCGCAGCAGCCCCACCGCC TCCACCTCCGAGCAGCAACAGCAGCCGCCCCCGCTCCCGACCCCTCCATGCCG CAGCAGGCGAGCCCGCGATGAAGTCTCGCCCCACCTTCATTGCCACCCAGGTGC CCGTCTGGAGCCCGCAGCTCCAGGAGCGTCTTTGACCCCATCGGCCATTCACCA GCCATCCTGCACCTGCCGAGCCTGAGCTGCCCTCACCTGCCCGAGCCGCTGAG CACAGCACTCCACCCCATCTCAACAGCAGCAGTGGTCTCTCCTCAGCTTTGCACA ACGCACTACCCCGCAGCCATCACGGCCAGCAACCGAGCCGCTGCCCTGCCTCCAA GCCGCGCCCGCCCGCAGCCGTGTCAACGCTTGACCCAAACCCCTGCCACAG CCCCCATGGCCCAACCCCAAGTGTGCTGGAGGATGAAGAGCCACTGCCCCAC CCCTCACCTCCATGCAGATGCACTGTACTGCAGCAGCTGCAGAAAGTGCAGCCCC TACGCCGCTACTCCTTCCGTGAAGGTGCACTCCAGCCCGCCACCCCGCTGCCGCCC CCACCCACCCCTCTGTGCAGCAGCAGTGCAGCAGCAGCCGCCACCCACCCACCCAC CCAGCCCCAGCCTCCACCCAGCAGCAGCATCAGCCCTCCAGCGCCGCTGCACTT GCAGCCCATGCAGTTTTCACCCACATCCAACAGCCCCCGCCACCCAGGGCCAGCAG CCCCCCCATCCGCCCGCAGGCCAGCAGCCACCCCGCGCAGCTGCCAAGCCTCAGC AAGTCATCCAGCACCACCATTCACCCCGGCAACCAAGTCCGAGCCCTACTCAACCGG TCACCTCCGCAAGCCCTCCCGCTTATGATACATTCACCCAGATGTCACAGTTT CAGAGCCTGACCCACAGTCTCCACCCAGCAAAACGTCCAGCCTAAGAAAAGGTTAA CTGGCAGGCTGGGCCAAGTCTGTGGGCCAGGGCCGGGGGTGCCCTGCCACTCACC GGCCGCTGTGCTGTGCCATCCAGGAGTGCCTGCTGCTCCTCGTGGTCCAGCCCCAG CCCTCGTGGTGGTGAAGGAGGAGAAGTCCACTACCCCATCATCCGAGCGAGCCCT TCAGCCCTCGCTGCGGCCGAGCCCGCAAGCACCCCGGAGAGCATCAGAGCCCGCT TTATGTTCCAGGGCCGGAATGAAGCCTGTGGATGTGGGAGGCTGTGATCCGGCCC CCAGAGCAGAACGCACCGCCACAGGGGCCCTGACAAGGACAAACAGAAACAGGAGC CGAAGACTCCAGTTGCGCCCAAAAGGACCTGAAAATCAAGAACATGGGCTCCTGGGC CAGCTTAGTGAGAAAGCATCCGACACCCCTCCTCCACAGCCCAAGTCATCAGCGAC AGCTTCGAGCAGTTCGCGCGCGCTCGGGAGAAAGAGGAGCGTGAAGAGCCCTGA AGGCTCAGGCCGAGCAGCTGAGAAGGAGAAGGAGCGGTGCGGCAGGAGCGCATGAG GAGCCGAGAGGACGAGGATGCGCTGGAGCAGGCCCGCGGGCCATGAGGAGGACGCT CGGCGCCAGGAGCAGCAGCAGCAGCGCCAGGAGCAACAGCAGCAGCAACAGC AAGCAGCTGCGGTGGCTGCCCGCCACCCACAGGCCAGAGCTCCAGCCCCAGTC CATGCTGGACAGCAGAGGGAGTTGGCCCGGAAGCGGGAGCAGGAGCGAAGACGCCG GAAGCCATGGCAGCTACCATGACATGAATTTCCAGAGTGTCTATTGTCAATATTG AAGAAAACTTTTCTGAGCGCACCTAG	

	ORF Start: ATG at 21	ORF Stop: TGA at 4191	
	SEQ ID NO: 224	1390 aa	MW at 154728.4kD
NOV79a, CG59452-01 Protein Sequence	MSAESGPGTRLRLNLPVMDGLSETSMSTTQAQAQPQANAASTNPPPPETSNNPKPKR QTNQLQYLLRVVLKTLWKHQFAWPFQPPVDAVKLNLPDYKIKTPMDMGTIKKRLN NYYWNAQECIQDFNTMFTNCYIYNKPGDDIVLMAEALFKLFLQKINELPTEETEIMIV QAKGRGRGRKETGTAKPGVSTVPNTTQASTPPQTQTPQPNPPVQATPHFPFAVTPDL IVQTPVMTVVPQPLQTPPPVPPQPPPPAPAPQPVQSHPIIAATPQPVKTKKGVKR KADTTTPTTIDPIHEPPSLPPPEKTTKLGRRESSRPVKPPKDVPPSQHHPAPEKSS KVSEQLKCCSGILKEMFAKHAAYAWPFYKPDVVEALGLHDYCDIHKHPMDMSTIKSK LEAREYRDAQEFQADVRLMFSNCYKYNPPDHEVVAMARKLQDVFEMFRAKMPDEPEEP VVAVSSPAVPPPTKVAVPPSSSDSSSDSSSDSSDSDSDSEERAQRLAEQLKAVH EQLAALSQPQNKPKKKEKDKKEKKKEKHKKKEVEENKSKAKEPPPKTKKNNSSN SNVSKKEPAPMKSPPPTYESSEEDKCKPMSYEEKRQLSLDINKLPGEKLGRRVHIQ SREPSLKNSNPDEIEIDFETLKPSTLRELERVYTSCLRKKRKPQAEKVDVIAGSSKMK GFSSSESESSSSSDSEDSETEMAPKSKKKHGPGRQKQHSHHHHQQMQQAPAVP QQPP PGSVFDPIGHFTQPIHLPPQLPPELPPHLPQPEHSTPPLNQHAAVSPALHNALPQPP SRPSNRAALPPKPARPPAVSPALTQTPLLPQPPMAQPPQVLEDEEPPAPPLTSMQM QLYLQQLQKVPPTPLLPVSVKVSQPPPPPLPPPPHPSVQQQLQQQPPPPPPPPPPPP QQQHQPVRPVHLQPMQFSTHIQQPPPPQPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP SPRHHKSDPYSTGHLEAPSPMLIHSPQMSQFQSLTHQSPQPNVQPKKQVTRAGPS FVGQGRGCLPTSPAAPVVPSPQELRAASVVPQPLVVVKEEKIHSPIIRSEPPSPSLRP EPPKHPESIKAPVYVPGPEMKPVDVGRPVIRPPEQNAPPPGAPDKDKQKQEPKTPVAP KKDLKIKNMGSWASLVQKHPTTPSTAKSSSDSFEQFRRAAREKEBREKALKAQAEHA EKEKERLRQERMRSREDEDALEQARRAHEEARRRQEQQQQQQEQQQQQQQQAAAVAA AATPQAQSSQPSMLDQRELARKREQERRRREMAATIDMNFQSDLLSI FEENLF		

Further analysis of the NOV79a protein yielded the following properties shown in Table 79B.

Table 79B. Protein Sequence Properties NOV79a	
PSort analysis:	0.9800 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV79a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 79C.

Table 79C. Geneseq Results for NOV79a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV79a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AA57898	Human transmembrane protein HTMPN-22 - Homo sapiens, 688 aa. [WO9961471-A2, 02-DEC-1999]	1..667 1..667	667/667 (100%) 667/667 (100%)	0.0
AA507027	Breast cancer associated antigen	44..724 13..708	407/732 (55%) 487/732 (65%)	0.0

	754 aa. [WO9904265-A2, 28-JAN-1999]			
AAY07114	WO9904265 Seq ID No: 685 - Homo sapiens, 947 aa. [WO9904265-A2, 28-JAN-1999]	35..738 4..686	357/761 (46%) 444/761 (57%)	e-170
AAW81168	Transcriptional regulatory factor RING3 - Homo sapiens, 947 aa. [WO9848015-A1, 29-OCT-1998]	35..738 4..686	357/761 (46%) 444/761 (57%)	e-170
AAU16206	Human novel secreted protein, Seq ID 1159 - Homo sapiens, 235 aa. [WO200155322-A2, 02-AUG-2001]	51..255 1..203	118/206 (57%) 137/206 (66%)	2e-59

In a BLAST search of public sequence databases, the NOV79a protein was found to have homology to the proteins shown in the BLASTP data in Table 79D.

Table 79D. Public BLASTP Results for NOV79a				
Protein Accession Number	Protein/Organism/Length	NOV79a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O60885	Bromodomain-containing protein 4 (HUNK1 protein) - Homo sapiens (Human), 1362 aa.	1..1390 1..1362	1357/1391 (97%) 1360/1391 (97%)	0.0
Q9ESU6	CELL PROLIFERATION RELATED PROTEIN CAP - Mus musculus (Mouse), 1400 aa.	1..1390 1..1400	1318/1400 (94%) 1338/1400 (95%)	0.0
AAL67833	BROMODOMAIN-CONTAINING PROTEIN BRD4 LONG VARIANT - Mus musculus (Mouse), 1400 aa.	1..1390 1..1400	1318/1400 (94%) 1338/1400 (95%)	0.0
O60433	R31546_1 - Homo sapiens (Human), 731 aa (fragment).	1..719 12..730	719/719 (100%) 719/719 (100%)	0.0
AAL67834	BROMODOMAIN-CONTAINING PROTEIN BRD4 SHORT VARIANT - Mus musculus (Mouse), 723 aa.	1..719 1..720	694/720 (96%) 700/720 (96%)	0.0

PFam analysis predicts that the NOV79a protein contains the domains shown in the Table 79E.

Table 79E. Domain Analysis of NOV79a

Pfam Domain	NOV79a Match Region	Identities/ Similarities for the Matched Region	Expect Value
bromodomain: domain 1 of 2	63..152	42/92 (46%) 82/92 (89%)	8.6e-45
bromodomain: domain 2 of 2	356..445	40/92 (43%) 81/92 (88%)	3e-40

Example 80.

The NOV80 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 80A.

Table 80A. NOV80 Sequence Analysis			
	SEQ ID NO: 225	1776 bp	
NOV80a, CG59572-01 DNA Sequence	TGGTTCGTTTATTCTCTGGGGTTGTCATATCATGGCTTATAATGACACAGACAGAAACC AGACTGAGAAGCTCCTAAAAAGAGTACGAGAACTGGAGCAAGAGGTGCAAAGACTTAA AAAGGAACAGGCCAAAAATAAGGAGGACTCAAACATTAGAGAAAAATTCAGCAGGAGCT GGAAAACTAAGCGTGCATTGATTTCAGTGTCTCATGGCCGAAGACACGTAGCCCTAA GAATAGCCTATATGGGCTGGGGATACCAGGGCTTTGCTAGTCAGGAAAAACAAATAA TACCATTGAAGAGAAACTGTTTGAAGCTCTAACCAAGACTCGACTAGTAGAAAGCAGA CAGACATCCAACATATCACCGATGTGGGAGAACAGATAAAGGAGTTAGTGCCCTTTGGAC AGGTGATCTCACTTGACCTTCGCTCTCAGTTTCCAAGGGGCAGGGATTCCGAGGACTT TAATGTAAAAGAGGAGGCTAATGCTGCTGCTGAAGAGATCCGTTATACCCACATTCTC AATCGGGTACTCCCTCCAGACATCCGTATATTGGCCTGGGCCCCCTGTAGAACCAAGCT TCAGTGTCTAGGTTAGCTGCCTTGAGCGGACTTACCGCTATTTTTCCCTCGTGCTGA TTTAGATATTGTAACCATGGATTATGCAGCTCAGAAGTATGTTGGCACCCATGATTTT AGGAAGTTGTGTAATAATGGATGTAGCCAACGGTGTGATTAAATTTTCAGAGGACTATTC TATCTGCTCAAGTACAGCTAGTGGGCCAGAGCCAGGTGAGGGGAGATGGCAAGAACCC TTTCCAGTTATGTCAGTTTGAAGTGAAGTGGCCAGGCATTCTTTATCATCAAGTCCGA TGATATGATGGCTATCCTCTTTCTGATTGGCCAAGGAATGGAGAAGCCAGAGATTATTG ATGAGCTGCTGAATATAGAGAAAAATCCCCAAAGCCTCAATATAGTATGGCTGTAGA ATTTCTCTAGTCTTATATGACTGTAAGTTTGAATAATGTCAAGTGGATCTATGACCAG GAGGCTCAGGAGTTCAATATTACCCACCTACAACAAGTGTGGGCTAATCATGCTGTCA AAACTCACATGTTGTATAGTATGCTACAAGGACTGGACACTGTTCCAGTACCCTGTGG AATAGGACCAAGATGGATGGAATGACAGAATGGGGAATGTTAAGCCCTCTGTGCATA AAGCAGACCAAGTGCCTTTGTAGAAGGAGTGAAGATGCGCACATATAAGCCCTCATGG ACCGTCTCTAAATGCCAAGGACTGGAATCCCGGATCCAGCATTTTGTACGTAGGGGACG AATTGAGCACCCACATTTATTCATGAGGAAGAAACAAAGCCAAAGGGACTGTAAT GACCACTAGAGGAAGAGAATACTAATTTGGAGACACCAACGAAGAGGGTCTGTGTTG ACACAGAAATTAAAGCATCATTTAACCATAGACAATTTGCCAGGATCTAGGAACCA CTAATGGTAGGTGGACAGAAAAGGAAAAAATTTACTTGCAGTACTAGGAA TTCAGATGATCAGCTCTTAAAAAAGAAAAAAGCAAAAGACTTAAGCCCTATTAAG GAAGTTATTGCTTTAATAAGAAATTTCAAATATTCTCTTATCCCGTCCAAAGGATT AAGCGATTAAAGAACGTAAAATGGAGATGTATTTACATACACGTGGAACCTGTGCCT TGTATTCAAATTCATTAAAGCCTAATCTGCAAGAA		
	ORF Start: ATG at 31	ORF Stop: TAA at 1474	
	SEQ ID NO: 226	481 aa	MW at 55646.8kD
NOV80a, CG59572-01 Protein Sequence	MAYNDTRDNRQTEKLLKRVRELEQEVQRLKKEQAKNKEDSNIRENSAGAGTKRAFDFS AHGRRHVALRIAYMGWYQGFASQENTNNTIEEKLFEALTKRLVESRQTSNYHRCGR TDKGVSAFGQVLSLDLRSQFPRGRDSEDFNVKEEANAEEIRYTHILNRVLPDPDIRI LAWAPVEPSFSARFSCLERTYRYFFPRADLDIVTMDYAAQYVVGTHDFRNLCKMDVAN GVINFQRTILSAQVQLVQSPGEGRWQEPFQLCQFEVTFQAFLYHQVRCHMAILFLIG QGMEKPEI IDELLNIEKNPQKPQYSMAVEFPLVLYDCKFENVKWIYDQEAQEFNITHL QQLWANHAVKTHMLYSMLQGLDTPVPCGIGPKMDGMTWGNVKKPSVIKQTSFVFBGV KMRTYKPLMDRPPKQGLSRIQHFRVRRGRIEHPHLFHEETKAKRDCNDTLEEENTNL ETPTKRVCVDTEIKSII		
	SEQ ID NO: 227	1508 bp	
NOV80b,	CATGGCTTATAATGACACAGACAGAAACAGACTGAGAAGCTCCTAAAAAGAGTAGCA GAAGCTGGAGCAAGAGGTGCAAAGACTTAAAAAGGAACAGGCCAAAAATAAGGAGGACT		

CG59572-02 DNA Sequence	CAAACATTAGAGAAAATTCAGCAGGAGCTGGAAAACTAAGCGTGCATTGATTTCAG TGCTCATGGCCGAAGACACGTAGCCCTAAGAATAGCCTATATGGGCTGGGGATACCAG GGCTTTGCTAGTCAGGAAAACACAAATAATACCATTTGAAGAGAACTGTTTGAAGCTC TAACCAAGACTCGACTAGTAGAAAGCAGACAGACATCCAATATCACCAGATGTTGGAG AACAGATAAAGGAGTTAGTGCTTTGGACAGGTGATCTCACTTGACCTTCGCTCTCAG TTTCCAAGGGGAGGGATTCCGAGGACTTTAATGTAAAAGAGGAGGCTAATGCTGCTG CTGAAGAGATCCGTTATACCCACATTCTCAATCGGGTACTCCCTCCAGACATCCGTAT ATTGGCCTGGGCCCCCTGTAGAACCAAGCTTCAGTGCTAGGTTTCACTGCTGAGCGG ACTTACCGCTATTTTTTCCCTCGTGTGATTTAGATATTGTAACCATGGATTATGCAG CTCAGAAGTATGTTGGCACCCTATGATTTTCAGGAACCTGTGTAAAATGGAGTATAGCCAA CGGTGTGATTAAATTTTCAGAGGACTATTCTATCTGCTCAAGTACAGCTAGTGGGCCAG AGCCCAAGGTGAGGGGAGATGGCAAGAACCTTTCCAGTTATGTAGTTTGAAGTGACTG GCCAGGCATTCTTTATCATCAAGTCCGATGTATGATGGCTATCCTCTTCTGATTGG CCAAGGAATGGAGAAGCCAGAGATTATTGATGAGCTGCTGAATATAGAGAAAAATCCC CAAAAGCCTCAATATAGTATGGCTGTAGAATTTCTCTAGTCTTATATAGCTGTAAGT TTGAAAATGTCAAGTGGATCTATGACCAGGAGGCTCAGGAGTTCAATATTACCCACCT ACAACAAGTGTGGCTAATCATGCTGTCAAACTCACATGTTGTATAGTATGCTACAA GGACTGGACACTGTTCCAGTACCCTGTGGAATAGGACCAAAGATGGATGGAATGACAG AATGGGGAAATGTTAGCCCTCTGTCTATAAGCAGACCAAGTGCCTTTGTAGAAGGAGT GAAGATGCGCACATATAAGCCCTCATGGACCGCTCCTAAATGCCAAGGACTGGAATCC CGGATCCAGCATTTTGTACGTAGGGGACGAATTGAGCACCCACATTTATTCATGAGG AAGAAACAAAAGCCAAAAGGACTGTAATGACACACTAGAGGAAGAGAATACTAATTT GGAGACACCAACGAAGAGGGTCTGTGTTGACACAGAAATAAAAGTATCATTTAACCA TAGACAAATTTGCCAGGATCTAGGAACCACTAATGGTAGGTGGACAGAAAAGGAAAAA		
	ORF Start: ATG at 2	ORF Stop: TAA at 1445	
	SEQ ID NO: 228	481 aa	MW at 55646.8kD
NOV80b, CG59572-02 Protein Sequence	MAYNDTDNRNTEKLLKRVRELEQEVQRLKKEQAKNKEDSNIRENSAGAGKTKRAFDFS AHGRRHVALRIAYMGWYQGFASQENTNNTIEEKLFEALTKTRLVESRQTSNYHRCGR TDKGVSFAFGQVLSLDLRSQFPRGRDSEDFNVKEEANAEEEEIRYTHILNRLVPPDIRI LAWAPVEPSFSARFSLERTYRYFFPRADLDIVTMDYAAQKYVGTDFRNLCKMDVAN GVINFQRTILSAQVQLVGQSPGEGRWQEPFQLCQFEVTVGQAFLYHQVRCMAILFLFIG QGMEKPEIIDELLNIEKNPKQPSMAVEFPLVLYDCKFENVKWIYDQEAQEFNITHL QQLWANHAVKTHMLYSMLQGLDTPVPVCGIGPKMDGMTWGNVVKPSVIKQTSFVGEV KMRTYKPLMDRPFKQGLSRIQHFVRRGRIEHPHLEETKAKRDCNDTLEEENTNL ETPTKRVCDTEIKSII		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 80B.

Table 80B. Comparison of NOV80a against NOV80b.		
Protein Sequence	NOV80a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV80b	1..481	459/481 (95%)
	1..481	459/481 (95%)

Further analysis of the NOV80a protein yielded the following properties shown in Table 80C.

Table 80C. Protein Sequence Properties NOV80a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0142 probability located in microbody (peroxisome)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV80a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 80D.

Table 80D. Geneseq Results for NOV80a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV80a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79457	Human protein SEQ ID NO 3103 - Homo sapiens, 490 aa. [WO200157190-A2, 09-AUG-2001]	1..481 10..490	478/481 (99%) 480/481 (99%)	0.0
AAM78473	Human protein SEQ ID NO 1135 - Homo sapiens, 481 aa. [WO200157190-A2, 09-AUG-2001]	1..481 1..481	478/481 (99%) 480/481 (99%)	0.0
AAG64907	Human depressed growth rate protein DEG1 - Homo sapiens, 248 aa. [CN1296014-A, 23-MAY-2001]	209..431 1..223	223/223 (100%) 223/223 (100%)	e-132
AAG02637	Human secreted protein, SEQ ID NO: 6718 - Homo sapiens, 96 aa. [EP1033401-A2, 06-SEP-2000]	361..456 1..96	96/96 (100%) 96/96 (100%)	5e-53
AAB96592	Putative P. abyssi pseudouridylylase synthase I - Pyrococcus abyssi, 263 aa. [FR2792651-A1, 27-OCT-2000]	65..367 3..261	79/305 (25%) 140/305 (45%)	4e-16

In a BLAST search of public sequence databases, the NOV80a protein was found to have homology to the proteins shown in the BLASTP data in Table 80E.

Table 80E. Public BLASTP Results for NOV80a				
Protein Accession Number	Protein/Organism/Length	NOV80a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BZE2	FKSG32 - Homo sapiens (Human), 481 aa.	1..481 1..481	481/481 (100%) 481/481 (100%)	0.0
Q96J23	HYPOTHETICAL 55.6 KDA PROTEIN - Homo sapiens (Human), 481 aa.	1..481 1..481	478/481 (99%) 480/481 (99%)	0.0
Q96NB4	CDNA FLJ31140 FIS, CLONE IMR322001218, HIGHLY SIMILAR TO MUS MUSCULUS PSEUDOURIDINE SYNTHASE 3 (PUS3) MRNA - Homo sapiens (Human), 481 aa.	1..481 1..481	478/481 (99%) 479/481 (99%)	0.0
Q9JI38	PSEUDOURIDINE SYNTHASE 3 - Mus musculus (Mouse), 481 aa.	5..480 4..480	407/479 (84%) 434/479 (89%)	0.0
Q9D0F7	2610020J05RIK PROTEIN - Mus musculus (Mouse), 316 aa.	5..314 4..315	276/312 (88%) 291/312 (92%)	e-158

Pfam analysis predicts that the NOV80a protein contains the domains shown in the Table 80F.

Table 80F. Domain Analysis of NOV80a			
Pfam Domain	NOV80a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PseudoU_synth_1: domain 1 of 1	88..307	70/249 (28%) 176/249 (71%)	4.7e-57

Example 81.

The NOV81 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 81A.

Table 81A. NOV81 Sequence Analysis		
	SEQ ID NO: 229	3080 bp
NOV81a, CG59522-01 DNA Sequence	TTCCAGCCGGCAGGATGGAGGACGAGGAAGGCCCTGAGTATGGCAAACCTGACTTTGT GCTTTTGGACCAAGTGACCATGGAGGACTTCATGAGGAACCTGCAGCTCAGGTTTCGAG AAGGGCCGCATCTACACCTACATCGGTGAGGTGCTGGTGTCCGTGAACCCCTACCAGG AGCTGCCCTGTATGGGCTGAGGCCATCGCCAGGTACCAGGGCCGTGAGCTCTATGA GCGGCCACCCCATCTCTATGCTGTGGCCAACGCCCTACAAGGCAATGAAGCACCGG	

	<p>TCCAGGGACACCTGCATCGTCATCTCAGGGGAGAGTGGGGCAGGGAAGACAGAAGCCA GTAAGCACATCATGCAGTACATCGCTGCTGTACCAATCCAAGCCAGAGGGCTGAGGT GGAGAGGGTCAAGGACGTGCTGCTCAAGTCCACCTGTGTGCTGGAGGCTTTGGCAAT GCCCCACCAACCGCAATCACAACCTCCAGCCGCTTTGGCAAGTACATGGACATCAACT TTGACTTCAAGGGGGACCCGATCGGAGGACACATCCACAGCTACCTACTGGAGAAAGT TCGGGTCCCTCAAGCAGCAAGTGGGTGAAAGAACTTCCACGCCCTTCTACCAATTGCTG AGAGGCAGTGAGGACAAGCAGCTGCATGAACCTGCACCTTGGAGAGAAACCTGCTGTAT ACAATTTACACACACAGGGAGCAGGACTCAACATGACTGTGAGTGATGAGCAGAGCCA CCAGGCAGTGACCGAGGCCATGAGGGTCATCGGCTTCAGTCTTGAAGAGGTGGAGTCT GTGCATCGCATCTCGCTGGCTGCCATATTGCACCTGGGAAACATCGAGTTTGTGGAGACGG AGGAGGGTGGGCTGCAGAAGGAGGGCTGGCAGTGGCCGAGGAGGCACTGGTGGACCA TGTGGCTGAGCTGACGGCCACACCCCGGGACCTCGTGCTCCGCTCCCTGCTGGCTCCG ACAGTTGCCCTCGGAGGCGAGGAACTCATAGAGAAGGGCCACACTGCAGCTGAGGCCA GCTATGCCCGGGATGCCCTGTGCCAAGGCAGTGTACCAGCGGCTTTGAGTGGGTGT GAACAGGATCAACAGTGTCTGGAACCCCGGGGCCGGATCCTCGGCGTGATGGCAAG GACACAGTCATTGGCGTGTGGACATCTATGGCTTCGAGGTGTTTCCGCTCAACAGTT TCGAGCAGTTTCTGCATCAACTACTGCAACGAGAAGCTGCAGCAGCTATTTCATCCAGCT CATCCTGAAGCAGGAACAGGAAGAGTACGAGCGGAGGGCATCACCTGGCAGAGCGTT GAGTATTTCAACACGCCACCATTTGTGGATCTGGTGGAGCGGCCACCGTGGCATCC TGGCCGTGCTGGACGAGGCTGTCAGCTCTGCTGGCACCATCACTGACCGAATCTTCCT GCAGACCTTGCAGATGCACACCGCCATCACCTACACTACACCGCCAGCTCTGCTG CCCACAGACAAGACCATGGAGTTTGGCCGAGACTTCCGGATCAAGCACTATGCAGGGG ACGTACGTAATCCGTGGAAGGCTTCATCGACAAGAACAGAGATTTCTCTTCCAGGA CTTCAAGCGGCTGCTGTACAACAGCACGGACCCCACTCTACGGGCCATGTGGCCGGAC GGGCAGCAGGACATCAAGAGGTGACCAAGCGCCCTGACGGCTGGCCACCTGTTCTTCA AGAAGTCCATGGTGGCCCTGGTGGAGAACCTTGCTTCCAAGGAGCCCTTCTACGTCCG CTGCATCAAGCCCAATGAGGACAAGGTAGCTGGGAAGCTGGATGAGAACCACTGTGCG CACCAGTGCATACCTGGGGCTGCTGGAGAATGTGAGGTCGCGAGGCTGGCTTCG CTTCCCGCCGCTTACTCTCGATTCTGCTCAGGTACAAGATGAGTGTGAATACAC ATGGCCCAACCACTGTGGGCTCCGACAAGGCAGCCGTGAGCGCTCTCTGGAGCAG CACGGGCTCAGGGGGACGTGGCCTTTGGCCACAGCAAGCTGTTTCATCCGCTCACCCC GGACACTGGTCACTGGAGCAGAGCGAGCCCGCTCATCCCCACTTGTGCTGTCT ATTGCAGAAGGCATGGCGGGCACCTTGGCGAGGTGGCGCTGCCGAGGCTGAGGGCT ATCTACACCATCATGCGCTGGTTCCGGAGACACAAGGTGCGGGCTCACCTGGCTGAGC TGCAGCGCGGATTCAGGCTGCAAGGCAGCCGCACTCTACGGGCGTGACCTTGTGTG GCCGCTGCCCCCTGCTGTGCTGCAGCCCTTCCAGGACACTGCCACGCACTTCTGTC AGGTGGCGGGCCCGGCAGCTGGTGAAGAACATCCCCCTTCCAGACATCCCCAGATCA AGGCCAAGGTGGCGCCATGGGGGCCCTGCAAGGGCTTCGTACGAGCTGGGGCTGCCG ACGGGCTGGGGCCGAGACTACCTGTCCTCTGCCACTGACAATCCCACAGCATCAAGC CTGTTTGTCTCAGGACTAAAGACACTTCAGGACAAGATGGCTTCGGGGCTGTGCTCT TTTCAAGCCATGTCCGCAAGGTGAACCGCTTCCACAAGATCCGGAACCGGGCCCTCT GCTCACAGACCAGCACTCTACAAGCTGGACCTGACCGGCAGTACCGGGTGAATGCGG GCCGTGCCCTTGAAGCGGTGACGGGGCTGAGCGTGACCAAGCGGAGGAGCAGCTGG TGGTGTGTCAGCCCGCGGCCAGGACGACCTCGTGGTGTGCTGCACCGCTCCCGGCC GCCATTGGACAACCGCGTTGGGGAGCTGGTGGGCGTGTGGCGGCACACTGCCGAGG GAGGGCCGACCTGGAGGTTCCGCTCTCCGACTGCATCCCAAGCATCGCGGGG TCCGGCGCTCATCTCGTGGAGCCAGGCGGAGCAGCAGAGCCGATTTCCGCTG CGCTCGGGCTCCTTACCCTGCTCTGGCCAGCGCTGAGCGCCGACCCGCGCA CCCCGA</p>
	<p>ORF Start: ATG at 15 ORF Stop: TGA at 3054</p>
	<p>SEQ ID NO: 230 1013 aa MW at 116044.5kD</p>
<p>NOV81a, CG59522-01 Protein Sequence</p>	<p>MEDEEGPEYKPDFVLLDQVTMEDFMRLQLRFEKGRIYTYIGEVLVSVNPYQELPLY GPEAIARYQGRELIERPPHLYAVANAAYKAMKHSRDTICVISGESAGKTEASKHIM QYIAAVTNPSQRAEVERVKDVLKSTCVLEAFGNARTNRNHNSSRFKYMINDIFDKG DPIGGHIHSYLLKSRVLKQHVGERNFHAFYQLLRGSEDKQLHELHLERNPAVYNFTH QGAGLNMTVSDEQSHQAVTEAMRVIGFSPPEEVSVHRI LAAILHLGNI EFVETEGLL QKEGLAVAEELVDHVAELTATPRDLVLRSLARTVASGGRELIEKGTAAEASYARD ACAKAVYQRLFEWVNRINSVMEPRGRDPRRDGKDTVIGVLDIYGFVFPVNSFEQFC INYCNEKLQQLFIQLILKQEQEYEREGITWQSVYFNNATI VDLVERPHRGILAVLD EACSSAGTITDRIFLQTLDMHRRHLHYTSRQLCPTDKTMEFGRDFRIKHVAGDVYS VEGFIDKNRDFLQDFKRLLYNSTDPTLRAMWPDGQDITETVTKRPLTAGTLFKNSMV ALVENLASKEPPYVRCIKPNEDKVAGKLDENHCRHQVAYLGLLENVRVRAGFASRQP YSRFLRLRYKMTCEYTPNHLGSDKAASALLEQHGLQGDVAFGHSKLFIRSPRTLV LEQSRARLPIIIVLLQKAWRGTLARWRCLRLRAIYTIMRFRHVKRAHLAEQLRRF QAARQPPLYGRDLVWPLP PAVLQPFQDTHALFCRWRARQLVKNIPPSDMPQIKAKVA AMGALQGLRQDWGCRRARAWDYLSATDNPTASSLFAQLRLKTLQDKDGFVAVLFSSHV RKVNRPHKIRNRALLTDQHLKLPDRQYRVMRAVPLEAVTGLSVTSGGQQLVVLHA RGQDDL VVCLHRSRPPLDNRVGLVGVLAHCRREGRTLEVRVSDCIPLSHRGVRRLLI SVEPRPEQPEPDFRCARGSFLLWPSR</p>

Further analysis of the NOV81a protein yielded the following properties shown in Table 81B.

Table 81B. Protein Sequence Properties NOV81a	
PSort analysis:	0.8800 probability located in nucleus; 0.3902 probability located in microbody (peroxisome); 0.2210 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV81a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 81C.

Table 81C. Geneseq Results for NOV81a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV81a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU23125	Novel human enzyme polypeptide #211 - Homo sapiens, 1026 aa. [WO200155301-A2, 02-AUG-2001]	1..1013 9..1026	1009/1018 (99%) 1011/1018 (99%)	0.0
AAU23128	Novel human enzyme polypeptide #214 - Homo sapiens, 909 aa. [WO200155301-A2, 02-AUG-2001]	1..853 9..866	851/858 (99%) 851/858 (99%)	0.0
AAM80123	Human protein SEQ ID NO 3769 - Homo sapiens, 764 aa. [WO200157190-A2, 09-AUG-2001]	243..1011 1..762	438/769 (56%) 570/769 (73%)	0.0
AAM79139	Human protein SEQ ID NO 1801 - Homo sapiens, 753 aa. [WO200157190-A2, 09-AUG-2001]	254..1011 1..751	434/758 (57%) 564/758 (74%)	0.0
AAM39991	Human polypeptide SEQ ID NO 3136 - Homo sapiens, 1063 aa. [WO200153312-A1, 26-JUL-2001]	10..933 47..986	410/966 (42%) 556/966 (57%)	0.0

In a BLAST search of public sequence databases, the NOV81a protein was found to have homology to the proteins shown in the BLASTP data in Table 81D.

Table 81D. Public BLASTP Results for NOV81a				
	Protein/Organism/Length			

Accession Number		Residues/ Match Residues	Similarities for the Matched Portion	Value
Q63357	MYOSIN I - Rattus norvegicus (Rat), 1006 aa.	1..1011 1..1004	606/1011 (59%) 780/1011 (76%)	0.0
A53933	myosin I myr 4 - rat, 1006 aa.	1..1011 1..1004	604/1011 (59%) 778/1011 (76%)	0.0
Q96RI6	UNCONVENTIONAL MYOSIN 1G VALINE FORM - Homo sapiens (Human), 633 aa (fragment).	33..646 1..619	612/619 (98%) 612/619 (98%)	0.0
Q96RI5	UNCONVENTIONAL MYOSIN 1G METHONINE FORM - Homo sapiens (Human), 633 aa (fragment).	33..646 1..619	611/619 (98%) 612/619 (98%)	0.0
Q23978	Myosin IA (MIA) (Brush border myosin IA) (BBMIA) - Drosophila melanogaster (Fruit fly), 1011 aa.	8..1012 6..1007	503/1017 (49%) 686/1017 (66%)	0.0

Pfam analysis predicts that the NOV81a protein contains the domains shown in the Table 81E.

Table 81E. Domain Analysis of NOV81a			
Pfam Domain	NOV81a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PRK: domain 1 of 1	97..109	8/13 (62%) 10/13 (77%)	3.7
Vir_DNA_binding: domain 1 of 1	575..592	5/18 (28%) 14/18 (78%)	8.2
myosin_head: domain 1 of 1	11..689	305/747 (41%) 531/747 (71%)	8.1e-288

Example 82.

The NOV82 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 82A.

Table 82A. NOV82 Sequence Analysis		
	SEQ ID NO: 231	1066 bp
NOV82a, CG59520-01 DNA Sequence	GAACGAATGGGAAACCAGAAATCAGATATTTATGCCCAAGCAAAGCAGGATTTTCGTTT AGCACTACTCCCAGATCGTTAGGGTGCTGACTGAGGATGAGATGGGGCACCCAGAGAC AGGAGATGCTACTGCCCGGCTCAAGGAGGTCCTGGAGTACAATGCCATTGGAGGCAAG TATCACCGAGGTTTGATGGTGCTAGTAGCGTTCCGGGAGCTGGTGGAGCCGAGGAAAC TGGATGCTGATAGTCTCCAGTGGGCACCGACTGTGGGCTGGTATGCGCAACTGCTGCA	

	AGCTTCTCTCCTGGTGGCAGATGACATTATGGATTATCCCTTACCTGCCAGGGACAG ATCTCCTGGTATCAGAAGCTGGGCATGGGTTTGGATGCCATCAATGATGCTATCCTTC TGGAAGCATGTATCTACTGCCTGCTGAAGCTGTATTGCCGGGAGCAGCCCTATTACCT GAACCTGATGGAGCTCTTCCAGCAGAATTCTTATCAGACTGAGATTGGGCAGACCTC GACCTCATCACAAACCCCGAGGCAATGTGGATCTTCGAGATGCACCGAAAAAAGGC ACAAATCTGTTGTCAAGTACAAGACAGCTTCTACTCCTTCTACCTTCTGTAGCTGC AGCCATGTACATGTCAAGAATGGATGACAAGAAGGAGCACACCAAGTCCCAAGAAGATC CTGCTGGAGATTCAAGAGTTCTTTCAGATTCAAGATGATTACCTTGACTTCTCTGGGG ACCCAGTGTGACTGGCAGAGTTGGCAATGACTTCCAGGACAACAAATGCAGCTGGCT GGTGGTTCAAGTGTCTGCTACAGGCCACTCCAGAACAGTACCAGATCCTGAAGGAAAAT TACAGGCAGAAGGAGGCCGAGAAGGTGGCCCGGGTGAAGGCACTATACGAGGAGCTGG ATCTGCCAGCCGTGTTCTTGCAGTATGAGAAAGACAGTTACAGCCACGTTATGGGTCT CATCGAACAGTACGACAGCCCTGCCCCCAGCCATCTTCTGGGGCTTGTGCACAAA ATCTACAAGTGGAAAAAGTGAC		
	ORF Start: ATG at 7	ORF Stop: TGA at 1063	
	SEQ ID NO: 232	352 aa	MW at 40740.3kD
NOV82a, CG59520-01 Protein Sequence	MGNQKSDIYAQAKQDFVQHSYQIVRVLTEDMGHPETGDATARLKEVLEYNAIGGKYH RGLMVLVAFRELVEPRKLDADSLQWAPTGVWYAQLLQAFFLVADDIMDSSLTCQQQIS WYQKLGMLDAINDAILLEACIYCLLKLYCREQPYLNLMEFLQQNSYQTEIGQTLDL ITTPQGNVDLRRCTEKRHSVVKYKTAFFSYFLPVAAAMYSRMDDKKEHTSAKKILL EIQEFFQIQDDYLDPSGDPSTGRVGNDFQDNKCSWLVVQCLLQATPEQYQILKENYR QKEAEKVARVKALYEELDLPAVFLQYEKDSYSHVMGLIEQYAEPLPPAIFLGLVHKIY KWKK		

Further analysis of the NOV82a protein yielded the following properties shown in Table 82B.

Table 82B. Protein Sequence Properties NOV82a	
PSort analysis:	0.4066 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV82a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 82C.

Table 82C. Geneseq Results for NOV82a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV82a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG29733	Arabidopsis thaliana protein fragment SEQ ID NO: 35427 - Arabidopsis thaliana, 342 aa. [EP1033405-A2, 06-SEP-2000]	10..352 2..342	147/343 (42%) 219/343 (62%)	7e-75

AAG29732	Arabidopsis thaliana protein fragment SEQ ID NO: 35426 - Arabidopsis thaliana, 349 aa. [EP1033405-A2, 06- SEP-2000]	10..352 9..349	147/343 (42%) 219/343 (62%)	7e-75
AAG29734	Arabidopsis thaliana protein fragment SEQ ID NO: 35428 - Arabidopsis thaliana, 305 aa. [EP1033405-A2, 06- SEP-2000]	47..352 1..305	138/306 (45%) 204/306 (66%)	4e-73
AAV43635	Amino acid sequence of the farnesyl pyrophosphate synthase enzyme - Phaffia rhodozyma, 355 aa. [EP955363-A2, 10-NOV-1999]	12..352 11..355	145/346 (41%) 208/346 (59%)	4e-69
AAB48971	Sunflower seedling farnesyl pyrophosphate synthase (FPS) - Helianthus annuus, 341 aa. [EP1063297-A1, 27-DEC-2000]	13..352 6..341	138/343 (40%) 204/343 (59%)	3e-64

In a BLAST search of public sequence databases, the NOV82a protein was found to have homology to the proteins shown in the BLASTP data in Table 82D.

Table 82D. Public BLASTP Results for NOV82a

Protein Accession Number	Protein/Organism/Length	NOV82a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96G29	FARNESYL DIPHOSPHATE SYNTHASE (FARNESYL PYROPHOSPHATE SYNTHETASE, DIMETHYLALLYLTRANSTRANSFERASE, GERANYLTRANSTRANSFERASE) - Homo sapiens (Human), 419 aa.	2..352 69..419	291/351 (82%) 317/351 (89%)	e-168
P14324	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) [Includes: Dimethylallyltransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)] - Homo sapiens (Human), 353 aa.	2..352 3..353	291/351 (82%) 317/351 (89%)	e-168
A35726	farnesyl-pyrophosphate synthetase - human, 353 aa.	2..352 3..353	290/351 (82%) 316/351 (89%)	e-168
AAL58886	FARNESYL DIPHOSPHATE SYNTHASE - Bos taurus (Bovine), 353 aa.	2..352 3..353	270/351 (76%) 308/351 (86%)	e-157
Q14329	FARNESYL PYROPHOSPHATE SYNTHETASE LIKE-4 PROTEIN - Homo sapiens (Human), 348 aa.	6..352 2..348	268/347 (77%) 295/347 (84%)	e-150

PFam analysis predicts that the NOV82a protein contains the domains shown in the Table 82E.

Table 82E. Domain Analysis of NOV82a

Pfam Domain	NOV82a Match Region	Identities/ Similarities for the Matched Region	Expect Value
polyprenyl_synt: domain 1 of 1	43..315	82/285 (29%) 237/285 (83%)	6.3e-91

Example 83.

The NOV83 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 83A.

Table 83A. NOV83 Sequence Analysis			
	SEQ ID NO: 233	411 bp	
NOV83a, CG59758-01 DNA Sequence	TGCCTACCCGAGACTGCTGCTGTTCCGAGACCTGCAGGTGAATGCCCATCACCATG TCTGACCTGGAGGCAAAACCTTCAACTGAGCATTGGGGGATAAGATAAAAGATGAAG ATATTAAACTCAGGGTTATTGGACAGGATAGCAGTGAGATTCAATTCAAAGTGAAAT GACAACACCTCTCAAGAACTCAAGAAATCGTACTGTGAGAGACAGGGCGTTCCAGTG AATTCCCTCAGGTTTCTCTTTGAAGGTCAGAGAATTGCTGATAATCATACTCCAGAAG AACTGGGAATGGAGGAAGAAGATGTGATTGAGGTTTATCAGGAACAAATCGGAGGTCA TTCAACAGTTTAGACATTCTTTTTTTTTTCTTTTCCCTCAATCCTTTTTTATTTT TTAAA		
	ORF Start: ATG at 56	ORF Stop: TAG at 359	
	SEQ ID NO: 234	101 aa	MW at 11526.0kD
NOV83a, CG59758-01 Protein Sequence	MSDLEAKPSTEHLGDKIKDEDIKLRVIGQDSSEIHFVKMTTPLKKLKSQCQRQGVF VNSLRFLFEGQRIADNHTPEELGMEEDVIEVYQEQIGGHSTV		
	SEQ ID NO: 235	658 bp	
NOV83b, CG59758-02 DNA Sequence	CTACCCCGAGACTGCTGCTGTTCCGAGACCTGCAGGTGAATGCCCATCACCATGTCT GACCTGGAGGCAAAACCTTCAACTGAGCATTGGGGGATAAGATAAAAGATGAAGATA TTAAACTCAGGGTTATTGGACAGGATAGCAGTGAGATTCAATTCAAAGTGAAATGAC AACACCTCTCAAGAACTCAAGAAATCGTACTGTGAGAGACAGGGCGTTCCAGTGAAT TCCCTCAGGTTTCTCTTTGAAGGTCAGAGAATTGCTGATAATCATACTCCAGAAGAAC TGGGAATGGAGGAAGAAGATGTGATTGAGGTTTATCAGGAACAAATCGGAGGTCAATC AACAGTTTAGACAATCGGAGGTCAATCAACAGTTTAGACAATCGGAGGTCAATCAACA GTTTAGACAATCGGAGGTCAATCAACAGTTTAGACAATCGGAGGTCAATCAACAGTTT AGACAATCGGAGGTCAATCAACAGTTTAGACAATCGGAGGTCAATCAACAGTTTAGAC AATCGGAGGTCAATCAACAGTTTAGACAATCGGAGGTCAATCAACAGTTTAGACAATC GGAGGTCAATCAACAGTTTAGACAATCGGAGGTCAATCAACAGTTTAGACAATCGGAG GTCATTCAACAGTTTAGACA		
	ORF Start: ATG at 53	ORF Stop: TAG at 356	
	SEQ ID NO: 236	101 aa	MW at 11526.0kD
NOV83b, CG59758-02 Protein Sequence	MSDLEAKPSTEHLGDKIKDEDIKLRVIGQDSSEIHFVKMTTPLKKLKSQCQRQGVF VNSLRFLFEGQRIADNHTPEELGMEEDVIEVYQEQIGGHSTV		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 83B.

Table 83B. Comparison of NOV83a against NOV83b.		
Protein Sequence	NOV83a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV83b	1..101	101/101 (100%)
	1..101	101/101 (100%)

Further analysis of the NOV83a protein yielded the following properties shown in Table 83C.

Table 83C. Protein Sequence Properties NOV83a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV83a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 83D.

Table 83D. Geneseq Results for NOV83a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV83a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79976	Human protein SEQ ID NO 3622 - Homo sapiens, 125 aa. [WO200157190-A2, 09-AUG-2001]	1..101 25..125	100/101 (99%) 100/101 (99%)	1e-52
AAM78992	Human protein SEQ ID NO 1654 - Homo sapiens, 101 aa. [WO200157190-A2, 09-AUG-2001]	1..101 1..101	100/101 (99%) 100/101 (99%)	1e-52
AAY49967	Human sentrin protein sequence - Homo sapiens, 101 aa. [US5985664-A, 16-NOV-1999]	1..101 1..101	89/101 (88%) 94/101 (92%)	2e-45
AAW87984	Ubiquitin-like domain of the protein SUMO1 - Mammalia, 101 aa. [WO9857978-A1, 23-DEC-1998]	1..101 1..101	89/101 (88%) 94/101 (92%)	2e-45
AAW60079	Homo sapiens sentrin-1 polypeptide - Homo sapiens, 101 aa. [WO9820038-A1, 14-MAY-1998]	1..101 1..101	89/101 (88%) 94/101 (92%)	2e-45

In a BLAST search of public sequence databases, the NOV83a protein was found to have homology to the proteins shown in the BLASTP data in Table 83E.

Table 83E. Public BLASTP Results for NOV83a				
Protein Accession Number	Protein/Organism/Length	NOV83a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q93068	Ubiquitin-like protein SMT3C precursor (Ubiquitin-homology domain protein PIC1) (Ubiquitin-like protein UBL1) (Ubiquitin-related protein SUMO-1) (GAP modifying protein 1) (GMP1) (Sentrin) - Homo sapiens (Human), and, 101 aa.	1..101 1..101	89/101 (88%) 94/101 (92%)	6e-45
Q9MZD5	SENTIN - Cervus nippon (Sika deer), 101 aa.	1..101 1..101	88/101 (87%) 93/101 (91%)	2e-44
O57686	SUMO-1 PROTEIN - Xenopus laevis (African clawed frog), 102 aa.	1..100 1..101	83/101 (82%) 90/101 (88%)	2e-39
Q9PT08	SMALL UBIQUITIN-RELATED PROTEIN 1 - Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), 101 aa.	1..97 1..97	72/97 (74%) 84/97 (86%)	9e-35
Q9D466	4933411G06RIK PROTEIN - Mus musculus (Mouse), 117 aa.	1..97 1..96	68/97 (70%) 80/97 (82%)	8e-30

Pfam analysis predicts that the NOV83a protein contains the domains shown in the Table 83F.

Table 83F. Domain Analysis of NOV83a			
Pfam Domain	NOV83a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ubiquitin: domain 1 of 1	20..95	14/83 (17%) 66/83 (80%)	4.7e-18

Example 84.

The NOV84 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 84A.

Table 84A. NOV84 Sequence Analysis

	SEQ ID NO: 237	912 bp
NOV84a, CG59586-01 DNA Sequence	ACTCACTAATGGGCTCGAGCGGCTGCCTGTGTTTCAGCGGCTCGGGGAAATCCACCGT GGGCGCCCTGCTGGCATCTGAGCTGGGATGGAAATCTATGATGCTGATGATTATCAC CCGGAGGAAATCGAAGGAAGATGGGAAAGGCATACCGCTCAATGACCAGGACCGGA TTCCATGGCTCTGTAACCTTGCATGACATTTTACTAAGAGATGTAGCCTCGGGACAGCG TGTGGTTCTAGCCTGTTTCAGCCCTGAAGAAAACGTACAGAGACATATTAACACAAGGA AAAGATGGTGTAGCTCTGAAGTGTGAGGAGTCGGGAAAGGAAGCAAAGCAGGCTGAGA TGCAGCTCCTGGTGGTCCATCTGAGCGGGTCGTTTGAGGTCACTCTGGACGCTTACT CAAAAGAGAGGGACATTTTATGCCCCCTGAATTATTGCAGTCCCAGTTTGAGACTCTG GAGCCCCCAGCAGCTCCAGAAAACCTTTATCCAATAAGTGTGGACAAAATGTTTCAG AGATAATTGCTACAATTATGGAAACCTTAAAAATGAAATGACAATGATTTTGTATCAG TGGTCCAAACAGAACTAAGCATAAATCATTGTGCCATCCCAACCTCGTTCCAGCCGC CTTGCCCATAGATTCTAAATGTTTCTAAAGCAAACCCCAATGTGTCAAGACAGA CTTGTTTAGGTGTAATTTTAGGAATTATGCTGGTTCATCAGGAAGCAGAGGGGGAGTT TTAAAGTCAAGCTTAAATTGAAGTTAAATTCATCTATAACCAAATCAAATGATCAG AGGAAATCTGTAATCAATGCTGGAAATCGTTACATTGTTTGAACATTCCTGCTCAT GCCTGTATTTGCACAAATAAATGAACTTCGCTGTAAAAAA	
	ORF Start: ATG at 9	ORF Stop: TGA at 561
	SEQ ID NO: 238	184 aa MW at 20352.2kD
NOV84a, CG59586-01 Protein Sequence	MGSSGCLCFSGSGKSTVGALLASELGWKFYDADDYHPEENRRKMGKGIPLNDQDRIPW LCNLHDILLRDVASGQRVVLACSALKKTYRDILTQKDGVALKCEESGKEAKQAEMQL LVVHLSGSFEVISGRLLKREGHFMPPELLQSQFETLEPPAAPENFIQISVDKNVSEI I ATIMETLKMK	

Further analysis of the NOV84a protein yielded the following properties shown in Table 84B.

Table 84B. Protein Sequence Properties NOV84a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.1000 probability located in plasma membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV84a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 84C.

Table 84C. Geneseq Results for NOV84a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV84a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG73989	Human colon cancer antigen protein SEQ ID NO:4753 - Homo sapiens, 193 aa. [WO200122920-A2, 05-APR-2001]	10..184 19..193	175/175 (100%) 175/175 (100%)	1e-97
AAB58998				1e-97

	antigen protein sequence SEQ ID 706 - Homo sapiens, 193 aa. [WO200055173-A1, 21-SEP-2000]	19..193	175/175 (100%)	
AAM89100	Human immune/haematopoietic antigen SEQ ID NO:16693 - Homo sapiens, 133 aa. [WO200157182-A2, 09-AUG-2001]	24..126 22..124	70/103 (67%) 77/103 (73%)	1e-34
AAG50675	Arabidopsis thaliana protein fragment SEQ ID NO: 64243 - Arabidopsis thaliana, 175 aa. [EP1033405-A2, 06- SEP-2000]	10..179 4..167	75/173 (43%) 102/173 (58%)	4e-28
AAG50674	Arabidopsis thaliana protein fragment SEQ ID NO: 64242 - Arabidopsis thaliana, 187 aa. [EP1033405-A2, 06- SEP-2000]	10..179 16..179	75/173 (43%) 102/173 (58%)	4e-28

In a BLAST search of public sequence databases, the NOV84a protein was found to have homology to the proteins shown in the BLASTP data in Table 84D.

Table 84D. Public BLASTP Results for NOV84a				
Protein Accession Number	Protein/Organism/Length	NOV84a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
BAB74785	GLUCONOKINASE - Anabaena sp. (strain PCC 7120), 160 aa.	10..183 9..160	72/174 (41%) 101/174 (57%)	1e-30
Q9RT56	THERMORESISTANT GLUCONOKINASE - Deinococcus radiodurans, 172 aa.	10..183 4..159	66/174 (37%) 101/174 (57%)	1e-29
CAC93415	PUTATIVE GLUCONOKINASE (EC 2.7.1.12) - Yersinia pestis, 167 aa.	10..174 12..159	68/166 (40%) 95/166 (56%)	2e-29
Q9CMM6	GLK - Pasteurella multocida, 172 aa.	10..182 15..169	68/174 (39%) 99/174 (56%)	2e-29
AAK86014	AGR_C_329P - Agrobacterium tumefaciens str. C58 (Cereon), 163 aa.	10..182 5..159	74/173 (42%) 98/173 (55%)	6e-29

PFam analysis predicts that the NOV84a protein contains the domains shown in the Table 84E.

Table 84E. Domain Analysis of NOV84a			
Pfam Domain	NOV84a Match Region	Identities/ Similarities for the Matched Region	Expect Value
SKI: domain 1 of 1	9..182	37/206 (18%) 114/206 (55%)	1.1

Example 85.

The NOV85 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 85A.

Table 85A. NOV85 Sequence Analysis		
	SEQ ID NO: 239	4332 bp
NOV85a, CG59704-01 DNA Sequence	GGCGTATTAACGCGCGGGTGCACACCCACGGGCGCGCAATGAACAACATATGTGCTT AATGACGAGATCGGCCAGGGTGCCTTCAGCACTATTTACAAGGGCCGCTATCGCACCA CCACCGAGTTCTACGCGATTGCTTCCATCGACAAGAAGCGAGCGCGTCTGTGAA CTGCGTTCAGCTGTACGCTCCATGCACTCAACCGTCATAGAGTTCCACAACCTGG TATGAGACCAACAATCACTTGTGGATCATTACGGAGTACTGCACCGGCGGAGACATGA GCACGATCCTCCGCTCGAACATTAATCTCACCCTCAGGCGGTCCAGGCGTTCGGCCG TGATGTGGCGATGGGCTCATGTACATCCACAGTAAGGGTGTCTGTATAACGACTTG CAGACTCGCAATCTGCTGATGGACTCCGCAGCAATGCTGCGCTTCCACGACTTTAGCT TGGCCTGTCTCTTCCAAGACGCGGCGACGCGCCACTGGTGGGAGCGCCACTGTACAT GGCCCCGAGTTGTTTCATGGCGGATCGCCCGCTGTACTCGATGGCATCAGACCTGTGG TCCTTCGGTTGTGTGTCACGAGCTGGCGACAGGCAAGCCGCTTGGCGCATCCG ACCTCGAGACGCTGCTGGCGCATACTGACGAGTCCGACGCCAGCGGTGCCTGGTGC GCCGAGTCTCTTCAAACGCTCCTGTGCGGCTGTCTGGAAAAGGACCGCTGAAGCGC TACCGTGGTTCGATGTTGTCCGACGAGTCTTGGGATGAGCCCTTGGCGTTCGCCA GCAACGCTTTCATCTCAGGTGGCGTGGGAGGACTACAAGCGTTCGCGTCTCGGAGC CGGTGCGAGTCAGTATAATTGGACGGAATCCGATGTGCTGTGGCAGTGGCTCACGCC GTGGGGGCGAGCAATCAAACGCTTCTACGCACAACGTGGAGGAGAGGAGCGAGCGG CTGCGACGTTGAACGTCGCGAAGGAGCTGGACTTCACTGCAAGCGCGGCGATGTTGT GGAACGGTTACCGGAGCGGACACAGGAGCGTGTGCGCACGCAACAGGCGATGTGCGG ACCGCGCACGCGAGCTGTGTCACGGCTGCCCATCCACGGCTCAGCGGCGACCTCGC CAAGACGTTCAAGGACAAGGCGCGCTGCTCAAGATTGTGGAAGAGGTCAAACCGCT GTGAGGGCTTCAAGCCGTGGGTGTCTTCCACGTCGCTGCGCCACCGGGCATGAGG GAGCGCACTGGACCGGCTTGTCTCAGAAGCTCGGGATGAAGCTGGTGCCTGGCGACA CACTGATGCTTCTGAGGAGTGCGAACCGCTGTAGCGCACCGCGACACATTATCAG CTACTGCGAGGTGGCCGGAAGGAGTGCAGATCGAGATGACGCTCAAGGACATGCGT GCCAAGTGGGAGACCAAGTGTCTCATCATCGAGGCATACAAGGAGACAGCAGTACA TCCTCAAGGACACCTCCGAGGTGGTGGAGCTCCTCGACGACACCTCAACGTCGTCCA GCAGTGCAGTTCTCTCAATTCAAGGGCTACTTCGAGGAGTCCATCAGCGATGGGAG CGCTCCTCAACCTCATCTCCGACATACTCGAACAATGGCTGGATGCGACGAGCGT GGCGTTATCTGGAGCCGATCCTCAACTCGGAGGACATCGCCATGCGACTACCGGACT GTCCACGCTGTTGAGAAGGTGGACCGCACATGGAGACGTGTATGGGCAACGCGCAC GCGCAGCCAAACGCACTCGAGTACTGCATTGGCACAACAAGCTCTTGGACCACTGC GCGAGGCGAACCGGCTCCTCGAAGTGTGCGAGCACTTGATGGCGCAGAAGGTCAACGT TGCCGCTGTTGGTCCGACTGGCACCGCAAGTCCATCTCACTCGCGCTCTCGTGCTT GGCGGCGGATGCGCGGCAACTTCTTGGCCTCAACTTCACTTCTCGGCGCAGACAA AGTGCACAGTGTGCGAATTCACTGATGGCCAAGTTCGATAAGCGGCGCTCGCAGCT CTACGCGCCCTGCGGTAAGCACTTCTCATCTTCAATGACGACGCGAAGCTGCGG CAGCCAGAGAAGTACGCGCGCAGCCCCCGTGGAGCTTCTGCGGCGAGATGCTCGCCC AAGGCGGCTTCTACAACCTTACAGGTGGCATCAAGTGGTCTCCATCATCGACTGCTC GCTTGCCTGGCGATGGGCGCGCTGCGGGGGCCGCGAGCGGGTTTCGAACCGCTTT ATGCGCTACTTCAATTACCTTGCCTTCCCGAGATGTGCGACATGTGGAAGCGAACGA TCTTGAGGCGCATCTCTGCGGCGGCTCGCGCAGAGCGGCTCGCTGACCGCTCGC GAACGTCGCTCCGCGGTGTCGATAGCACGTTGCGGGTGTTCGCAAGTGCACCCAG GTCTTCTGCGGACCCCGCGCACGTGCACACTCTTCAACATGCGGGATGTGATGC GTGTTTTTCCCTCTTGTACACAGCAGACAAGTCGGTGTGCGAGTCGGAGGAATCCAT CGTGGCGCTGTGGATGCACGAGATGCAGCGCTCTTCTACGATCGCCTCGTCAGCGG ACAGACAAGGTCTGTTCATCGAGTACTCAATGCCGAGCTGCGCTCATGGGGGTGG ACAAGTCTTACAACGAGGTAGTGAAGGCTGACCGCTCATCTTGGCCGATCTGAG CGACAAGGGCGGTACGAGCAGATTACGACATGAACGCCCTCAGCACGCGATGAAT GAGCTGCTGGAGGCGTAAATGACGAGAATGAAGTGAAGATGAACCTCGTGCTCTTCC TCGACGCCATCGAGCATGTCTGCGGTATCTCGCGGTGTCTGCGCATGCCGACGGCA CTGCCTCTCTCGCGTGGCGGGTGGGACGCAAGTCACTCACGCGCTGGCTGTG	

	TCTCTGATTGCCGAGATGGAGGTGTTACGATTGAGCTGTGCAAGAAGCTTCGGTGTCA AGGAATGGCAGAGAGCTCGCGAAGTTGCTGCTCGAGTGTGGCAAGGACGAGAAGAA GCGGACGTTTTCTTTCGCCGACACCCAGCTGGCGCATCCGACGTTTTCTGGAGGATGTG GCGGGCCTGCTCACATCGGGTGTGTGCGAACCCTCTTTGAGGACCAAGATATCGAGC TCATCAACGACAAGTTTCGCGGCGTCTGCCTAAGCGAGAACCTGCCAACGACGAAGGT GTCGGTGTACGCGCGCTTTGTGAAGGAGGCGCGAGCCAACCTGCACCTTGTGCTCGCC TTCTCTCCCATCGGAGAGGCGTTTCGAGCCGCTGCGTATGTTCCCATCGCTCATTG CGTGCTGCACATCGACTGGTTTGTGAGTGGCCATCCGAGGCGCTACTGTGCGTAGC CGCAGTGCAGCTGAACGCCGCGGACGTTACTGACGTATGGGGCGGCAAGCCATGCC GACTTGCCGGGCTGCTTCCAGGCAGTGCACCGCGCGGCGGAGGTGACGGAGCGCT TCTTACGGAACCGCTGCTCGCTCGTACGTGACGCCGACGTCCTATCTGTGCTCCT CTCCAACCTCAAAGTGATGGCGGCGGCAAAACGCCGCTTCGTTCCGAGAGCGCGGG CGCCTCGAGAAGGGGCTGGAGAAGCTGCGGCACACCGAGGTGCAAGTGGCGGAGTGG AGGCCAGCTCAAGCGCGAGCAGCGGTTCTGGTGCAGAAAAGGAGAGATTGATCAGTC GATGATGGAGCGGCTGACGGTGGACCGAAAGGAGGCGCGGTGAAGGAGCGGACGCG CGCAGGAGGCGGAGCTTCCCGTGGCGGTGTGCATACGGCGGTGAAGATGACGAAT GAGCGCGGATGGGCTGCGGGCGAAGCTGATGCGCTCTACTACGGCTTCACTCCCG AGGACCTCGAGCAGGAGGAGAAGCCCGCGAGTTCAAAAAGATGTTGATGGCATCCGC ATGCCTGGTCCCATACCCGAGCACTGAAGAGCAGGGTCTCTGGAGCTGCGATCGTGG GGTGGCCCTCAGCTTCCCACTCACTGTGGGAAGTTTCTTAGTGTCTCTGAGCCTGT TTCCTCATCGTTGCTGAGGATAAACCTGCTTCAGGATTGTTGGTGAAGAAGACTTCC CTCACCTAGCTTCTGTACGCCACTGCATGCCACCCTGCTGAGTACTGTTGTTTGC TAGGTTGGTGTCTATTCTATTTTACCAGAAAGTGAAGCTC		
	ORF Start: ATG at 41 ORF Stop: TGA at 3944		
	SEQ ID NO: 240	1301 aa	MW at 146115.7kD
NOV85a, CG59704-01 Protein Sequence	MNHYVLNDEIGQAFSTIYKGRYRTTTEFYAIASIDKKRRERVVNCVQLLRSMHNSV IEFHNWYETNNHLWIITEYCTGGDMSTILRSNINLTQAVQAFGRDVMGLMYIHSKG VYNDLQTRNLLMDSAAMLRFHDFSLACLFQDAATRLVGTPLYMAPELFMADRPLYS MASDLSWFGCVLHELATGKPPFAASDLETLGDIILTSPTPAVPGAPESFQTLCLLLE KDPLKRYAWVDVVRSEFWDPEPLPLPSNGFPQVWEDYKRSRSGRGASQYNWTDSDVR VAVAHAVGAAKSNASTHNVEERERAAATLNVAKELDFTASAMLLERLPERTQERAAH ATGHVATAHGLVHGPCPTASAATSPPRSRTRRRCSRLWKRSLKPLSRASSRGCPSTSL RHPGMRERHWTGLSQKLGMLVPGDTLMLLEDCEPLLAHRDTIISYCEVAAKESQIEM TLKDMRAKWETKCFIIEAYKETGTIILKDTSEVVELLDEHLNVVQQLQFSPFKGYFEE STTDWERSLNLISDILEQWLEQRAWRYLEPIINSEDIAMQLPRLSTLFEKVDRTWRR VMGNAHAQPNALCYCIGNKLLDHLREANRLLEVQLHLMAQKVNVAAGVPTGTGKSIS LARLVLGGMPPANFLGLNFTFSAQTKCTVLQNSLMKFDKRRSHVYGAPAGKHFLIFI DDANLPQPEKYGAQPPVELLRQMLAQGGFYNTGGIKWSSIIDCSLALAMGPPGGGRS RVSNRMRYFNILAFPEMSDMSKRTILQAILVGGLAQSLADRLANVASAVVDSLTRV FRKCTQVFLPTPAHVHYSFNMVDVVRVPLLYTADKSVLQSEESIVRLWMHEMQRVY DRLVDATDKGLFIEYLNAELPSMGVDKSYNEVVKADRLIFADVLSDKGVEQITDMNA LITRMNELLEAYNDENEVMNLVFLDAIEHVCRISRVLRPLNGHCLLVGGSGRSK LTRLACSLIAEMEVFTIELSKNFGVKEWHESLAKLLECGKDEKRTFLFADTQLAHP TFLEDVAGLLTSGDVPNLFEDQDIELINDKFRGVCLSENLPPTKVSVAARFVKEARAN LHLVLAFSPIGEAFRSRLRMFPSLIACCTIDWFAEWPSEALLSVAAVQLNAGDVTDM GAASHADLPGCFQAVHRAAAEVTERFFTTETRRRSYVTPTSYLSLLSNFKVMAAKRRF VREQRGRLEKGLEKLRHTEVQVAELEAQLKAQPPVLVQKKAETQSMMERLITVDRKEAA VKEADARREQLPGGRAAYGGEDDE		

Further analysis of the NOV85a protein yielded the following properties shown in Table 85B.

Table 85B. Protein Sequence Properties NOV85a	
PSort analysis:	0.8800 probability located in nucleus; 0.3562 probability located in microbody (peroxisome); 0.1671 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV85a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 85C.

Table 85C. Geneseq Results for NOV85a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV85a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79863	Human protein SEQ ID NO 3509 - Homo sapiens, 2127 aa. [WO200157190-A2, 09-AUG-2001]	602..1287 168..847	218/692 (31%) 347/692 (49%)	1e-89
AAM79862	Human protein SEQ ID NO 3508 - Homo sapiens, 2127 aa. [WO200157190-A2, 09-AUG-2001]	602..1287 168..847	218/692 (31%) 347/692 (49%)	1e-89
AAM78879	Human protein SEQ ID NO 1541 - Homo sapiens, 2143 aa. [WO200157190-A2, 09-AUG-2001]	602..1287 108..787	218/692 (31%) 347/692 (49%)	1e-89
AAM78878	Human protein SEQ ID NO 1540 - Homo sapiens, 2067 aa. [WO200157190-A2, 09-AUG-2001]	602..1287 108..787	218/692 (31%) 347/692 (49%)	1e-89
AAM80293	Human protein SEQ ID NO 3945 - Homo sapiens, 1774 aa. [WO200157190-A2, 09-AUG-2001]	910..1293 33..405	153/393 (38%) 227/393 (56%)	5e-70

In a BLAST search of public sequence databases, the NOV85a protein was found to have homology to the proteins shown in the BLASTP data in Table 85D.

Table 85D. Public BLASTP Results for NOV85a				
Protein Accession Number	Protein/Organism/Length	NOV85a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL37427	CILIARY DYNEIN HEAVY CHAIN 7 - Homo sapiens (Human), 4024 aa.	628..1293 1975..2655	271/692 (39%) 395/692 (56%)	e-132
Q27812	DYNEIN HEAVY CHAIN ISOTYPE 7B (EC 3.6.1.3) - Tripneustes gratilla (Hawaian sea urchin), 1314 aa (fragment).	601..1247 654..1310	264/667 (39%) 389/667 (57%)	e-127
Q9MBF8	1 BETA DYNEIN HEAVY CHAIN - Chlamydomonas reinhardtii, 4513 aa.	611..1293 2486..3159	257/693 (37%) 377/693 (54%)	e-117
Q9VJC6	DHC36C PROTEIN - Drosophila melanogaster (Fruit fly), 4010 aa.	596..1275 1913..2604	249/699 (35%) 383/699 (54%)	e-116
Q9VWZ3	DHC16F PROTEIN - Drosophila melanogaster (Fruit fly), 4081 aa.	618..1301 2022..2709	248/704 (35%) 380/704 (53%)	e-108

PFam analysis predicts that the NOV85a protein contains the domains shown in the Table 85E.

Table 85E. Domain Analysis of NOV85a			
Pfam Domain	NOV85a Match Region	Identities/ Similarities for the Matched Region	Expect Value
pkinese: domain 1 of 1	4..250	80/286 (28%) 190/286 (66%)	6.8e-62
DEAD: domain 1 of 1	613..637	7/25 (28%) 22/25 (88%)	0.83
dNK: domain 1 of 1	865..1020	32/179 (18%) 101/179 (56%)	6.8

Example 86.

The NOV86 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 86A.

Table 86A. NOV86 Sequence Analysis			
	SEQ ID NO: 241	1420 bp	
NOV86a, CG59628-01 DNA Sequence	GTCCAGCTTTAGCTCTCTGCTCGCCGCCCGCTGTGCGCCGCCACCTCCTCTGATCTA CGAAAGTCATGTTACCCAACACCGGAGGCTGGCAGGATGTACAGTTTTTATCACAGG TGCAAGCCGTGGCATTGGCAAAGCTATTGCATTGAAAGCAGCAAAGGATGGAGCAAAT ATTGTTATTGCTGCAAAGACCGCCAGCCACATCCAAAACCTCTAGGCACAATCTATA CTGCTGCTGAAGAAATTGAAGCAGTTGGAGGAAAGGCCCTTGCCATGTATTGTTGATGT GAGAGATGAACAGCAGATCAGTGTCTGAGTGGAGAAAGCCATCAAGAATTTGGAGGA ATTGATATTCTGGTAAATAATGCCAGTGCCATTAGTTTGACCAATACATTGGACACAC CTACCAAGAGATTGGATCTGATGATGAACGTGAACACCAGAGGCACCTACCTTGCACT TAAAGCATGTATTCTTTATTGAAAAGAGCAAAGTTGCTCATATCCTCAATATCAGT CCACCACTGAACCTAAATCCAGTTTGGTTCAAACAGCACTGTGCTTATACCATTTGCTA AGTATGGTATGTCTATGTATGTGCTTGGAAATGGCAGAAGAATTTAAAGGTGAAATTGC AGTCAATGCATTATGGCCTAAAACAGCCATACACACTGCTGCTATGGATATGCTGGGA GGACCTGGTATCGAAAGCCAGTGTAGAAAAGTTGATATCATTGCAGATGCAGCATATT CCATTTTCCAAAGCCAAAAAGTTTTACTGGCAACTTTGTCAATTGATGAAAATATCTT AAAAAGAAGAAGGAATAGAAAATTTTGACGTTTATGCAATTAAACAGGTCATCCTTTG CAACCAGATTTCTTCTTAGATGAATACCCAGAAGCAGTTAGCAAGAAAGTGAATCAA CTGGTGTCTGTTCCAGAATTCAAAGAAGAGAAACTGCAGCTGCAACCAAAACACGTTT TGGAGCTGTGGAAGAAACATTTAGAATTGTTAAGGACTCTCTCAGTGATGATGTTGTT AAAGCCACTCAAGCAATCTATCTGTTTGAACCTCTCCGTTGAAGATGGTGGCAGCTGGT TTCTTGATCTGAAAAGCAAGGGTGGGAATGTCGGATATGGAGAGCCTTCTGATCAGGC AGATGTGGTGATGAGTATGACTACTGATGACTTTGTAAAAATGTTTTCAGGTAAACTA AAACCAACAATGGCATTTCATGTGAGGGAATTTGAAGATTAAAGGTAACATGGCCCTAG CAATCAAATTGGAGAAGCTAATGAATCAGATGAATGCCAGCTGTGAAGGAAATATA AAAAAAAAGTCGACTGCTATGCTCAAAAAGTAAAAAAGCTCAACAGTTAAAATCTAA TGTTTGTTTCTTCTGTTATATTATA		
	ORF Start: ATG at 67	ORF Stop: TGA at 1321	
	SEQ ID NO: 242	418 aa	MW at 45394.2kD
NOV86a, CG59628-01 Protein Sequence	MLPNTGRLAGCTVFITGASRGIGKAIKAAKDGANIVIAAKTAQPHPKLLGTIYTAA EEIEAVGGKALPCIVDVREQQISAAVEKAIKKFGGIDILVNNASAI SLNTLDTPTK RLDLMMNVNTRGTYLASKACIPYLKKSVAHILNISPLNLNPVWFKQHCAYYTIKAYG MSMYVLGMAEEFKGEI AVNALWPKTAIHTAAMDMLGGPGIESQCRKVDIIADAAYSIF QKPKSFTGNFVIDENILKEEGIENFDVYAIKPGHPLQPDFFLDEYPEAVSKKVESTGA VPEFKEEKLQLQPKPRSGAVEETFRI VKDSLSDDVVKATQAIYLFELSGEDGGTWFLD LKS KGGNVGYGEPDQADVVMSMTTDDFVKMFSGKLKPTMAFMSGKLKIKGNMALAIK LEKLMMQMNARL		

Further analysis of the NOV86a protein yielded the following properties shown in Table 86B.

Table 86B. Protein Sequence Properties NOV86a	
PSort analysis:	0.5500 probability located in endoplasmic reticulum (membrane); 0.5000 probability located in microbody (peroxisome); 0.1900 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV86a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 86C.

Table 86C. Geneseq Results for NOV86a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV86a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG81260	Human AFP protein sequence SEQ ID NO:38 - Homo sapiens, 418 aa. [WO200129221-A2, 26-APR-2001]	1..418 1..418	418/418 (100%) 418/418 (100%)	0.0
AAB84367	Amino acid sequence of human alcohol dehydrogenase 21612 - Homo sapiens, 418 aa. [WO200144446-A2, 21-JUN-2001]	1..418 1..418	418/418 (100%) 418/418 (100%)	0.0
AAG81258	Human AFP protein sequence SEQ ID NO:34 - Homo sapiens, 383 aa. [WO200129221-A2, 26-APR-2001]	1..382 1..382	382/382 (100%) 382/382 (100%)	0.0
ABB10251	Human cDNA SEQ ID NO: 559 - Homo sapiens, 278 aa. [WO200154474-A2, 02-AUG-2001]	141..418 1..278	271/278 (97%) 274/278 (98%)	e-156
AAU23020	Novel human enzyme polypeptide #106 - Homo sapiens, 278 aa. [WO200155301-A2, 02-AUG-2001]	141..418 1..278	271/278 (97%) 274/278 (98%)	e-156

In a BLAST search of public sequence databases, the NOV86a protein was found to have homology to the proteins shown in the BLASTP data in Table 86D.

Table 86D. Public BLASTP Results for NOV86a

Protein Accession Number	Protein/Organism/Length	NOV86a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC38510	SEQUENCE 37 FROM PATENT WO0129221 - Homo sapiens (Human), 418 aa.	1..418 1..418	418/418 (100%) 418/418 (100%)	0.0
CAC38508	SEQUENCE 33 FROM PATENT WO0129221 - Homo sapiens (Human), 383 aa.	1..382 1..382	382/382 (100%) 382/382 (100%)	0.0
Q99LV2	HYPOTHETICAL 54.9 KDA PROTEIN - Mus musculus (Mouse), 496 aa.	1..418 1..496	355/496 (71%) 390/496 (78%)	0.0

Q9BT58	SIMILAR TO RIKEN CDNA 2610207I16 GENE - Homo sapiens (Human), 345 aa.	163..418 90..345	253/256 (98%) 254/256 (98%)	e-143
Q9VB10	CG5590 PROTEIN (GH01709P) - Drosophila melanogaster (Fruit fly), 412 aa.	4..418 3..412	238/422 (56%) 300/422 (70%)	e-128

Pfam analysis predicts that the NOV86a protein contains the domains shown in the Table 86E.

Table 86E. Domain Analysis of NOV86a			
Pfam Domain	NOV86a Match Region	Identities/ Similarities for the Matched Region	Expect Value
beta-lactamase: domain 1 of 1	222..236	4/15 (27%) 14/15 (93%)	6.5
adh_short: domain 1 of 1	9..321	74/339 (22%) 211/339 (62%)	2.4e-29
SCP2: domain 1 of 1	306..415	41/114 (36%) 87/114 (76%)	1.5e-25

Example 87.

The NOV87 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 87A.

Table 87A. NOV87 Sequence Analysis			
	SEQ ID NO: 243	888 bp	
NOV87a, CG59516-01 DNA Sequence	TTCAACAAGGGCCCCTCCTACAGGCTCTTGGCGGACGTCCAGAACAGGCTTCTGTTCA AATATGACTCCCAGAAGGAGGCAGAGCTCCGCAGCTGGATCAAGGGATTCACTGGCCT CTCCATCCGCCCCGACTTCCAGAAGGGCCTGAAGGACGGGATTATTTTATGCACTC GTGAACAACTGCAGCCGGGCTCAGTCCCAAGATCAACCGCTTCCGTGTAGAAGTGG CACCAGCTAGAAAACCTCTCCAACATCCTCAAGGCAATGGTCAGTACGGCATGATCC CGTGGACCTATTTGAGGCCAACGACCTGTTTGAGAGTGGGAACAATATGCAGGTGCGG GTGTCTCTTCTCGCCCTGGCAGGGAAGGCCAAGACTAAGGGCTGCAGAGCGGGTGG ACATCCGTGACAAGTACTCAGAGAAGCAGAACTTCAACGACACCACCATGAAGGCCAG GCTGTGCGTCATCCGGCTGCAGATTACCAACAAATGTGCCAGCCAGTCAGGCATGACC GCATACGTACAGAGGAGGCATCTCTACGACCCCAAGAACCAGCATCCTGCCCCCATGG ACAACCTCGACCATCAGCCTCCGGATGGGTACAAACAAGTGCGCCAGCCAGGTGGGCAT GACGGCTCCCGGGAACAGTGGCACATCTATGACACCAAGTTGGGAATCGACAAGTGT GAGAACTCCTCCATGTCCCTGAAGATGGGCTACACGCAGGTCGCCAATCACAGCAGAC AGGTTCTTGGCCTAGGCCGGCAAATATATGAACCCAAGTACCAGCCGGGTGGCCAGT GGCCACAGGGGCTCCCTCCGCCGGCAACTGCCAGGGCCAGGGGAGGCCCTTAGTAC CAGGAGGAGACCAGCTAC		
	ORF Start: TTC at 1	ORF Stop: TAG at 865	
	SEQ ID NO: 244	288 aa	MW at 31831.2kD
NOV87a, CG59516-01 Protein Sequence	FNKGPSYRLLADVQNRLLFKYDSQKEAELRSWIKGFTGLSIRPDFQKGLKDGIILCTL VNKLQPGSVPKINGFRVELAPARKPLQHPQNGQLRHPVDLFEANDLFESGNMQRV VSLALAGKAKTKGLQSGVDIRDKYSEKQNFNDTMMKARLCVIRLQITNKCASQSGMT		

	AYVTRRHLYDPKNRILPPMDNSTISLRMGTNKCASQVGMTAPGNQWHIYDTKLGIIDKC ENSSMSLKMGYTQVANHSRQVFLGRQIYEPKYQPGGPVAHGAPSAAGNCPGPGEAP		
	SEQ ID NO: 245	888 bp	
NOV87b, CG59516-02 DNA Sequence	TTCAACAAGGGCCCTCTCTACAGGCTCTTGGCGGACGTCCAGAACAGGCTTCTGTTC AATATGACTCCCAGAAGGAGGCAGAGCTCCGACGTGGATCAAGGGATTCACTGGCCT CTCCATCCGCCCGACTTCCAGAAGGCCCTGAAGGACGGGATTATTTATGCACACTC GTGAACAAACTGCAGCCGGGCTCAGTCCCCAAGATCAACGGCTTCCGTGTAGAACTGG CACCAGCTAGAAAACCTCTCCAACATCCTCAAGGCAATGGTCAGTACGGCATGATCC CGTGGACCTATTGAGGCCAACGACCTGTTTGAGAGTGGGAACAATATGCAGGTGCGG GTGTCTCTTCTCGCCCTGGCAGGGAAGGCCAAGACTAAGGGGTGCAGAGCGGGGTGG ACATCCGTGACAAGTACTCAGAGAAGCAGAACTTCAACGACACCACCATGAAGGCCAG GCTGTGCGTCATCCGGCTGCAGATTACCAACAAATGTGCCAGGCAGTCAGGCATGACC GCATACGTACAGGAGGGCATCTCTACGACCCCAAGAACCGCATCCTGCCCCCATGG ACAACCTCGACCATCAGCCTCCGGATGGGTACAACAAGTGCAGCAGGTGGGCAT GACGGCTCCCGGAACCAAGTGGCACATCTATGACACCAAGTTGGGAATCGACAAGTGT GAGAACTCCTCCATGTCCCTGAAGATGGGCTACACGCAGGTGCGCAATCAGCAGAC AGGTCTTTGGCCTAGGCCGGCAAATATATGAACCAAGTACCAGCCGGGTGGCCAGT GGCCACCGGGGCTCCTCCGCGGCAACTGCCAGGGCAGGGGAGGCCCTTAGTAC CAGGAGGAGACCAGCTAC		
	ORF Start: TTC at 1	ORF Stop: TAG at 865	
	SEQ ID NO: 246	288 aa	MW at 31831.2kD
NOV87b, CG59516-02 Protein Sequence	FNKGPSYRLADVQNRLLFKYDSQKEAELRSWIKGFTGLSIRPDFQKGLKDGIIILCTL VNKLQPGSVPKINGFRVELAPARKPLQHPQGNQQLRHPVDLFEANDLFESGNNMQVR VSLALAGKAKTKGLQSGVDIRDKYSEKQNFNDTMMKARLCVIRLQITNKASQSGMT AYVTRRHLYDPKNRILPPMDNSTISLRMGTNKCASQVGMTAPGNQWHIYDTKLGIIDKC ENSSMSLKMGYTQVANHSRQVFLGRQIYEPKYQPGGPVAHGAPSAAGNCPGPGEAP		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 87B.

Table 87B. Comparison of NOV87a against NOV87b.		
Protein Sequence	NOV87a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV87b	1..288	288/288 (100%)
	1..288	288/288 (100%)

Further analysis of the NOV87a protein yielded the following properties shown in Table 87C.

Table 87C. Protein Sequence Properties NOV87a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.2110 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV87a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 87D.

Table 87D. Geneseq Results for NOV87a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV87a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAR94888	Carponin - Homo sapiens, 297 aa. [JP08073380-A, 19-MAR-1996]	1..265 6..272	136/269 (50%) 176/269 (64%)	7e-63
AAR72588	Carponin protein - Homo sapiens, 297 aa. [WO9509010-A, 06-APR-1995]	1..265 6..272	136/269 (50%) 176/269 (64%)	7e-63
AAB43807	Human cancer associated protein sequence SEQ ID NO:1252 - Homo sapiens, 163 aa. [WO200055350-A1, 21-SEP-2000]	164..273 4..116	67/113 (59%) 82/113 (72%)	6e-30
AAM73074	Human bone marrow expressed probe encoded protein SEQ ID NO: 33380 - Homo sapiens, 71 aa. [WO200157276-A2, 09-AUG-2001]	157..225 2..71	49/70 (70%) 55/70 (78%)	4e-21
AAM60434	Human brain expressed single exon probe encoded protein SEQ ID NO: 32539 - Homo sapiens, 71 aa. [WO200157275-A2, 09-AUG-2001]	157..225 2..71	49/70 (70%) 55/70 (78%)	4e-21

In a BLAST search of public sequence databases, the NOV87a protein was found to have homology to the proteins shown in the BLASTP data in Table 87E.

Table 87E. Public BLASTP Results for NOV87a

Protein Accession Number	Protein/Organism/Length	NOV87a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q08094	Calponin H2, smooth muscle - Sus scrofa (Pig), 296 aa (fragment).	1..287 6..296	219/291 (75%) 237/291 (81%)	e-116
Q99439	Calponin H2, smooth muscle (Neutral calponin) - Homo sapiens (Human), 309 aa.	1..288 6..297	218/292 (74%) 235/292 (79%)	e-115
Q08093	Calponin H2, smooth muscle - Mus musculus (Mouse), 305 aa.	1..288 6..293	214/291 (73%) 231/291 (78%)	e-112
O93547	CALPONIN H3 - Xenopus laevis (African clawed frog), 295 aa.	1..269 5..276	179/273 (65%) 208/273 (75%)	6e-91
Q922F8				8e-83

	MGC:8135) - Mus musculus (Mouse), 242 aa.	1..230	179/233 (76%)	
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PFam analysis predicts that the NOV87a protein contains the domains shown in the Table 87F.

Table 87F. Domain Analysis of NOV87a

Pfam Domain	NOV87a Match Region	Identities/ Similarities for the Matched Region	Expect Value
CH: domain 1 of 1	23..123	27/124 (22%) 65/124 (52%)	0.068
calponin: domain 1 of 2	159..183	17/26 (65%) 21/26 (81%)	3.8e-07
calponin: domain 2 of 2	198..223	15/26 (58%) 19/26 (73%)	3e-08

Example 88.

The NOV88 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 88A.

Table 88A. NOV88 Sequence Analysis

Table 88A. NOV88 Sequence Analysis		
	SEQ ID NO: 247	2213 bp
NOV88a, CG59671-02 DNA Sequence	CGTGAGGCACCCACTCTGGGAGCACAGAGAGCTCAGGTAGCCTGCCTAGATGGCGGGC CGCACCTCTGGGCGCGCGCTCGGGAGGCTGCTGGGCAGCTGCGAGGGCTCTCGGGGC AGCCCGCGCGGCGCGCGTGC GGGGTGAGCGCGCGCGCAGGGCGGGCTCGGGACCTC GGGCAGCGCTCCGCGAGTTGCAGCAGCAGCAGCAGCAGCGAGCTCGTATCCCGCGCTG AGTGACAGGCGAGCCGGGAGCCGGCCGCTTCTGGGGGCTCTGGCGGGGACACTC TCGTGTGGGACACCCCTACCAACACGCTCTGGGACTGCGACTTCAGCACTGGCAAGAT CGGCTGGTCTCTGGGAGGCCAGTTAAATGTCTCTGTCACTGCTTGGACGACATGTT CGGAAGTCCCCGAGAGCGTTGCTTTGATCTGGGAGCGCATGAGCCTGGAACGGAAG TGAGGATCACCTACAGGGAACCTACTGGAGACCAACGTCGCCCTGGCCAACACGCTGAA GAGGCATGGAGTCCACCGTGGGGACCGTGTGGCATCTACATGCCCGTGTCCCCATTG GCTGTGGCAGCAATGCTGGCCTGTGGCCAGGATCGGAGCTGTCCACACAGTCATCTTTG CTGGCTTCAGTGACAGAGTCTTTGGCTGGGAGGATCAATGATGCCAAGTGCAAGGTGGT TATCACTTCAACCAAGGACTCCGGGGTGGGCGCGTGGTGGAGCTGAAGAAAATAGTG GATGAGGCTGTGAAGCACTGCCCCACCGTGCGAGCATGTCTCGTGGTGCTCACAGGACAG ACAACAAGGTCCACATGGGGGATCTGGACGTCCCCTGGAGCAGGAAATGGCCAAGGA GGACCTGTTTGCGCCCCAGAGAGCATGGGCAGTGAGGACATGCTCTTCATGCTGTAC ACCTCAGGAGGACACCGGAATGCCCAAGGGCATCGTCCATACCCAGGCGAGGCTACCTGC TCTATGCGCGCCCTGACTCACAAGCTTGTGTTTGACACCAGCAGGTCAGATCTTTGG CTGTGTGGCCGACATCGGTTGGATTACAGGACACAGCTACGTGGTGTATGGGCTCTC TGCAATGGTGCCACAGCGTCTTTTGTAGAGCACCCAGTTTATCCCAATGCTGGTGT GGTACTGGGAGACAGTAGAGAGGTGAAGATCAATCAGTTCTATGGCGCCCAACGGG TGTCCGGCTGTGTGCTGAAATACGGTGATGCCTGGGTGAAGAAGTATGATCGCTCCTCC CTGCGGACCTGGGGTCACTGGGAGAGCCCATCAACTGTGAGGCTTGGGAGTGGCTTC ACAGGCTGGTGGGGACAGCAGGTGCACGCTGGTGGACACCTGGTGCCAGACAGAAAC AGGTGGCATCTGCATCGCACCAACCGCCCTCGGAAGAAGGGCGGAAATCCTCCTGCC ATGGCGATGAGGCCCTTCTTTGGCATCGTCCCGCTCTCATGGATGAGAAGGGCAGCG TCGTGGAGGGCAGCAACGCTCTCCGGGGCCCTGTGCATCTCCAGGCGCTGGCCGGGCAT GGCCAGGACCATCTATGGCGACCACAGCGATTGTGTGAGCGCTACTTCAAGGCTTAC CCAGGCTATTACTTCACTGGAGACGGGGCTTACCGAACTGAGGGCGGCTATTACCAGA TCAAGGGCGGATGGATGATGTATCAACATCAGTGGCCACCGCGTGGGGACCGCAGAG GATTGAGGACGCCATGCCGACCCCTGCAGTACCAGAAAGTGTGTCATTGGCTAC CCCCACGACATCAAGGAGAAAGCTGCCTTTGCGCTTCAATTGGTGGTGAAGATAGTGC	

	GTGACTCAGATGTGGTGGTGCAGGAGCTCAAGTCCATGGTGGCCACCAAGATCGCCAA ATATGCTGTGCCTGATGAGATCCTGGTGGTGAACGTCTTCCAAAAACAGGTCTGGG AAGGTGATGCGGCGGCTCCTGAGGAAGATCATCACTAGTGAGGCCAGGAGCTGGGAG ACACTACCACCTTGGAGGACCCAGCATCATCGCAGAGATCCTGAGTGTCTACCAGAA GTGCAAGGACAAGCAGGCTGCTGCTAAGTGAGCTGGCACCTTGTGGGGCTCTTGGGAT GGGCGGGCACCAAGCCCTGGCTTGTCTTCCAGAAGGTACCCCTGAGGTTGGCGTC TTCCTACGT		
	ORF Start: ATG at 50	ORF Stop: TGA at 2117	
	SEQ ID NO: 248	689 aa	MW at 74855.9kD
NOV88a, CG59671-02 Protein Sequence	MAARTLGRGVGRLGSLRGLSGQPARPPCGVSAPRRASGPSGSAPAVAAAAAQPGSY PALSAQAAREPAAFWGLPLARDTLVWDTPTYHTVWDCDFSTGKIGWFLGGQLNVSVNCLD QHVRKSPESVALIWERDEPGTEVRITYRELLETTCLRLANTLKRHGVRGDRVAIYMPV SPLAVALACARIGAVHTVIFAGFSAESLAGRINDAKCKVITFNQGLRGGRVVELK KIVDEAVKHCPTVQHVLAHRTDNKVHMGDLDPLEQEMAKEDPVCAPESMGSEDMLF MLYTSGSTGMPKGI VHTQAGYLLYAALTHKL VFDHQPGDIFGCVADIGWITGHSYVVY GPLCNGATSVLPFESTPVYPNAGRYWETVERLKNQFYGAPTAVRLLLKYGDAWVKKYD RSSLRTLGSGVEPINCEAWEWLHRVVGDSRCTLVDTWWQTETGGICIAPRPSEEGAEI LPAMAMRPFFGIVPVLMDKGSVVEGSNVSGALCISQAWPGMARTIYGDHQRFDVAYF KAYPGYYFTGDGAYRTEGGYYQITGRMDDVINISGHR LGTAIEDAIDH PAVPESAV IGYPHDIKGEAAFAFIVVKDSAGSDV VVQELKSMVATKIAYAVPDEILVVKRLPKT RSGKVMRRLLRKIITSEAQELGDTTTLLEDPSIIAEILSVYQKCKDKQAAAK		

Further analysis of the NOV88a protein yielded the following properties shown in Table 88B.

Table 88B. Protein Sequence Properties NOV88a	
PSort analysis:	0.6500 probability located in plasma membrane; 0.6000 probability located in nucleus; 0.4340 probability located in mitochondrial inner membrane; 0.3000 probability located in Golgi body
SignalP analysis:	Likely cleavage site between residues 23 and 24

A search of the NOV88a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 88C.

Table 88C. Geneseq Results for NOV88a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV88a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value

AAU23058	Novel human enzyme polypeptide #144 - Homo sapiens, 664 aa. [WO200155301-A2, 02-AUG-2001]	26..689 1..664	663/664 (99%) 663/664 (99%)	0.0
AAB34712	Human secreted protein encoded by DNA clone vo9 1 - Homo sapiens, 518 aa. [WO200055375-A1, 21-SEP-2000]	172..689 1..518	518/518 (100%) 518/518 (100%)	0.0
AAU23050	Novel human enzyme polypeptide #136 - Homo sapiens, 479 aa. [WO200155301-A2, 02-AUG-2001]	224..689 18..479	459/466 (98%) 461/466 (98%)	0.0
ABB12253	Human acetate-coA ligase homologue, SEQ ID NO:2623 - Homo sapiens, 446 aa. [WO200157188-A2, 09-AUG-2001]	1..446 1..446	446/446 (100%) 446/446 (100%)	0.0
AAR23968	facA gene product - Penicillium chrysogenum, 669 aa. [WO9207079-A, 30-APR-1992]	58..684 45..669	305/629 (48%) 407/629 (64%)	e-175

In a BLAST search of public sequence databases, the NOV88a protein was found to have homology to the proteins shown in the BLASTP data in Table 88D.

Table 88D. Public BLASTP Results for NOV88a				
Protein Accession Number	Protein/Organism/Length	NOV88a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q99NB1	ACETYL-COA SYNTHETASE 2 - Mus musculus (Mouse), 682 aa.	1..687 1..680	599/687 (87%) 638/687 (92%)	0.0
Q9BEA3	ACETYL-COA SYNTHETASE 2 - Bos taurus (Bovine), 675 aa.	1..689 1..675	575/689 (83%) 625/689 (90%)	0.0
Q9NUB1	DJ568C11.3 (NOVEL AMP-BINDING ENZYME SIMILAR TO ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE)) - Homo sapiens (Human), 478 aa (fragment).	212..689 1..478	478/478 (100%) 478/478 (100%)	0.0
Q96JI1	KIAA1846 PROTEIN - Homo sapiens (Human), 354 aa (fragment).	336..689 1..354	354/354 (100%) 354/354 (100%)	0.0
Q9HV66	ACETYL-COENZYME A SYNTHETASE - Pseudomonas aeruginosa, 645 aa.	58..675 24..639	326/619 (52%) 433/619 (69%)	0.0

PFam analysis predicts that the NOV88a protein contains the domains shown in the Table 88E.

Table 88E. Domain Analysis of NOV88a			
Pfam Domain	NOV88a Match Region	Identities/ Similarities for the Matched Region	Expect Value
AMP-binding: domain 1 of 1	142..580	121/441 (27%) 341/441 (77%)	7.1e-117

Example 89.

The NOV89 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 89A.

Table 89A. NOV89 Sequence Analysis			
	SEQ ID NO: 249	1268 bp	
NOV89a, CG56870-01 DNA Sequence	ACTTCTTTCTTTTCTGTTTCAGAGTTACTGATTTATTCTTGAGATTCTCTACTCTCG TTATCTGACCTCATGGATGAACTTCAGGATGTTTCAGCTCACAGAGATCAAACCACTTC TAAATGATAAGAATGGTACAAGAACTTCAGGACTTTGACTGTCAGGAACATGATAT AGAAACAACCTCATGGTGTGGTCCACGTCACTATAAGAGGCTTACCCAAAGGAAACAGA CCAGTTATACTAACATATCATGACATTGGCCTCAACCGTAAATCCTGTTTCAATGCAT TCTTTAACTTTGAGGATATGCAAGAGATCACCCAGCACTTTGCTGTCTGTCAATGTGGA TGCCCCAGGCCAGCAGGAAGGTGCACCCTCTTTCCCAACAGGGTATCAGTACCCCA ATGGATGAGCTGGCTGAAATGCTGCCTCCTGTTCTTACCCACTAAGCCTGAAAAGCA TCATTGGAATTGGAGTTGGAGCTGGAGCTTACATCCTCAGCAGATTGCACTCAACCA TCCAGAGCTTTGGAAGGCCTTGCTCTCATTAAATGTTGACCCCTTGCCTAAAGGCTGG ATTGACTGGGCAGCTTCCAACTCTCTGGCCTGACAACCAATGTTGTGGACATTATTT TGGCTCATCACTTTGGGCAGGAAGAGTTACAGGCCAACCTGGACCTGATCCAAACCTA CAGAATGCATATTGCCCAAGACATCAACCAAGACAACCTGCAGCTCTTCTTGAATCC TACAATGGGCGCAGAGACCTGGAGATCGAAAGACCCATACTGGGCCAAAATGATAACA AATCAAAAACATTAAAGTGTCTACTTTACTGGTGGTAGGGGACAATTGCGCTGCACT TGAGGCTGTGGTCAATGCAATTCCCGCTGAACCTTATAATACAATTGCTAAAG ATGGCGGACTGTGGGGGACTGCCCCAGGTAGTTTCAGCCTGGGAAGCTCACCGAGGCT TCAAGTACTTTTGCAGGAATGGGCTACGTCCTGTCAGCATGACTCGGCTCGC CCGATCAGCAACCCACTCAACCTCGAGTAGCCTCGGCTCTGGAGAAAGTCCCTTCAGC CGGTCTGTCAACAGCAATCAGTCAGATGGAATCAAGAATCCTGTGAGTCCCTCGATG TCCTGGACAGACACCAGACCATGGAGGTGTCCTGCTAAGCAGATGCTCTCCCTCGGA CCATTGCAAGTCCATCCTTCAAATGACCATTCCATAATATAACATTTCAT		
	ORF Start: ATG at 71	ORF Stop: TAA at 1196	
	SEQ ID NO: 250	375 aa	MW at 41413.3kD
NOV89a, CG56870-01 Protein Sequence	MDELQDVQLTEIKPLNDKNGTRNFQDFDCQEHDIETTHGVVHTIRGLPKGNRPVIL TYHDIGLNRKSCFNFFNFEDMQEITQHFVCHVDAPGQEGAPSPFTGYQYPTMDEL AEMLPPVLTHLSLKSIIIGVGVAGAYILSRFALNHPPELVEGLVLINVDPCAKGWIDWA ASKLSGLTTNVVDIIIAHFGQEEQLQANLDLIQTYRMHIAQDINQDNLQFLNSYNGR RDLEIERPILGQNDNKSITLKCSTLLVVGDNSPAVEAVVECNRLNPINTLLKMAADC GGLPQVVQPGKLTFAFKYFLQGMGYVPSASMTLRARSRTHSTSSSLGSGESPFSRSVT SNQSDGTQESCESPDVLDRHQTMVSC		
	SEQ ID NO: 251	1175 bp	
NOV89b, CG56870-02 DNA Sequence	TCGTTATCTGACCTCATGGATGAACTTCAGGATGTTTCAGCTCACAGAGATCAAACCA TTCTAAATGATAAGAATGGTACAAGAACTTCAGGACTTTGACTGTCAGGAACATGA TATAGAAAACACTCATGGTGTGGTCCACGTCACTATAAGAGGCTTACCCAAAGGAAAC AGACCAGTTATACTAACATATCATGACATTGGCCTCAACCATAAATCCTGTTTCAATG CATTCCTTTAACTTTGAGGATATGCAAGAGATCACCCAGCACTTTGCTGTCTGTCAATG GGATGCCCCAGGCCAGCAGGAAGGTGCACCCTCTTTCCCAACAGGGTATCAGTACCCC ACAATGGATGAGCTGGCTGAAGTGTGCTGCTCTGTTCTTACCCACTAAGCCTGAAAA GCATCATGGAATTGGAGTTGGAGCTGGAGCTTACATCCTCAGCAGATTGCACTCAA		

	CCATCCAGAGCTTGTGGAAGCCTTGTGCTCATTAAATGTTGACCCTTGGCGTAAAGGC TGGATTGACTGGGCAGCTTCCAAACTCTCTGGCCTGACAACCAATGTTGTGGACATTA TTTTGGCTCATCACTTTGGGCAGGAAGAGTTACAGGCCAACCTGGACCTGATCCAAAC CTACAGAATGCATATTGCCAAGACATCAACCAAGACAACCTGCAGCTCTTCTTGAAT TCCTACAATGGACGCGAGAGACCTGGAGATCGAAAGACCCTACTGGGCCAAAATGATA ACAAATCAAAAACATTAAAGTGTCTACTTTACTGGTGGTAGGGGACAATTTCGCCTGC AGTTGAGGCTGTGGTGAATGCAATTCCTGGCTGAACCTATAAATACAACCTTTGCTA AAGATGGCGGACTGTGGGGGACTGCCCCAGGTAGTTACGCTGGGAAGCTCACCAGG CCTTCAAGTACTTTTTCAGGGAATGGGCTACATACCATCTGCCAGCATGACTCGGCT CGCCGATCAGAACCCACTCAACCTCGAGTAGCCTCGGCTCTGGAGAAAGTCCCTTC AGCCGGTCTGTACCAGCAATCAGTCAGATGGAACCAAGAAATCCTGTGAGTCCCTTG ATGTCTGGACAGACCCAGACCATGGAGGTGTCTGCTAAGCAGATGCTCCTCCCT GGACCATTGCAAGTC		
	ORF Start: ATG at 16	ORF Stop: TAA at 1141	
	SEQ ID NO: 252	375 aa	MW at 41376.2kD
NOV89b, CG56870-02 Protein Sequence	MDELQDVQLTEIKPLNDKNGTRNFQDFDCQEHDIETTHGVVHTIRGLPKGNRPVIL TYHDI GLN HKSCFNAPFNEDMQEITQHFAVCHVDAPGQEGAPSFPTGYQYPTMDEL AEVLPPVLTHLSLKSIIIGIVGAGAYILSRFALNHPVELVGLVLINVDPCAKGWIDWA ASKLSGLTTNVVDIILAHFQGEEQLQANLDLIQTYRMHIAQDINQNLQLFLNSYNGR RDLEIERPILGQNDKSKTLKCSLLVVGDNSPAUEAVVECNRLNPINTLLKMACD GGLPQVVPQPKLTEAFKYFLQGMGYIPASMTLRARSRTHSTSSSLGSGESPFSSVT SNQSDGTQESCESPDVLDHRHQTMEVSC		
	SEQ ID NO: 253	1232 bp	
NOV89c, CG56870-03 DNA Sequence	ACTTCTTTCTTTTCTGTTTCAGAGTTACTGATTATTCTTGAGATTCTCTACTCTCG TTATCTGACCTCATGGATGAACCTCAGGATGTTGAGCTCAGAGATCAAAACCACTTC TAAATGATAAGGAACATGATATAGAAACAACCTCATGGTGTGGTCCACGTCATAAG AGGCTTACCCAAAGGAAACAGACCAGTTATACTAACATATCATGACATTGGCCTCAAC CATAAATCTCTGTTTCAATGCATTCTTTAACTTTGAGGATATGCAAGAGATCACCAGC ACTTTGCTGTCTGTCAATGTGGATGCCCCAGGCCAGCAGGAAGGTGCACCCTCTTTCCC AACAGGGTATCAGTACCCCAATGGATGAGCTGGCTGAAATGCTGCCTCTGTCTTCTT ACCCACCTAAGCCTGAAAAGCATCATTGGAATTGGAGTTGGAGCTGGAGCTTACATCC TCAGCAGATTGCACTCAACCATCCAGAGCTTGTGGAAGGCCCTTGTGCTCATTAAATGT TGACCTTGGCTAAAGGCTGGATTGACTGGGCAGCTTCCAACTCTCTGGCCTGACA ACCAATGTTGTGGACATTATTTGGCTCATCACTTTGGGCAGGAAGAGTTACAGGCCA ACCTGGACCTGATCCAAACCTACAGAATGCATATTGCCCAAGACATCAACCAAGACAA CCTGCAGCTCTTCTTGAATTCCTACAATGGGCGCAGAGACCTGGAGATCGAAAGACCC ATACTGGGCCAAAATGATAACAAATCAAAAACATTAAAGTGTCTACTTTACTGGTGG TAGGGGACAATTTCGCTGCAGTTGAGGCTGTGGTGAATGCAATTCGCCCTGAACCC TATAAATACAACCTTTGCTAAAGATGGCGGACTGTGGGGGACTGCCCGAGTAGTTTCAG CTTGGAAGCTCACCAGGCTTCAAGTACTTTTGCAGGGAATGGGCTACGTCCTCGT CTGCCAGATGACTCGGCTCGCCGATCACGAACCCACTCAACCTCGATGAGCTCGG CTCTGGAGAAAGTCCCTTCAGCCGGTCTGTACCAGCAATCAGTCAGATGGAACCTCAA GAATCCTGTGAGTCCCTGTATGTCTGGACAGACACAGACCATGGAGGTGTCTGTCT AAGCAGATGCTCTCTCCCTGGACCATTGCAAGTCCATCCTTCAAATGACCACTCCATA ATATAACATTTTCAT		
	ORF Start: ATG at 71	ORF Stop: TAA at 1160	
	SEQ ID NO: 254	363 aa	MW at 39967.8kD
NOV89c, CG56870-03 Protein Sequence	MDELQDVQLTEIKPLNDKEHDIETTHGVVHTIRGLPKGNRPVILTYHDI GLN HKSC FNAFFNFEDMQEITQHFAVCHVDAPGQEGAPSFPTGYQYPTMDELAELMPVLTHLS LKSIIIGIVGAGAYILSRFALNHPVELVGLVLINVDPCAKGWIDWAASKLSGLTTNV DIILAHFQGEEQLQANLDLIQTYRMHIAQDINQNLQLFLNSYNGRRDLEIERPILGQ NDNKSCTLKCSLLVVGDNSPAUEAVVECNRLNPINTLLKMACDGGLPQVVPQPKL TEAFKYFLQGMGYVPSASMTLRARSRTHSTSSSLGSGESPFSSVTSNQSDGTQESCE SPDVLDHRHQTMEVSC		
	SEQ ID NO: 255	1220 bp	
NOV89d, CG56870-04 DNA Sequence	ACTTCTTTCTTTTCTGTTTCAGAGTTACTGATTATTCTTGAGATTCTCTACTCTCG TTATCTGACCTCATGGATGAACCTCAGGATGTTGAGCTCAGAGATCAAAACCACTTC TAAATGATAAGAAATGGTACAAGAACTTCAGGACTTGTACTGTGAGGAACATGATAT AGAAACAACCTCATGGTGTGGTCCACGTCATAAGAGGCTTACCCAAAGGAAACAGA CCAGTTATACTAATATATCATGACATTGGCCTCAACCGTAAATCCTGTTTCAATGCAT TCTTTAACTTTGAGGATATGCAAGAGATCACCCAGCACTTGTCTGTCTGTATGTTGGA TGCCCCAGGCCAGCAGGAAGGTGCACCCTCTTCCCAACAGGGTATCAGTACCCACCA ATGGATGAGCTGGCTGAAATGCTGCCTCCTGTTCTTACCCACCTAAGCCTGAAAAGCA TCATTGGAATTGGAGTTGGAGCTGGAGCTTACATCCTCAGCAGATTGCACTCAACCA TCCAGAGCTTGTGGAAGGCTTGTGCTCATTAAATGTTGACCTTGGCTGCTAAAGGCTGG ATTGACTGGGCAGCTTCCAACTCTCTGGCCTGACAACCAATGTTGTGGACATTATTT TGGCTCATCACTTTGGGCAGGAAGAGTTACAGGCCAACCTGGACCTGATCCAAACCTA CAGAATGCATATTGCCAAGACATCAACCAAGACAACCTGCAGCTCTTCTTGAATTC TACAATGGACGACGAGACCTGGAGATCGAAAGACCCATACTGGGGCCAAAATGATAACA		

	AATCAAAAACATTAAAGTGTCTACTTTACTGGTGGTAGGGGACAATTCGCCTGCAGT TGAGGCTGTGATGGCGGACTGTGGGGGACTGCCCCAGGTAGTTCAGCCTGGGAAGTTTC ACCGAGGCCCTTCAAGTACTTTTTCAGGGAATGGGCTACACACCATTCTGCCAGCATGA CTCGGCTCGCCCGATCACGAACCCACTCAACCTCGAGTAGCCTCGGCTCTGGAGAAAG TCCCTTCAGCCGGTCTGTCAACAGCAATCAGTCAGATGGAACCTCAAGAATCCTGTGAG TCCCTGTATGTCTGGACAGACACCAGACCATGGAGGTGTCCTGCTAAGCAGATGCTC CTCCCTGGACCATTGCAAGTCCATCCTTCAAATGACCACTCCATAATATAACATTTC AT		
	ORF Start: ATG at 71	ORF Stop: TAA at 1148	
	SEQ ID NO: 256	359 aa	MW at 39652.2kD
NOV89d, CG56870-04 Protein Sequence	MDELQDVQLTEIKPLLNDKNGTRNFQDFDCQEHDIETTHGVVHVTIRGLPKGNRPVIL TYHDIGLNRKSCFNFFNFMQEIQTQHFVCHVDAPGQEGAPSFPTGYQYPTMDEL AEMLPPVLTHLSLSKSIIGVGVGAGAYILSRFALNHPPELVGLVLINVDPCAKGWIDWA ASKLSGLTTNVVDIILAHHFGQEELQANLDLIQTYRMHIAQDINQDNLQLFLNSYNGR RDLEIERPILGQNDNKSITLKCSTLLVVGDNSPAVEAVMADCGGLPQVVQPGKFTFAF KYFLQGMGYTPSASMTLRASRTHSTSSSLGSGESPFSSRVTSNQSDGTQESCESPDV LDRHQTMEVSC		
	SEQ ID NO: 257	970 bp	
NOV89e, CG56870-05 DNA Sequence	ATGGATGAACCTCAGGATGTTCACTCACAGAGATCAAACCACTTCTAAATGATAAGA ATGGTACAAGAACTTCCAGGACTTTGACTGTCTAGTATCAGTACCCCAATGGATGA GCTGGCTGAAATGCTGCCTCCTGTTCTTACCCACCTAAGCCTGAAAAGCATCATTGGA ATTGGAGTTGGAGCTGGAGCTTACATCCTCAGCAGATTGCACTCAACCATCCAGAGC TTGTGGAAGGCCTTGTGCTCATTAAATGTTGACCTTGCCTAAAGGCTGGATTGACTG GGCAGCTTCAAACCTCTCTGGCCTGACAACCAATGTTGTGGACATTATTTGGCTCAT CACTTTGGGCAGGAAGAGTTACAGGCCAACCTGGACCTGATCCAAACCTACAGAATGC ATATTGCCCAAGACATCAACCAAGACAACCTGCAGCTCTTCTTGAATTCCTACAATGG GCGCAGAGACCTGGAGATCGAAAGACCCATACTGGGCCAAAATGATAACAAATCAAAA ACATTAAGTGTCTTACTTTACTGGTGGTAGGGGACAATTGCGCTGCACTTGAGGCTG TGGTCGAATGCAATTCCCGCCTGAACCTTATAAATACAACCTTTGCTAAAGATGGCGGA CTGTGGGGGACTGCCCCAGGTAGTTCAGCCTGGGAAGCTCACCGAGGCCTTCAAGTAC TTTTTGCAGGGAATGGGCTACGTCCTGCTGCCAGCATGACTCGGCTCGCCCGATCAC GAACCACTCAACCTCGAGTAGCCTCGGCTCTGGAGAAAGTCCCTTCAGCCGGTCTGT CACCAGCAATCAGTCAGATGGAACCTCAAGAATCCTGTGAGTCCCCTGATGTCTGGAC AGACACCAGACCATGGAGGTGTCCTGCTAAGCAGATGCTCCTCCCTGGACCATTTGCA AGTCCATCCTTCAAATGACCACTCCATAATATAACATTTCAT		
	ORF Start: ATG at 1	ORF Stop: TAA at 898	
	SEQ ID NO: 258	299 aa	MW at 32956.9kD
NOV89e, CG56870-05 Protein Sequence	MDELQDVQLTEIKPLLNDKNGTRNFQDFDCQYQYPTMDELAEMLPVVLTHLSLSKSIIG IGVGAGAYILSRFALNHPPELVGLVLINVDPCAKGWIDWAASKLSGLTTNVVDIILAH HFGQEELQANLDLIQTYRMHIAQDINQDNLQLFLNSYNGRRDLEIERPILGQNDNKS ITLKCSTLLVVGDNSPAVEAVVECNRLNPINTLLKMAADCGGLPQVVQPGKLTFAFKY FLQGMGYVPSASMTLRASRTHSTSSSLGSGESPFSSRVTSNQSDGTQESCESPDVLD RHQTMEVSC		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 89B.

Table 89B. Comparison of NOV89a against NOV89b through NOV89e.		
Protein Sequence	NOV89a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV89b	1..375	336/375 (89%)
	1..375	338/375 (89%)
NOV89c	1..375	326/375 (86%)
	1..363	326/375 (86%)

NOV89d	1..375	321/375 (85%)
	1..359	321/375 (85%)
NOV89e	104..375	233/272 (85%)
	28..299	233/272 (85%)

Further analysis of the NOV89a protein yielded the following properties shown in Table 89C.

Table 89C. Protein Sequence Properties NOV89a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1685 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV89a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 89D.

Table 89D. Geneseq Results for NOV89a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV89a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM94019	Human stomach cancer expressed polypeptide SEQ ID NO 108 - Homo sapiens, 363 aa. [WO200109317-A1, 08-FEB-2001]	1..375 1..363	360/375 (96%) 361/375 (96%)	0.0
AAG64392	Human reducing agent and tunicamycin-responsive protein 40 - Homo sapiens, 363 aa. [WO200155375-A1, 02-AUG-2001]	1..375 1..363	360/375 (96%) 361/375 (96%)	0.0
AAB94494	Human protein sequence SEQ ID NO:15186 - Homo sapiens, 363 aa. [EP1074617-A2, 07-FEB-2001]	1..375 1..363	360/375 (96%) 361/375 (96%)	0.0
AAU31598	Novel human secreted protein #2089 - Homo sapiens, 395 aa. [WO200179449-A2, 25-OCT-2001]	68..374 1..307	282/323 (87%) 286/323 (88%)	e-154
AAB95462	Human protein sequence SEQ ID	133..375 44..286	240/243 (98%) 242/243 (98%)	e-138

	[EP1074617-A2, 07-FEB-2001]			
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In a BLAST search of public sequence databases, the NOV89a protein was found to have homology to the proteins shown in the BLASTP data in Table 89E.

Table 89E. Public BLASTP Results for NOV89a				
Protein Accession Number	Protein/Organism/Length	NOV89a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UGV2	NDRG3 protein - Homo sapiens (Human), 375 aa.	1..375 1..375	373/375 (99%) 374/375 (99%)	0.0
Q96PL8	NDR1-RELATED DEVELOPMENT PROTEIN NDR3 - Homo sapiens (Human), 375 aa.	1..375 1..375	372/375 (99%) 373/375 (99%)	0.0
Q9QYF9	NDRG3 protein (Ndr3 protein) - Mus musculus (Mouse), 375 aa.	1..375 1..375	358/375 (95%) 368/375 (97%)	0.0
AAH18504	SIMILAR TO N-MYC DOWNSTREAM REGULATED 3 - Mus musculus (Mouse), 388 aa.	1..375 1..388	359/388 (92%) 368/388 (94%)	0.0
Q96SM2	CDNA FLJ14759 FIS, CLONE NT2RP3003290, MODERATELY SIMILAR TO MUS MUSCULUS NDR1 RELATED PROTEIN NDR3 - Homo sapiens (Human), 363 aa.	1..375 1..363	360/375 (96%) 361/375 (96%)	0.0

Pfam analysis predicts that the NOV89a protein contains the domains shown in the Table 89F.

Table 89F. Domain Analysis of NOV89a			
Pfam Domain	NOV89a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Orn_Arg_deC_N: domain 1 of 1	62..89	7/33 (21%) 24/33 (73%)	1.9
abhydrolase: domain 1 of 1	87..310		0.0066

		142/239 (59%)	
Ndr: domain 1 of 1	22..346	210/340 (62%) 311/340 (91%)	3.7e-211

Example 90.

The NOV90 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 90A.

Table 90A. NOV90 Sequence Analysis			
	SEQ ID NO: 259	632 bp	
NOV90a, CG59764-01 DNA Sequence	GAAACTATAAAGGGTCCGAACCCCTCTTTTAAAGGATCCCAATGCATTTCCTTGATCCCGCGCGGTGCGACGGTACCACCATCCCAGCTGTGAGGCTGCCATCAACACCCACATCA GCCTGGAGCTCCACGCATCCTATGTGTACCTGTCCATGGCCTTCTACTTCGACCAGGAGCAGCGCGGCCCTGGAGCACTTTGACCGCTACTTCCTGCGCCAGTCGCAGGAGAAAAGG GAGCACGCCAGGAGCTGATGAGCCTGCAGAACCTGCGCGGTGGCCGCATCTGCCTTC ATGACATCAGGAAGCCAGAGGGCCAAGGCTGGGAGAGCGGGCTCAAGGCCATGGAGTG CACCTTCCACCTGGAGAAGAACATCAACCAGAGCCTCCTGGAGCTGCACCACTGGCC AGGGAAGAACGGCGACCCCCAGCTCTGCGCACTTCCTGGAGAACGACTTCCTGAACCAGC AGGCCAAGACCATCAAAGAGCTGGGTGGCTACCTGAGCAACCTGCACAAGATGGGGGC CCCGAAGCAGGCTGGCAGAGTACCTCTTTAACAAGCTCACCTGGGCGCAGCGCAA CCACTTCCTTGAACCAGCAGGCCAAGACCATCAAAGAGATTGGTGGCTACCT		
	ORF Start: ATG at 41	ORF Stop: TGA at 590	
	SEQ ID NO: 260	183 aa	MW at 21159.6kD
NOV90a, CG59764-01 Protein Sequence	MHFFDPSPVRRYHHPSCAAINTHISLELHASVYVLSMAFYFDQDDAALHFDRYFLR QSQEKREHAQELMSLQNLRRGGRICLHDIRKPEGQGWESGLKAMECTFHLEKNINQSL ELHQLARENGDPQLCDFLENDPLNQAKTIKELGGYLSNLHKMGAPEAGLAELYFNKL TLGRSEPLP		

Further analysis of the NOV90a protein yielded the following properties shown in Table 90B.

Table 90B. Protein Sequence Properties NOV90a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.1400 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV90a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 90C.

Table 90C. Geneseq Results for NOV90a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV90a	Identities/	Expect Value

		Match Residues	the Matched Region	
AAU07889	Polypeptide sequence for human hspG34a - Homo sapiens, 221 aa. [WO200166752-A2, 13-SEP-2001]	7..180 45..218	159/174 (91%) 164/174 (93%)	4e-91
AAU07890	Polypeptide sequence for human hspG34b - Homo sapiens, 183 aa. [WO200166752-A2, 13-SEP-2001]	6..177 6..177	125/172 (72%) 149/172 (85%)	6e-70
AAB90804	Human shear stress-response protein SEQ ID NO: 108 - Homo sapiens, 183 aa. [WO200125427-A1, 12-APR-2001]	7..180 7..180	114/174 (65%) 141/174 (80%)	6e-64
AAR71567	Human monocyte growth factor - Homo sapiens, 183 aa. [JP07031482-A, 03-FEB-1995]	7..180 7..180	114/174 (65%) 141/174 (80%)	6e-64
AAU27741	Mouse full-length polypeptide sequence #66 - Mus musculus, 182 aa. [WO200164834-A2, 07-SEP-2001]	6..180 6..180	112/175 (64%) 141/175 (80%)	5e-63

In a BLAST search of public sequence databases, the NOV90a protein was found to have homology to the proteins shown in the BLASTP data in Table 90D.

Table 90D. Public BLASTP Results for NOV90a				
Protein Accession Number	Protein/Organism/Length	NOV90a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BXU8	Ferritin heavy polypeptide-like 17 - Homo sapiens (Human), 183 aa.	6..177 6..177	125/172 (72%) 149/172 (85%)	2e-69
P29389	Ferritin heavy chain (Ferritin H subunit) - Cricetulus griseus (Chinese hamster), 185 aa.	6..180 10..184	115/175 (65%) 142/175 (80%)	6e-64
A26886	ferritin heavy chain - chicken, 180 aa.	6..180 5..179	112/175 (64%) 142/175 (81%)	1e-63
P08267	Ferritin heavy chain (Ferritin H subunit) - Gallus gallus (Chicken), 179 aa.	6..180 4..178	112/175 (64%) 142/175 (81%)	1e-63
Q95MP7	FERRITIN - Canis familiaris (Dog), 183 aa.	6..180 6..180	112/175 (64%) 143/175 (81%)	2e-63

PFam analysis predicts that the NOV90a protein contains the domains shown in the Table 90E.

Table 90E. Domain Analysis of NOV90a			
Pfam Domain	NOV90a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Bacteriofer: domain 1 of 1	14..159	35/172 (20%) 76/172 (44%)	6.7
ferritin: domain 1 of 1	17..173	92/161 (57%) 138/161 (86%)	4.7e-87

Example 91.

The NOV91 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 91A.

Table 91A. NOV91 Sequence Analysis			
	SEQ ID NO: 261	487 bp	
NOV91a, CG59710-01 DNA Sequence	TGCTGTGCGTTGTCTTTTCCTTCTCACTCAAGCCTGTGAAATCTCTCTTTTCAGGTTGAC AGACTAATGGAGTTGCATTTTAAATATCTGGGTGCAATGCAGGTGGCGGACAAGAAGA TTGAAGGGGAAAAACACGACATGGTCCGGCGAGGAGAGATCATCGACAATGACACCGA GGAGGAGTTCTACCTCCGGCGCCTGGATGCGGGGCTCTTTGTTCTCCAGCACATCTGC TACATCATGGCCGAGATCTGCAATGCCAATGTCCCCAGATTGCGCCAGAGGGTTCCACC AGATCCTAAACATGCGAGGAAGCTCCATCAAAATGTTCAGGCATATCATCAAGGAGTA TGCAGAGAACATCGGGGACGGCCGGAGCCCGGAGTTCGGGAGAACGAGCAAAAGCGC ATCCTGGGCTTGCTGGAGAACTTCTAGAGGCACCTTGGCCCTGCGCATCATGGACTCT CTCAGCTTCCCTCCCAGGATCAG		
	ORF Start: ATG at 65	ORF Stop: TAG at 431	
	SEQ ID NO: 262	122 aa	MW at 14385.4kD
NOV91a, CG59710-01 Protein Sequence	MELHFKYLGAMQVADKKIEGEKXDMVRRGEIIDNDEEFYLRRLDAGLFLVQHICYI MAEICNANVPQIRQRVHQILNMRGSSIKIVRHIIKEYAENIGDGRSPEFRENEQKRIL GLLENF		

Further analysis of the NOV91a protein yielded the following properties shown in Table 91B.

Table 91B. Protein Sequence Properties NOV91a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV91a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 91C.

Table 91C. Geneseq Results for NOV91a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV91a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU28058	Novel human secretory protein, Seq ID No 227 - Homo sapiens, 518 aa. [WO200166689-A2, 13-SEP-2001]	1..122 397..518	122/122 (100%) 122/122 (100%)	1e-66
AAM93729	Human polypeptide, SEQ ID NO: 3689 - Homo sapiens, 563 aa. [EP1130094-A2, 05-SEP-2001]	1..122 442..563	122/122 (100%) 122/122 (100%)	1e-66
AAB63116	Human secreted protein sequence encoded by gene 39 SEQ ID NO:126 - Homo sapiens, 401 aa. [WO200061748-A1, 19-OCT-2000]	1..119 283..401	119/119 (100%) 119/119 (100%)	1e-64
AAU28246	Novel human secretory protein, Seq ID No 603 - Homo sapiens, 360 aa. [WO200166689-A2, 13-SEP-2001]	1..118 197..316	104/120 (86%) 106/120 (87%)	2e-51
ABB21673	Protein #3672 encoded by probe for measuring heart cell gene expression - Homo sapiens, 32 aa. [WO200157274-A2, 09-AUG-2001]	24..55 1..32	32/32 (100%) 32/32 (100%)	1e-11

In a BLAST search of public sequence databases, the NOV91a protein was found to have homology to the proteins shown in the BLASTP data in Table 91D.

Table 91D. Public BLASTP Results for NOV91a				
Protein Accession Number	Protein/Organism/Length	NOV91a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96KD2	TESTES DEVELOPMENT-RELATED NYD-SP19 - Homo sapiens (Human), 376 aa.	1..122 255..376	122/122 (100%) 122/122 (100%)	5e-66
Q9H7A5	CDNA: FLJ21108 FIS, CLONE CAS05257 - Homo sapiens (Human), 225 aa.	1..122 104..225	121/122 (99%) 121/122 (99%)	5e-65
O62703	P14 - Bos taurus (Bovine), 122 aa.	1..122 1..122	116/122 (95%) 119/122 (97%)	2e-62
Q9CWL8	5730471K09RIK PROTEIN - Mus musculus (Mouse), 563 aa.	1..122 442..563	115/122 (94%) 118/122 (96%)	3e-62
Q9Y3M7	DJ633O20.1 (P14L, SIMILAR TO BOS TAURUS P14) - Homo sapiens (Human), 284 aa (fragment).	1..93 192..284	93/93 (100%) 93/93 (100%)	3e-48

PFam analysis predicts that the NOV91a protein contains the domains shown in the Table 91E.

Table 91E. Domain Analysis of NOV91a			
Pfam Domain	NOV91a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 92.

The NOV92 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 92A.

Table 92A. NOV92 Sequence Analysis		
	SEQ ID NO: 263	6527 bp
NOV92a, CG59754-02 DNA Sequence	CCACAGAGGGGAAATGCCAGCTTCCCTCTCCCTGGGGCTCCGTGCCCCCTCTGATCCA GCCCTTCGAATTCACCCCGCCTCCATCGGCCAGCTGCTCTACATTCCTGTGTGGTG TCCTCGGGGGACATGCCCATCCGTATCACCTGGAGGAAGGACGGACAGGTGATCATCT CAGGCTCGGGCGTGACCATCGAGAGCAAGGAATTCATGAGCTCCCTGCAGATCTCTAG CGTCTCCCTCAAGCACAACGGCAACTATACATGCATCGCCAGCAACGCAGCCGCCACC GTGAGCATTGTGTCTCCAGAACACAGGTTTTTTATTACCTACCACGGCGGGCTGTACA TCTCTGACGTACAGAAGGAGGACGCCCTCTCCACCTATCGCTGCATCACCAAGCACAA GTATAGCGGGGAGACCCGGCAGAGCAATGGGGCACGCCTCTCTGTACAGACCCGTGCT GAGTCGATCCCCACCATCCTGGATGGCTTCCACTCCCAGGAAGTGTGGGCCGGCCACA CCGTGGAGCTGCCCTGCACCGCCTCGGGCTACCCTATCCCCGCCATCCGCTGGCTCAA GGATGGCCGGCCCTCCCGGCTGACAGCCGCTGGACCAAGCGCATCACAGGGCTGACC	

ATCAGCGACTTGCGGACCGAGGACAGCGGCACCTACATTTGTGAGGTACCAACACCT
TCGGTTTCGGCAGAGGCCACAGGCATCCTCATGGTCATTGATCCCCCTCATGTGACCT
GACACCAAAGAAGCTGAAGACCGGCATTGGCAGCACGGTCATCCTCTCTGTCCTTG
ACGGGCTCCCCAGAGTTACCATCCGCTGGTATCGCAACACGGAGCTGGTGCCTG
ACGAGGCCATCTCCATCCGCGGGCTCAGCAACGAGACGCTGCTCATCACTCCGGCCCA
GAAGAGCCATTCCGGGGCTACCACTGCTTCGCTACCCGCAAGGCCACAGCCGCCAG
GACTTTGCCATCATTGCACTTGAGGATGGCAGCCCCCGCATCGTCTCGTCTTCAGCG
AGAAGGTGGTCAACCCCGGGGAGCAGTTCTCACTGATGTGTGCGGCCAAGGGCGCCCC
GCCCCCACGGTCACCTGGGCCCTCGACGATGAGCCCATCGTGGGGATGGCAGCCAC
CGCACCAACCAGTACACCATGTCCGACGGCACCAACCATCAGCCACATGAACGTCAACG
GCCCCAGATCCGCGACGGGGCGTGTACCGGTGCACAGCGCGGAACCTTGGTGGGCAG
TGCTGAATATCAGGCGCGAATAAAGCTAAGAGGCCACCCAGCATCCGGGCTATGCGG
AACATCACAGCAGTCCCGGGCGGGACACCTTATCAACTGCAGGGTCATCGGCTATC
CCTACTACTCCATCAAGTGGTACAAGGATGCCTTGTGTGTCGCGGACCAACCGCCA
GGTGGTGTGAGAAATGGGACCTCAAGCTGACTGACGTGCAGAGGGCATGGATGAG
GGGGAGTACCTGTGCACTGTCTCATCCAGCCCCAGCTCTCCATCAGCCAGAGCGTTTC
ACGTAGCCGTCAAAGTGGCCCTCTGATCCAGCCCTTCGAATTCACCCCGCTCCAT
CGGCCAGTGTCTACATTCCTGTGTGTGTCTCGGGGGACATGCCATCCGTATC
ACCTGGAGGAAGACGGACAGGTGATCATCTCAGGCTCGGGCGTGACCATCGAGAGCA
AGGAATTCATGAGTCCCTGCAGATCTCTAGCGTCTCCCTCAAGCAACCGCAACTA
TACATGCATCGCCAGCAACGAGCGGCCACCGTGAGCCGGGAGCTCAGCTCATCGTG
CGTGTGCCCCCTCGATTGTGGTGCAACCAACCAACAGGATGGCATCTACGGCAAG
CTGGTGTGCTCAACTGTCTGGTGGACGGCTACCCCCACCCAGGTATGTGGAAGCA
TGCCAAGGGGAGCGGGAACCCCGAGCAGTACCACCTGTGCCCTCACTGGCCGCATC
CAGATCTGCCCAACAGCTCGCTGTGATCCGCCACGTCTTAGAGAGGACATCGGCT
ACTACCTCTGCCAGGCCAGCAACGGCGTAGGCACCGACATCAGCAAGTCCATGTTCT
CACAGTCAAGATCCCGCCATGATCACTTCCACCCCAACACCACTCGCCATCAAG
GGCCATGCGAAGGAGTAAACTGCACGGCACGGGGTGAAGCGCCATCATCTCGCT
GGGAGAAGGGGACACAGTCTACGACCTGACCGGTGATGCGGTATGCCATCGCCAC
CAAGGACAACGGCGACGAGGTGCTTCCACACTGAAGCTCAAGCCCGTGACCGTGGG
GACTCTGTGTTCTTCACTGCCATGCCATCAACTCGTATGGGGAGGACCGGGCTTGA
TCCAACCTCACTGTGCAAGAGCCCCGACCCCGAGAGCTGGAGATCCGGAGGTGA
GGCCCGGAGCATGAACCTGCGCTGGACCCAGCGATTGACGGGAACAGCATCATCAG
GGCTTCGACATTGAATACAAGAACAAATCAGATTCTGGGACTTCAAGCAGTCCACAC
GCAACATCTCCCCACCATCAACAGGCCAACATTGTGGACTTGCACCCGGCATCTGT
GTACAGCATCCGCTGACTTCTTCAACAAGATTGGCCGAGTGAACCAAGGAG
CTCACCATCAGCACTGAGGAGGCGCTCCCGATGGGCCCCCATGGATGTTACCTTGC
AGCCAGTGACCTCACAGAGCATCCAGGTGACCTGGAAGGCACCAAGAGGAGCTGCA
GAACGGTGTATCCGGGGCTACAGATTGGCTACAGAGAGAACAGCCCCGCGAGCAAC
GGGCAGTACAGCATCGTGGAGATGAAGGCCAGGGGGACAGCGAGGTCTACACCTGG
ACAACTCAAGAGTTCCGCCAGTATGGGGTGGTGTCAAGCCTTCAATCGGGCTGG
CACGGGGCCCTCTTCCAGCGAGATCAATGCCACCACTCTGGAGGATGTGCCAGCCAG
CCCCCTGAGAAGCTCGGGCCCTGTCCATCACTTCTGACGTGGCGCTCATCTCTGGT
CAGAGCCCCCGCGCAGCACCTCAATGGCGTCTCTCAAAGGCTATCGGGTCATCTTCTG
GTCCCTCTATGTTGATGGGGAGTGGGGCAGATGCAGAACATCACCAACAGCGGGAG
CGGGTGGAGTGGGGGATGGAGAAGTTCAACCACTACAGCGTCCAGGTGCTGGCCT
ACACCAAGCTGGGGACGGCGTACGAGCAGTGTGCTCTACATCTCAGCAAGGAGA
CGTTCAGGTCCCCCTGCTGGCATCAAAGCTGTCCCTTCACTAGCTAGCAGTGTGGTT
GTGTCTTGGCTCCCCCTACCAAGCCCAACGGGGTGTCCGCAAGTACACCATCTTCT
GTTCCAGCCCCGGTCTGGCCAGCGGCTCCAGCGAGTACGAGAGTCCAGAGCA
GCTCTTCTACCGGATCGCCACCTAAACCGCGGTACAGCATCTCTGCTGTGGGTGGCC
GCCGTCACTCTGCGCGCCGGGGCAACAGCAGCGAGAAGGTGACCATCGAGCTGTCTG
GCAAGGCCCCAGCAAAGATCATCTCTTGGGGGACCGTGACAACCTTGGATGAA
AGATGTTCGGCTGCTTGAATTCAAGTGGGAGATCCAGCCCTGTGTGAAGTGGAC
AAGGACAGTGAAGACTCGGCCATTCCAGTGTCCATGGATGGGACCGGCTCATCCACA
CCAATGGCACACTGTGCTGCTGCGTGAAGGCTGAGGACTCTGGCTACTACACGTG
CACGGCCACCAACTGGTGGCTTGTACACCATCATCTGCAACCTTCTGGTGAAGTT
CCCCCGGACCAAGCCCCGCTCACTGTCTCAAAACCTCAGCTTCGTCCATCACCTGA
CCTGGATTCCAGGTGACAATGGGGCAGCTCCATCCGAGGCTTCGTGCTACAGTACTC
GGTGGACAACAGCGAGGAGTGAAGGATGTGTTTATCAGCTCCAGCGAGCGCTCCTTC
AAGCTGGACAGCCTCAAGTGTGGCAGTGGTACAAGGTGAAGTGGCGGCCAAGAACA
GCGTGGGCTCTGGGCGCATCAGCGAGATCATCGAGGCCAAGACCCACGGGCGGGAGCC
CTCCTTCAGCAAAGACCAACCTCTTCAACCCACATCAACTCCACGCATGCTCGGCTT
AACTGCAAGGGTGGAAATGGGGGCTGCCCTATCACAGCCATCGTTCTGGAGTACC
GGCCAAAGGGACCTGGGCTGGCAGGGCTCGGGCCAAACAGCTCCGGGGAGGTGT
TCTGACGGAATGCGAGAGGCCACGTGGTACGAGCTGCGCATGAGGGCTTGAACAGT
GCGGGCTGCGGCAATGAACAGCCAGTTTCGCCACCTGGACTACGATGGCAGCACA
TTCCACCCATCAAGTCTGCTCAAGTGAAGGGGATGATGTGAAGAAGCTGTTACCAT
CGGCTGCTGTCTGCTGGCCACACTGGGGGTGGCACTGCTCTTCACTGTCAGCAAG
AAGAGGAAGGAGAAACGGCTGAAGCGACTCCGAGATGCAAAGAGTTTGGCAGAAATGT
TGATAAGCAAGAAATAGAAGCTTGAACACCTGTGAAAGGGCCACCCAGGGCCC
ACGGCTACACATTGACATCCCCAGGCTCCAGTGTCTCATCGAGGACAAGAAGGCATC
AAGCAACTGGGAGATGACAAGGCCACCATCCCTGTGACAGATGCTAGTTCAGCCAG
CTGTCAACCCACAGAGCTTCTGTACTGGGCTCTCTTGCACCAACCAACCTCATCCA
GAGCACAGGACCCCTCATCGACATGTCTGACATCCGGCCAGGAACCAATCAGTGTCC
AGGAAGAAATGGAAGTCAGCCACAGCACCCGGAACCGGTACTCAAGCCAGTGGACCC
TGACCAAGTGCCAGGCTCCACACTGCCCGCACCTCACCTCCGACTGGCGCACCGT

	GGGCTCCCAGCATGGTGTACGGTCACTGAGGTGACAGCTACAGTGCACGCTGTCC CAGGACACAGACAAAGGAAGGAACAGCATGGTGTCCACTGAGAGTGCCTCTTCCACCT ACGAGGAGCTGGCCCGGCCTATGAGCATGCCAAGCTGGAGGAGCAGCTGCAGCACGC CAAGTTTGAGATCACCAGAGTGCTTCATCTCTGACAGTTCTCTGACCAGATGACCACA GGCACCAACGAGAACGCCGACAGCATGACATCCATGAGCACACCTCAGAGCCTGGCA TCTGCCGCTTTACCGCCTCACCACCCAAGCCCCAGGATGCGGACCGGGGGCAAAAACGT GGCTGTGTGCCATCCCTACCGGGCCAACAGAGTGAAGTACTGCAACCTGCCCTGTAT GCCAAGTCAGAGGCTTCTTTGAAAGGCAGATGGACGTGAGCCCTGCCCGTGGTCC CACCCCGTGAGGCTCCATCCGGAACCTGGCTCGAACCTACCAACACGAGGCTCGCCA CCTGACCCCTGGACCTGCCAGCAAGTCTTGGGCCCTTCCCCACCAGGGGCCCCCGGT GCCGCTCCACAGCCACCTTACCTCAGAGGACTCTGGCCATGCCAGCCCCCCCCAGCGC GCACAGCCCCCCCCAGCCCCCGGCCCAACCCCTGCTGAGCCACCCAGCCCCAGCGC TGCCCTCCGGCCCCCAGCACCAGAGCTCCACGAGCCGGGGGCCACACACCAAAATG GGGGCTCCAGGACTCGCTTCTCGAGATGAGCACATCGGGGTAGGGAGGTCTCAGA AGCAGGGGGCCGGGCTACTCCAATCCTACACCCTGGTGTAGGGCCGCGCAGGAAGA GCAGCCACGCTGGGCGCGCGCCGCGCAGCCCCACAGCCAGCTGGTGTGTTTTTC TGCATTATTATATTCAACTGACAGACAAAAACCAACCAACGACAAAAACAAAACCCC CAATCATGAACGCTGTACATAGAATCTTTTGTACAAATGAAACTATTTTCTCTCTC TCCATGAAGCCAGGCCACAAAGAAATTGACAGTACAAGTCAAAATCCCCACCCACAA AATATGTGTGGAGATATATATACATATATAGACAGACAGGAACGCCTCCACGAGCTAT ATATCTATATATTTCTCTCACCTATTTTGAGACAGAGGCACAAAGACTCAGCAATTT TTTTCCCTCCTCTCACCTTCCCCCAGTCTAGGTGGTTTTGACAAAGACCAAAATCC CAACTCAGAGACTGCATGCGATTTTACTGTTCCAAGAAAACAGGAGTTGCTTCAA TTTGCAGATGCTTATGTGTTAATACCTTTTCTATGAAAAAGACCCAGCGCGTGTG CAATAAAGGTTATGTTTCCAAAAAAGCTT		
	ORF Start: ATG at 129 ORF Stop: TAG at 5958		
	SEQ ID NO: 264	1943 aa	MW at 211904.3kD
NOV92a, CG59754-02 Protein Sequence	MPIRITWRKDGQVVISGSGVTIESKEFMSSLQISSVSLKHNGNYTCIASNAAATVSI SPEHRFFITYHGLYISDVQKEDALSTYRCITKHYSGETRQSNARLSVTDPAESIP TILDFPHSQEVWAGHTVELPCTASGYPIPAIRWLKDGRLPADSRWTKRITGLTISDL RTEDSGTYICEVNTNFGSAEATGILMVIDPLHVTLPKKLKTGIGSTVILSCALTGSP EFTIRWYRNTLVLPEAISISIRGLSNETLLITSAQKSHSGAYQCFATRKQAQDFAI IALEDGTPRIVSSFSEKVVNPGEQFSLMCAAKGAPPPTVTWALDDEPIVRDGSHTNQ YTMDSGTTISHMNVTPQIRIDGGVYRCTARNLVGSAEQARINVRGPPSIRAMRNITA VAGRDTLINCVRIGYPYISIKWYKDALLLPDNHRQVVFENGTLKLTVDVQKMGDEBYL CSVLIQPOLSIQSQSVHAVKVPPLIQPFEPFPPASIGQLLYIPCVVSSGDMPIRITWRK DGQVVISGSGVTIESKEFMSSLQISSVSLKHNGNYTCIASNAAATVSRERQLIVRVP RFVVQPNQDGIYKAGVLNCSVDGYPPPKVMWKHAKGSGNPQQYHPVPLTGRIQILP NSSLLIRHVLEEDIGYLLCQASNGVGTDISKSMFLTVKIPAMITSHPNITIAIKGHAK ELNCTARGERPIIIRWEKGDVTVIDPDRVMRYAIATKNDGEVSTLKLKPADRGDSVF FSCHAINS YGEDRGLIQLTVQEPDPPELEIREVKARSMNLRTQRFDGNSIITGFDI EYKNKSDSWDFKQSTRNISPTINQANIVDLHPASVYSIRMYSFNKIGRSEPSKELTIS TEEAAPDGPMPDVTLQPVTSQSIQVTKAPKKELQNGVIRGQIGYRENSPGSNGQYS IVEMKATGDSEVYTLNLLKFAQYGVVQAFNRAGTGPSSSEINATLLEDVPSQPPEN VRALSITSDVAIVISWSEPPRSTLNGVLKGYRVIFWSLYVDGEWGMQNITTRRVEL RGMEKFTNYSVQVLAITQAGDGVRSVLYIQTKEDVPGPPAGIKAVPSSASSVVSWL PPTKPNGVIRKYTIFCSSPGSQPAPSEYETSPEQLFYRIAHNLNRGQQLLVAAVTS AGRGNSSEKVTIEPAGKAPAKIISFGGTVTPWMKDVRLPCNSVGDPAVAVKWKDSE DSAI PVSMGDGHLIHTNGTLLLRVAKAEDSGYYTCTATNTGGFDITIVNLLVQVPPDQ PRLTVSKTSASSITLWIPGDNGGSSIRGFVLQYSVDNSEWVKDVFISSSERSFKLDS LKCGTWYKVLAAKNSVSGSRISEIEAKTHGREPSFSKDQHLFTHINSTHARLNLQG WNNGGCPITAI VLEYRPGKTWAWQGLRANSSGEVFLTELREATWYELMRACNSAGCG NETAQFATLDYDGSTIPIKSAQEGDDVKLFTIGCPVILATLGVALLFIVRKKRKE KRLKRLDAKSLAEMLISKNNRSFDPVKGPPQGPRLHIDI PRVOLLIEDKEGIGQLG DDKATIPVTDAEFSQAVNPQSFCTGVSLHHPTLIQSTGPLIDMSDIRPNTNPSVRKNV KSAHSTRNRYSSQWTLTKCQASTPARTLSDWRTVGSQHGVTVTESDSYSASLSQDTD KGRNSMVSTESASSTYEELARAYEHAKLEEQLOHAKFEITECFISDSSSDQMTTGTNE NADSMSTMSPTSEPGICRFTASPPKPQDADRGKNVAVPIPHRANKSDYCNLPYAKSE AFFRKADGREPCPVVPPREASIRNLARTYHTQARHLTLDPAKSLGLPHPGAPAAAST ATLPQRTLAMPAPPAGTAPPAGPTPAEPPTAPSAAPPAPSTEPPRAGGPHTKMGGR DSLLEMSTSGVGRSQKQAGAYSYSYTLV		
	SEQ ID NO: 265	6049 bp	
NOV92b, CG59754-01 DNA Sequence	CCACAGAGGGGAAATGCCAGCTTCCCTCTCCCTGGGGCTCCGTGCCCCCTCTGATCCA GCCCTTCGAATCCCACCCGCTCCATCGGCCAGCTGCTCTACATTCCTGTGTGGTG TCCTCGGGGACATGCCATCCGTATCACTGGAGGAAGGACGAGGTGATCATCT CAGGCTCGGGCGTGACCATCGAGAGCAAGGAATTCATGAGCTCCCTGCAGATCTCTAG CGTCTCCCTCAAGCACAAACGGCAACTATACATGCATCGCCAGCAACGAGCCGCCACC GTGAGCATTTGTGTCTCCAGAACACAGGTTTTTATTACCTACCACGGCGGGCTGTACA TCTCTGACGTACAGAAGGAGGACGCCCTCTCCACCTATCGTGCATCACCAAGACAA GTATAGCGGGGAGACCCGGCAGAGCAATGGGGCAGCCTCTCTGTGACAGACCCTGCT GAGTCGATCCCCACCATCTGGATGGCTTCCACTCCCAGGAAGTGTGGGCGGGCCACA CCGTGGAGCTGCCCTGCACCGCTCGGGCTACCCTATCCCCGCTATCCGCTGGCTCAA GGATGGCGGGCCCTCCCGGTGACAGCCGCTGGACCAAGCGCATCACAGGCTGACC		

ATCAGCGACTTGCGGACCGAGGACAGCGGCACCTACATTTGTGAGGTACCAACACCT
 TCGGTTTCGGCAGAGGCCACAGGCATCCTCATGGTCATTGATCCCCCTCATGTACCCT
 GACACCAAAGAAGCTGAAGACCGGCATTGGCAGACGGTCATCCTCTCTGTGCCCTG
 ACGGGCTCCCCAGAGTTACCATCCGCTGGTATCGCAACAGGAGCTGGTGTGCCTG
 ACGAGGCCATCTCCATCCGCGGGCTCAGCAACGAGAGCGTGCTCATACCTCGGCCCA
 GAAGAGCCATTTCGGGGCCTACCAGTGCTTCGCTACCCGCAAGGCCACCGCCAG
 GACTTTGCCATCATTGCACTTGAGGATGGCAGCCCCGCATCGTCTCGTCTTCAGCG
 AGAAGGTGGTCAACCCCGGGGAGCAGTTCTCACTGATGTGTGCGGCCAAGGGCGCCCC
 GCCCCCAGTCACCTGGGCCCTCGACGATGAGCCCATCGTGCGGGATGGCAGCCAC
 CGCACCAACAGTACACCATGTGCGACGGCACCAACCATCAGCCACATGAACGTACAG
 GCCCCAGATCCGCGACGGGGCGGTGTACCGGTGCACAGCGGGAACCTGGTGGGAG
 TGCTGAATATCAGGCGCAATAAACGTAAGAGGCCACCCAGCATCCGGGCTATGCGG
 AACATCACAGCAGTCGCGGGCGGGACACCTTATCAACTGCAGGGTCATCGGCTATC
 CCTACTACTCCATCAAGTGGTACAAGGATGCCTTGCTGTGTCGACAGCAACCGCCA
 GGTGGTGTGAGAAATGGGACCTCAAGCTGACTGACGTGCAGAGGGCATGGATGAG
 GGGGAGTACCTGTGAGTGTCTCATCCAGCCCCAGCTCTCCATCAGCCAGAGCGTTTC
 ACGTAGCCGTCAAAGTGCCTCTGTATCCAGCCCTTCGAATTCACCCCGCTCCAT
 CGGCCAGCTGTCTACATTTCCCTGTGTGGTGTCTCGGGGGACATGCCCATCCGTATC
 ACCTGGAGGAAGGACGGACAGGTGATCATCTCAGGCTCGGGCGTGACCATCGAGAGCA
 AGGAATTCATGAGTCCCTGCAGATCTCTAGCGTCTCCCTCAAGCACAACGGCAACTA
 TACATGCTCGCCAGCAACGCGCGCCACCGTGAGCCGGGAGCGTCAGCTCATCGTG
 CGTGTGCCCCCTCGATTTGTGGTGCAACCCAAACAGGATGGCATCTACGGCAAAG
 CTGGTGTGCTCAACTGCTCGGTGGACGGCTACCCCCACCAAGGTGATGTGAAGCA
 TGCCAAGGGTAGCGGAACCCCGCAGCAGTACCACCTGTGCCCTCACTGGCGCATC
 CAGATCTGCCCCAACAGCTCGCTGTGATCCGCCACGTCCTGAAGAGGACCTCATCGGT
 ACTACCTCTGCCAGGCCAGCAACGGCGTAGGCACCGACATCAGCAAGTCCATGTTCTCT
 CACAGTCAAGATCCCCACCATCTCGGATGGCTTCCACTCCAGGAAGTGTGGGCGCGC
 CACACCGTGGAGCTGCCCTGCACCGCTCGGGCTACCTATCTCCCGCATCCGCTGGC
 TCAAGGATGGCCGGCCCCCTCCCGGCTGACAGCCGCTGGACCAAGCGCATCACAGGGCT
 GACCATCAGCGACTTGCGGACCGAGGACAGCGGCACCTACATTTGTGAGGTACCAAC
 ACCTTCGGTGAGGCCACAGGCATCCTCATGGTCATTGGTGAGGAGCCCCCGACCCCC
 CAGAGCTGGAGATCCGGGAGGTGAAGGCCCGGAGCATGAACCTCGCTGGAGCCAGCG
 ATTGAGCGGAACAGCATCATCAGGGCTTCGACATTGAATACAAGAACAATCAGAT
 TCCTGGGACTTCAAGCAGTCCACACGCAACATCTCCCCACCATCAACAGGCCAACA
 TTGTGGACTTGACCCGGCATCTGTGTACAGCATCCGATGTACTTTTCAACAAGAT
 TGGCGCAGTGAACCAAGCAAGGAGCTCACCATCAGCACTGAGGAGGCTCAGCTCCC
 GATGGGCCCCCATGGATGTTACCTTGACAGCCAGTGACCTCACAGAGCATCCAGGTGA
 CCTGGAAGCAGGCACCAAGAAGGAGCTGCAGAACGGTGTATCCGGGGCTACAGAT
 TGGCTACAGAGAGAACAGCCCCGGCAGCAACGGGCAGTACAGCATCGTGAGATGAAG
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 GGGTGGTGTCCAGGCCTTCAATCGGGCTGGCACGGGGCCCTCTTCCAGCGAGATCAA
 TGCCACCACTCTGGAGGATGTGCCAGCCAGCCCCCTGAGAACGTCGGGGCCCTGTCC
 ATCACTTCTGACGTGGCCGTCATCTCTGGTGCAGAGCCCCCGGCGACACCTCAATG
 GCGTCTCAAAGGCTATCGGGTCATCTTCTGGTCCCTCTATGTTGATGGGAGTGGGG
 CGAGATGCAGAACTACCAACACGCGGGAGCGGGTGGAGCTCGGGGCATGGAGAAG
 TTCACCAACTACAGCGTCCAGGTGCTGGCTACACCCAGGCTGGGGACGGCGTACGCA
 GCAGTGTGCTCTACAGACCAAGGAGGACGTTCCAGGTCCCCCTCTGGCATCAA
 AGCTGTCCCTTCATCAGCTAGCAGTGTGGTGTGCTTGGCTCCCCCTACCAAGCCC
 AACGGGGTGATCCGCAAGTACACCATCTTCTGTTCCAGCCCCCGCCCGAGGCTCCCA
 GCGAGTACGAGACGAGTCCAGAGCAGCTCTTACCGGATCGCCACCTAAACCGCGG
 TCAGCAGTATCTGTGGGTGGCCGCGCTCACCTTCGCGGCGGGGCAACAGCAGC
 GAGAAGGTGACCATCGAGCCTGCTGGCAAGGCCCGAGCAAGATCATCTCTTTGGGG
 GCACCGTGACAACCTTGGATGAAAGATGTTGGCTGCTTGGCAATTGAGTGGGAGA
 TCCAGCCCCCTGTGTGAAGTGGACCAAGGACAGTGAAGACTCGGCCATTCAGTGTCC
 ATGGATGGGCACCGGCTCATCCACCAATGGCACACTGCTGTGCTGCGTGCAGTGAAGG
 CTGAGGACTCTGGCTACTACAGTGCACGGCCACCAACACTGGTGGCTTTGACACCAT
 CATCGTCAACCTTCTGGTGCAAGTTCCCCCGAGCAGCCCCGCTCACTGTCTCCAAA
 ACCTCAGCTTTCGTCATCACCTGACCTGGATTCCAGGTGACAAATGGGGGCGAGTCCA
 TCCGAGGTTTGTGCTACAGTACTCGGTGGACAACAGCGAGGAGTGAAGGATGTGTT
 CATCAGCTCCAGCGAGCGCTCTTCAAGCTGGACAGCCTCAAGTGTGGACGTTGGTAC
 AAGGTGAAGCTGCGAGCCAAGAACAGCGTGGGCTTGGGGCATCAGCGAGATCATCG
 AGGCCAAGACCCAGGGCGGGAGCCCTCTTTCAGCAAGACCAACACCTCTTACCCCA
 CATCAACTCCACGATGCTCGGCTTAACCTGCAGGGCTGGAACAATGGGGGCTGCCCT
 ATCAGGCCATCGTTCTGGAGTACCGGCCCAAGGGGACCTGGGCTGGCAGGGCCTCC
 GGGCCACAGCTCCGGGGAGGTGTTTCTGACGGAACTGCGAGGGCCAGCTGGTACGA
 GCTGCGCATGAGGGCTTGCAACAGTGGGGCTGCGGCAATGAACAGCCAGTTCCGCC
 ACCCTGGACTACGATGGCAGTACCATTCCACCCATCAAGTCTGCTCAAGGTGAAGGGG
 ATGATGTGAAGAAGCTGTTACCATCGGCTGCCCTGTCTCTTGGCCACACTGGGGGT
 GGCAGTCTTCTCATCGTACGCAAGAAGAGGAAGGAGAAGCGCTGAAGCGACTCCGA
 GATGCAAGAGTTTGGCAGAAATGTTGATAAGCAAGAACAATAGAAGCTTTGACACCC
 CTGTGAAAGGGGCCACCCAGGGCCACGGCTACACATTGACATCCCCAGGGTCCAGCT
 GCTCATCGAGGACAAAGAAGGCATCAAGCAACTGGGTGAGGACAAAGGCCACCATCCCT
 GTGACAGATGCTGAGTTGAGCCAAAGCTGTCAACCCACAGAGCTTCTGTACTGGCGTCT
 CCTTGACACCAACCAACCTCATCCAGAGCACAGGACCCCTCATCGACATGTCTGACAT
 CCGGCCAGGAACCGATCCAGTGTCCAGGAAGAATGTGAAGTCAGCCACAGCACCCGG
 AACCGGTACTCAAGCCAGTGGACCTGACCAAGTGCCAGGCTCCACACCTGCCCGCA
 CCTCACCTCCGACTGGCGCACCGTGGGCTCCAGCATGGTGTACGGTCACTGAGAG

	TGACAGCTACAGTGCCAGCCTGTCCCAGGACACAGACAAAGGAAGGAACAGCATGGTG TCCACTGAGAGTGCCCTCTTCCACCTACGAGGAGCTGGCCCGGCCCTATGAGCATGCCA AGCTGGAGGAGCAGCTGCAGCAGCCAAAGTTTGAGATCACCGAGTGCTTCTCTCTGA CAGTTTCTCTGACCAGATGACCACAGGCACCAACGAGAACGCCGACAGCATGACATCC ATGAGCACACCCCTCAGAGCCTGGCATCTGCCGCTTTACCGCCTCACCACCCAAAGCCCC AGGATGCGGACCGGCTGCTGATGCTGGTCCCAGGTGCCACCTCCCTCCTCAGTCCAT CCATGTTGTAGCATATGTCAGAATTTCTTCTTACTGAACAAGGGTGGGGGAGACCTG GCTTCTGATCTTAGCTCCGGCAGAGCTTGCACTGAGCCGAGATCACCGGCCACCCGGC CACCACACTGGTGGCTTTGACACCATCATCGTCAACCTGTGAGGCAGGTGACCCAG GTGGGGACAGGGATGGAGAAAGGGTAGGGATTCCATCATGCGAGAGGGTCATCGAATG GAAGAAGCCAAACCAAGGGAGAGACAGACCTCTGGAGAAACAGAGGTGCACATGGAAG GGGAGGCAGGAGAGCTGGGGAGTGGGAGTGGGAGTGGGGTGTGGGAGAGCCAGCACC TTCCCGTCACGGGGGGACTCCCCACCCCATCACAGGGTCCGCGCTTGTGCTAAGGG GTGGTGGCTTTCCCTCACAGTTCCCCCGACCGCCCGCCTCACTGCTCTCAAAC CTCAGCTTCGTCCATCACCTGACCTGGATTCCAGGTGACAAATGGGGGAGCTCCATC CGAGGTGAGGAGGGTCTGGATGCGGGGGAAGATAGGGGAAGGAATCTGGGCCCGGG GCAGGGAAGGGGCTTCA		
	ORF Start: ATG at 129		ORF Stop: TAA at 5853
	SEQ ID NO: 266	1908 aa	MW at 208575.3kD
NOV92b, CG59754-01 Protein Sequence	MPIRITWRKDGQVVISGSGVTIESKEFMSSLQISSVSLKHNGNYTCIASNAAATVSIV SPEHRFFITYHGGLYISDVQKEDALSTYRCITKHKYSGETRQSGNARLSVTDPAESIP TILDGFHSQEVWAGHTVELPCTASGYPIPAIRWLKDGRLPADSRWTKRITGLTISDL RTEDSGTYICEVTNTFGSAEATGILMVIDPLHVTLPKKLKTIGISTVILSCALTGSP EFTIRWYRNTLVLPEAISISIRGLSNETLLITSAQKSHSGAYQCFATRKAQTAQDFAI IALEDGTPRIVSSFSEKVVNPGEQFSLMCAAKGAPPPTVTWALDDEPIVRDGSHTNQ YTMSDGTITSHMNVGTGPQIRDGGVYRCTARNLVGSAEYQARINVRGPPSIRAMRNITA VAGRDTLINCVRIGYPYYSIKWKDALLLPDNRHQVVFENGTLKLTDVQKGMDEGEYL CSVLIQPLSISQSVHVAVKVPPLIQPFEPFPASIGQLLYIPCVSSGDMPIRITWRK DGQVVISGSGVTIESKEFMSSLQISSVSLKHNGNYTCIASNAAATVSRRQLIVRVPP RFVVQPNNDGIYKAGVLNCSVDGYPPPKVMWKHAKGSGNPQQYHPVPLTGRIQILP NSSLLIRHVEEDIGYYLCQASNGVGTDISKSMFLTVKIPTILDGFHSQEVWAGHTVE LPCTASGYPIPAIRWLKDGRLPADSRWTKRITGLTISDLRTEDSGTYICEVTNTFGE ATGILMVIGEPPDPPELEIREVKARSMNLRWTQRFDGNSIITGFDIEYKNKSDSWDF KQSTRNISPTINQANIVDLHPASVYSIRMYSFNKIGRSEPSKELTISTEASAPDGP MDVTLQPVTSQSIQVTWKQAPKKELOQNGVIRGYQIGYRENSPGSNGQYSIVEMKATG SEVYTLNKKFAQYGVVVQAFNRAGTGPPSSSEINATTLLEDVPSQPPENVRLSITSD VAVISWSEPPRSTLNGVLKGYRVI FWSLYVDGEWGMQNTITRERVELRGMKEFTNY SVQVLAYTQAGDGVRSVLYIQTKEDVPGPPAGIKAVPSSASSVVVSWLPPTKPNQVI RKYTIFCSPAPQAPSEYETSPEQLFYRIAHLNRGQYLLWVAAVTSAGRGNSSSEKVT IEPAGKAPAKIISFGGTVTPWMDVRLPCNSVGDPAVAVKWKDSEDSAPVSMGDH RLIHTNGTLLLRVKAEDSGYTTCTATNTGGFDITIVNLLVQVPPDQPRLTVSKTSAS SITLTWIPGDNNGSSIRGFLVQYSVDNSEEWKDFVFISSERSFKLDSLKCGTWYKVL AAKNSVSGRISIEIAKTHGREPSFSKDQHLFTHINSTHARLNLQGWNNGGCPITAI VLEYRPGKTWAWQGLRANSSGEVFLTELREATWYELMRACNSAGCGNETAQFATLDY DGSTIPPIKSAQGEEDVKKLFTIGCPVILATLGVALLFIVRKKRKEKRLKRLRDAKS LAEMLISKNNRSDFTPVKPPQGPRLHIDI PRVQLLIEDKEGIKQLGEDKATIPVTD EFSQAVNPQSFCSTGSLHPTLIQSTGPLIDMSDIRPGTDPVSRKNVKSASHTNRNYS SQWTLTKQCASTPARTLTSWRTVGSQHGVTVTESDSYASLSQDTPDKGRNSMVSTES ASSTYEEELARAYEHAKLEEQLQHAKEITECFISDSSSDQMTGTNENADSMTSMSTP SEPGICRFTASPPKQDADRLMLVPGAHLPPQSIHVVAIVRISFLNKGKGGDLASDL SSGRACSEPRSRGTRPPTLVALTPSSSTCEAGDPRWGQWRKGRDSIMREGHRMEEAK PRERQTSGETEVHMEGAGELGSGSGSEGVGEPAAPSRHGGTPHTPSQGPPLC		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 92B.

Table 92B. Comparison of NOV92a against NOV92b.		
Protein Sequence	NOV92a Residues/ Match Residues	Identities/ Similarities for the Matched Region

NOV92b	1..1771	1663/1773 (93%)
	1..1760	1681/1773 (94%)

Further analysis of the NOV92a protein yielded the following properties shown in Table 92C.

Table 92C. Protein Sequence Properties NOV92a	
PSort analysis:	0.7000 probability located in plasma membrane; 0.3000 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.2000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV92a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 92D.

Table 92D. Geneseq Results for NOV92a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV92a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU28091	Novel human secretory protein, Seq ID No 260 - Homo sapiens, 1744 aa. [WO200166689-A2, 13-SEP-2001]	200..1943 1..1744	1744/1744 (100%) 1744/1744 (100%)	0.0
AAM78713	Human protein SEQ ID NO 1375 - Homo sapiens, 1744 aa. [WO200157190-A2, 09-AUG-2001]	200..1943 1..1744	1744/1744 (100%) 1744/1744 (100%)	0.0
AAM39040	Human polypeptide SEQ ID NO 2185 - Homo sapiens, 1744 aa. [WO200153312-A1, 26-JUL-2001]	200..1943 1..1744	1744/1744 (100%) 1744/1744 (100%)	0.0
AAW42086	Human Down syndrome-cell adhesion molecule DS-CAM1 - Homo sapiens, 1910 aa. [WO9817795-A1, 30-APR-1998]	44..1778 154..1890	1085/1745 (62%) 1357/1745 (77%)	0.0
AAW42087	Human Down syndrome-cell adhesion molecule DS-CAM2 - Homo sapiens, 1571 aa. [WO9817795-A1, 30-APR-1998]	44..1457 154..1564	890/1416 (62%) 1109/1416 (77%)	0.0

In a BLAST search of public sequence databases, the NOV92a protein was found to have homology to the proteins shown in the BLASTP data in Table 92E.

Table 92E. Public BLASTP Results for NOV92a				
Protein Accession Number	Protein/Organism/Length	NOV92a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL57166	DOWN SYNDROME CELL ADHESION MOLECULE DSCAML1 - Homo sapiens (Human), 2053 aa.	44..1943 155..2053	1889/1900 (99%) 1892/1900 (99%)	0.0
Q9ULT7	KIAA1132 PROTEIN - Homo sapiens (Human), 1822 aa (fragment).	122..1943 1..1822	1822/1822 (100%) 1822/1822 (100%)	0.0
O60469	Down syndrome cell adhesion molecule precursor (CHD2) - Homo sapiens (Human), 2012 aa.	44..1943 154..2012	1123/1920 (58%) 1410/1920 (72%)	0.0
Q9ERC8	DOWN SYNDROME CELL ADHESION MOLECULE - Mus musculus (Mouse), 2013 aa.	44..1943 154..2013	1119/1921 (58%) 1405/1921 (72%)	0.0
AAL57167	DOWN SYNDROME CELL ADHESION MOLECULE DSCAM - Rattus norvegicus (Rat), 2013 aa.	44..1943 154..2013	1119/1921 (58%) 1405/1921 (72%)	0.0

PFam analysis predicts that the NOV92a protein contains the domains shown in the Table 92F.

Table 92F. Domain Analysis of NOV92a			
Pfam Domain	NOV92a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ig: domain 1 of 10	1..48	12/49 (24%) 38/49 (78%)	2.7e-05

ig: domain 2 of 10	72..90	8/19 (42%) 14/19 (74%)	85
ig: domain 3 of 10	130..186	22/60 (37%) 46/60 (77%)	2.1e-14
ig: domain 4 of 10	219..278	16/63 (25%) 44/63 (70%)	4.9e-09
ig: domain 5 of 10	312..377	14/69 (20%) 50/69 (72%)	1.5e-07
ig: domain 6 of 10	409..467	12/61 (20%) 41/61 (67%)	4.8e-05
ig: domain 7 of 10	500..561	17/64 (27%) 49/64 (77%)	3.2e-11
ig: domain 8 of 10	594..659	19/69 (28%) 47/69 (68%)	9.4e-07
ig: domain 9 of 10	693..759	9/70 (13%) 47/70 (67%)	7.9e-06
fn3: domain 1 of 6	777..864	22/89 (25%) 65/89 (73%)	3e-16
fn3: domain 2 of 6	876..968	33/93 (35%) 68/93 (73%)	3.1e-16
fn3: domain 3 of 6	980..1069	26/93 (28%) 69/93 (74%)	2.9e-16
fn3: domain 4 of 6	1081..1167	24/88 (27%) 64/88 (73%)	3.7e-17
ig: domain 10 of 10	1194..1255	17/65 (26%) 46/65 (71%)	4.3e-09
fn3: domain 5 of 6	1274..1357	30/86 (35%) 67/86 (78%)	1.2e-18
fn3: domain 6 of 6	1371..1453	27/86 (31%) 53/86 (62%)	0.045

Example 93.

The NOV93 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 93A.

Table 93A. NOV93 Sequence Analysis		
	SEQ ID NO: 267	1272 bp
NOV93a, CG59800-01 DNA Sequence	AGAGCCTGGTATGCAGGAGGTGCTCTGTAAATACCTGCCCCATACATACCCGCCCCAT ACATACCCACCCCATACATACCCACCCCATACATACCTGCCCTGTCCATACCTGCCCC CTACATACCTGCCCCGTCCATACCTGCCCCCTACATACCTGCCCCGTCCATACCTGCC CCCTACATACCTGCTCTGTCTATACCTGTGGCTAGGACTGTGGCCTTGCTTCTTAGCC GCTCAGAGCCTGCCTCCTCCTCTGCAGAGTGGCGGTGGTAGCAGGGCTTCCCGCGCGC	

	CGATGCTGCTCGTGGCCCTGGTGTCTGGGCGCTACTGCCTCTGCGCCCTCCCGGGCCG CTGCCCGCGGCCGCGCCCGCGCCCGCGCCCGCGCCCTCCGAGCCGTCCAGC TCCGTCCACCGCCCGGAGCACCCGGCCTGCCTTTGGCCAGCGGTCCCGGCCGCGGC GCTTCCCGCAAGCGCTCATCGTTGGCGTGAAGAAGGGCGGCAGCGCGCCCTGCTGGA GTTTCTGCGGCTGCACCCGACCTCCGCGCGCTGGGCTCTGAGCCCCACTTCTTCGAC AGGTGCCCCGACCGCGCCTCGCCTGGTCCCGGAGTCTGATGCCCCGAACCTGGATG GGCAGATCACCATGGAGACGACCCCGGGCTACTTCGTGACGCGAGAGGCCCCCGCG CATCCACGCCATGTCCCGGACACGAAGCTGATCGTGGTGGTGGGAAACCCGTGACC CGGGCCATCTCCGACTAGGCCCAGACGCTCTCCAAGACCCGGGCGCTGCCAGCTTCC GCGCCCTGGCCTTCCGCCACGGCCTGGGCCCCGTGGACACAGCTGGAGCGCGTCCG CATCGGCCTGTACGCCAGCACCTGGACCACTGGCTGCGCTACTTCCCCCTGTCCAC TTCCTGTTCTGTCAGCGGGGAGCGTCTGGTCAGCGACCCGGCCGGAGAGGTGCGCCGCG TGCAAGACTTCTGGGCTGAAACGGGTCGTACGGACAAGCACTTCTACTTCAACGC CACCAAGGGCTTCCCTGCGCTCAAGAAGGCCAGGGCGGAGCGCTCCCGCTGCCTG GGCAAGTCCAAGGGCCGCCACCCACGCGTGGCCAGGCCGTGTCGGCGCGCTGC AGGAGTTCTACGGCCCTTCAACCGCAGGTTCTACCAGATGAGGGCCAGGACTTCGG CTGGGGCTGAGCGGCACCCTGGGGATGCTCAGCACCTTGATTGACACCCGCTCG		
	ORF Start: GAG at 2 ORF Stop: GGC at 1217		
	SEQ ID NO: 268	405 aa	MW at 43994.8kD
NOV93a, CG59800-01 Protein Sequence	MQEVLCKYLPHTYPPHTYPPHTYLPHTYLPCTYLPHTYLPHTYLPHTYLPHTYLPHTY LLCLYLWLGLWPCFLAAQSLPPPLQSGGSRASRAPMLLVALVLGAYCLCALPGRCP AARAPAPAPAPSEPSSSVHRPGAPGLPLASGPGRRRFPQALIVGVKKGGTRALLEFLR LHPDXRALGSEXHFDRCCXXGLXWXRSLMPRTLDGQITMEXTPXIFYVTREAPRIHA MSPDTKLIIVVRNPVTRAISDXQTLSTPGLPSFRALAFRHGLGPVDTAWSAVRIGL YAQHLDHWRLYFPLSHFLFVSGERLVSDPAGEVGRVQDFLGLKRVVTDKHFYFNATKG FPCLKKAQGGSRPRCLGKSKGRPHPRVPQAXVRRQLQEFYRPFNRRFYQMTGQDFGWG		

Further analysis of the NOV93a protein yielded the following properties shown in Table 93B.

Table 93B. Protein Sequence Properties NOV93a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 7 and 8

A search of the NOV93a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 93C.

Table 93C. Geneseq Results for NOV93a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV93a Residues/	Identities/ Similarities for	Expect Value

		Residues	Region	
AAB95507	Human protein sequence SEQ ID NO:18067 - Homo sapiens, 390 aa. [EP1074617-A2, 07-FEB-2001]	31..253 11..237	121/229 (52%) 146/229 (62%)	4e-55
AAY17066	Human 3-OST-3B protein - Homo sapiens, 390 aa. [WO9922005-A2, 06-MAY-1999]	31..253 11..237	121/229 (52%) 146/229 (62%)	4e-55
AAB70115	Human 3-OST-3B - Homo sapiens, 391 aa. [WO200113910-A2, 01-MAR-2001]	31..253 11..238	121/230 (52%) 146/230 (62%)	9e-54
AAB70114	Murine 3-OST-3B - Mus sp, 391 aa. [WO200113910-A2, 01-MAR-2001]	31..253 11..238	119/231 (51%) 147/231 (63%)	2e-51
AAU12275	Human PRO5004 polypeptide sequence - Homo sapiens, 367 aa. [WO200140466-A2, 07-JUN-2001]	86..253 45..214	102/170 (60%) 117/170 (68%)	9e-48

In a BLAST search of public sequence databases, the NOV93a protein was found to have homology to the proteins shown in the BLASTP data in Table 93D.

Table 93D. Public BLASTP Results for NOV93a				
Protein Accession Number	Protein/Organism/Length	NOV93a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96QI5	C439A6.1 (NOVEL PROTEIN SIMILAR TO HEPARAN SULFATE (GLUCOSAMINE) 3-O-SULFOTRANSFERASES) - Homo sapiens (Human), 381 aa (fragment).	85..253 61..229	160/169 (94%) 162/169 (95%)	2e-89
Q96RX7	HEPARAN SULPHATE D-GLUCOSAMINYL 3-O-SULFOTRANSFERASE-3B LIKE - Homo sapiens (Human), 311 aa.	95..253 1..159	153/159 (96%) 155/159 (97%)	1e-85
Q9Y662	HEPARAN SULFATE D-GLUCOSAMINYL 3-O-SULFOTRANSFERASE-3B (EC 2.8.2.23) - Homo sapiens (Human), 390 aa.	31..253 11..237	121/229 (52%) 146/229 (62%)	1e-54
Q9QZS6	D-GLYCOSAMINYL 3-O-SULFOTRANSFERASE-3B - Mus musculus (Mouse), 390 aa.	31..253 11..237	119/230 (51%) 147/230 (63%)	3e-52

Q9Y278	HEPARAN SULFATE D-GLUCOSAMINYL 3-O-SULFOTRANSFERASE-2 (EC 2.8.2.23) - Homo sapiens (Human), 367 aa.	86..253 45..214	102/170 (60%) 117/170 (68%)	3e-47
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PFam analysis predicts that the NOV93a protein contains the domains shown in the Table 93E.

Table 93E. Domain Analysis of NOV93a			
Pfam Domain	NOV93a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 94.

The NOV94 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 94A.

Table 94A. NOV94 Sequence Analysis		
	SEQ ID NO: 269	2949 bp
NOV94a, CG59761-01 DNA Sequence	GTCCGCTCCGGGCGCGGAGCCGAGCCGCGGAGATGGGGGCGGCGCGGCGCGC CCGCGCGGGTCCCGCGCGCGCTGCCGCTGAGCGCATGGGCGCGGACCGCGCGC GCCGCTCCGGGAGCCGGGCGCGGTCCCGCCACCACCGCGCGGGACAGATTGATT CACTTTGGAGCTGTAGTACTGATGTATTAGGGTGACGCGCTATTGTTTCATTGACGC AGAGTCCCAAAATGAATATCCAAGAGCAGGGTTTCCCTTGGACCTCGGAGCAAGTTT CACCGAAGATGCTCCCGACCCCGAGTGCCTGGTGAGGAGGAGAACTGGTGTCCACA GACCCGAGGCGCGGAGCTACAGTTTCTGCTCCGGGAAAGGTGTTGGCATTAAAGGTG AGACTTCGACGGCCACTCCGAGGCGCTCGGATCTGGACCTGGGGTATGAGCCTGAGGG CAGTGCCTCCCCACCCACCATCTTGAAGTGGGCTGAGTCACTGCATTCCCTGCTG GATGACCAAGATGGGATAAGCCTGTTGAGGACTTCTGAAGCAGGAGGGCTGTGCCG ACTTGCTGGACTTCTGGTTTGCCTGCACTGGCTTCAGGAAGCTGGAGCCCTGTGACTC GAACGAGGAGAAAGAGCTGAAGCTGGCGAGAGCCATCTACCGAAAGTACATTCTTGAT AACAAATGGCATCGTGTCCCGGAGACCAAGCCAGCCACCAAGAGCTTCATAAAGGGCT GCATCATGAAGCAGCTGATCGATCCTGCCATGTTGACCAAGCCAGACCGAAATCCA GGCCACTATGGAGGAAACACCTATCCCTCCTTCTTAAGTCTGATATTTATTGGAA TATACGAGGACAGGCTCGGAGAGCCCCAAAGTCTGTAGTGACCAAGCTCTGGGTGAG GGACAGGGAAGGGCATATCTGGATACCTGCCGACCTTAAATGAAGATGAGGAATGGAA GTGTGACCAGGACATGGATGAGGACGATGGCAGAGACGCTGCTCCCCCGGAAGACTC CCTCAGAAGCTGCTCCTGGAGACAGCTGCCCGAGGGTCTCCTCCAGTAGACGGTACA GCGAAGGCAGAGAGTTCAAGTATGGATCCTGGCGGGAGCCAGTCAACCCCTATTATGT CAATGCCGGCTATGCCCTGGCCCCAGCCACCAAGTGCCAAACGACAGCGAGCAGCAGAGC CTGTCCAGCGATGCAGACACCTGTCCCTCACGGACAGCAGCGTGGATGGGATCCCCC CATAAGAGATCCGTAAGCAGCACCGCAGGGAGATGCAGGAGAGCGTGCAGGTCAATGG GCGGGTGCCCTACCTCACATTCCCGCACGTACCGGGTGCCGAAGGAGGTCCCGGTG GAGCTCTCAGAAGTTTCGCGGAGGAGCTCATCCACCGCTGGAGGCTGTGCAGCGCAGC GGGAGGCCGAGGAGAAGCTGGAGGAGCGGCTGAAGCGCGTGCATGGAGGAGGAAGG TGAGGACGGCGATCCATCATCAGGGCCCCAGGGCGGTGTCAAGCTGCCTCCCGCC CCGCTTGGCACCACTTCCCGCCCGCTGTGTGGACATGGGCTTGTGCCGGGCTCC GGGATGCACACGAGGAGAACCTGAGAGCATCCTGGACGAGCAGTACAGCTGTGCT GAGGACACCTGGCCGCGAGTCCGCTGGGCTGGCCATCGCTCCCCGGACAGTGGGCAC GTGGCCAAGATGCCAGTGGCACTGGGGGGTGGCGCTCGGGGCACGGGAAGCACGTAC CCAAGTCAGGGCGAAGCTGGACGCGGCGGCTGCACCAACACCGACAGCTCCACCA CCACGTCCACCACAGCACAGCCCCGGCCCAAGGAGCAGGTGGAGGCCGAGGCCACCCGC AGGGCCAGAGCAGCTTCGCTGGGGCTGGAACCAACACAGCATGGGGCAAGGTCCC GAGGCTACTCAGAGAGTGTGGCGCTGCCCCCAACGCCAGTGTGGCTCGCCACAG TGGGAAGTGGCGGTGGCGTGCAAAAGAAATGCCAAGAAGGCCGAGTCTGGGGGAAGAGC GCCAGCACCGAGGTGCCAGTGCCTCGAGGATGCGGAGAAGAACCAGAAAATCATGC	

	AGTGGATCATTGAGGGGAAAAGGAGATCAGCAGGCACCGCAGGACCGGCCACGGGTC TTCCGGGACGAGGAAGCCACAGCCCCATGAGAACTCCAGACCGTTGTCCCTTGAGCAC CCCTGGGCGGGCCCTCAGCTCCGGACCTCCGTGCAGCCCTCCACCTCTTCATCCAAG ACCCACCATGCCACCCACCCAGCTCCCAACCCCTAACCCAGCTGGAGGAGGCGCG CCGACGTCTGGAGGAGGAAGAAAAGAGAGCCAGCCGAGCACCTCCAAGCAGAGGTAT GTGCAGGAGGTTATGCGGCGGGGACGCGCTGCGTCAGGCCAGCGTGCCTGCGGCGGTGC TGCACGTGGTACCAGCCGTGTGCGACATGGAGCTCTCCGAGACAGAGACAAGATCGCA GAGGAAGGTGGGCGGCGGAGTGCCAGCCGTGTGACAGCATCGTTGTGGCGTACTAC TTCTGCGGGGAACCCATCCCTACCGCACCCCTGGTGAGGGGCGCGCTGTCAACCCTGG GCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTTCAAGAAAGT GAGCGACGAGTTTACTGTGGGGTGGTGTGAGGAGGTTGAGAGGACGAGGCCGTC CTGCCCGTCTTTGAGGAGAAGATCATCGGCAAAGTGGAGAAGTGGACTGATAGGCTG GTGGGCTGGCCGCTGTGCCAGGCGAGGCCCTTGGCGGGCAGGGGTGTACGCCCCAGGC AGATGACCTCGTACTCAGGAGCCCGATGGGGAACAGTGTGGGTGTACC		
	ORF Start: ATG at 97	ORF Stop: TGA at 2833	
	SEQ ID NO: 270	912 aa	MW at 101118.1kD
NOV94a, CG59761-01 Protein Sequence	MGPDRAAPLREPGPSRHHRRARDRLIHFGAVSTDVLGCSAHCSLTQSPKMNIEQGF LDLGASFTEDAPRPVPGEELVSTDPRPASYSFCSGKGVGKGETSTATPRSDLD LGYEPEGSASPTPYLKWAESLHSLDDQDGLSLFRTFLKQEGCADLLDFWFACTGFR KLEPCDSNEEKRLKLARAIYRKYIILDNNGIVSRQTKPATKSFIKGCKIMQLIDPAMFD QAQTEIQATMEENTYPSFLKSDIYLEYTRTGSESPKVCSDQSSSGTGKIGYLPTL NEDEEWKCDQDMDDEDGRDAAPGRLPQKLLLETAAPRVSSRRYSEGREFRYGSWRE PVNPYYVNAGYALAPATSANDSEQQSLSSDADTSLSDSSVDGIPPYRIRKQHRREM ESVQVNGRVPLPHIPRTYRVPEVRVEPQKFAEELIHRLEAVQRTREAEKLEERLKR VRMEEGEDGDPSSGPPGCHKLPPAPAWHHFPPRLCWTWACAGLRDAHENPESILD EHVQRVLRTPGRQSPGPHRSPDSGHVAKMPVALGGAASGHGKHVPKSGAKLDAAGLH HHRVHHVHHSTARPEQVEAEATRRRAQSSFAWGLEPHSHGARSRGYSESVAAPNA SDGLAHSGKVGVACKRNAKKAESGKSASTEVPGASEDAEKNQKIMQWIIIEGEKISR RRTGHGSSGTRKPQPHENSRLSLEHPWAGPQLRTSVQPSHLFIQDPTMPHPAPNPL TQLEEARRRLEEEKRASTRAPSKQRYVQEVMMRGRACVRPACAPVLHVPAVSDMELS ETETRSQRKVGGGSAQPCDSIVVAYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKGSY RYYFKVSDEFDCGVVFEEVREDAVLPVFEEKIIGKVEKVD		

Further analysis of the NOV94a protein yielded the following properties shown in Table 94B.

Table 94B. Protein Sequence Properties NOV94a	
PSort analysis:	0.6000 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV94a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 94C.

Table 94C. Geneseq Results for NOV94a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV94a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value

AAG68175	Wnt signaling protein SEQ ID NO:91 - Homo sapiens, 900 aa. [WO200177327-A1, 18-OCT-2001]	13..912 1..900	898/900 (99%) 898/900 (99%)	0.0
AAW96264	Human axin - Homo sapiens, 900 aa. [WO9902179-A1, 21-JAN-1999]	13..912 1..900	898/900 (99%) 898/900 (99%)	0.0
AAW96265	Murine axin - Mus musculus, 992 aa. [WO9902179-A1, 21-JAN-1999]	6..912 84..992	781/914 (85%) 820/914 (89%)	0.0
AAW93569	Human conductin protein - Homo sapiens, 840 aa. [WO9911780-A2, 11-MAR-1999]	60..912 12..840	378/892 (42%) 506/892 (56%)	e-171
AAW93570	Human conductin protein - Homo sapiens, 840 aa. [WO9911780-A2, 11-MAR-1999]	60..912 12..840	378/892 (42%) 506/892 (56%)	e-171

In a BLAST search of public sequence databases, the NOV94a protein was found to have homology to the proteins shown in the BLASTP data in Table 94D.

Table 94D. Public BLASTP Results for NOV94a				
Protein Accession Number	Protein/Organism/Length	NOV94a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O15169	Axin 1 (Axis inhibition protein 1) (hAxin) - Homo sapiens (Human), 900 aa (fragment).	13..912 1..900	898/900 (99%) 898/900 (99%)	0.0
Q96S28	AXIN - Homo sapiens (Human), 862 aa.	50..912 1..862	858/863 (99%) 858/863 (99%)	0.0
O35625	Axin 1 (Axis inhibition protein 1) (Fused protein) - Mus musculus (Mouse), 992 aa (fragment).	6..912 84..992	781/914 (85%) 820/914 (89%)	0.0
O70239	Axin 1 protein (Axis inhibition protein 1) (rAxin) - Rattus norvegicus (Rat), 893 aa (fragment).	6..912 21..893	756/914 (82%) 793/914 (86%)	0.0
T08422	negative regulator axin [imported] - rat, 832 aa.	46..912 2..832	726/872 (83%) 760/872 (86%)	0.0

PFam analysis predicts that the NOV94a protein contains the domains shown in the Table 94E.

Table 94E. Domain Analysis of NOV94a			
Pfam Domain	NOV94a Match Region		Expect Value

		Similarities for the Matched Region	
RGS: domain 1 of 2	137..198	23/75 (31%) 44/75 (59%)	5.6e-06
RGS: domain 2 of 2	231..260	13/30 (43%) 21/30 (70%)	0.12
TP2: domain 1 of 1	585..709	33/147 (22%) 52/147 (35%)	9.6
DIX: domain 1 of 1	830..912	40/86 (47%) 83/86 (97%)	5.6e-44

Example 95.

The NOV95 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 95A.

Table 95A. NOV95 Sequence Analysis			
	SEQ ID NO: 271	2223 bp	
NOV95a, CG59756-01 DNA Sequence	TTGCAGGCATCACCCACGCCCTCTGCACCCACGCTGGAGGACGGGGAGGTTGTTCAGGG GCTATGATGAGATGAGTGGGGGCGCTTCGACTTTGATGATGGAGGGGCGTACTGCGG GGGCTGGGAGGGGGGAAAGGCCCATGGGCATGGACTGTGCACAGGCCCCAAGGGCCAG GGCGAATACTCTGGCTCCTGGAACCTTTGGCTTTGAGGTGGCAGGTGTCTACACCTGGC CCAGCGGAAACACCTTTGAGGGATACTGGAGCCAGGGCAAACGGCATGGGCTGGGCAT AGAGACCAAGGGGCGCTGGCTCTACAAGGGCGAGTGGACACATGGCTTCAAGGGACGC TACGGAATCCGGCAGAGCTCAAGCAGCGGTGCCAAGTATGAGGGCACCTGGAACAATG GCCTGCAAGACGGCTATGGCACCGAGACCTATGCTGATGGAGGGACGTACCAAGGCCA GTTCAACACGGCATGCGCCATGGCTACGGAGTACGCCAGAGCGTGCCTACGGGATG GCCGTGGTGGTGGCTCGCCGCTGCGCACGTCGCTGTCTGCTCCCTGCGCAGCGAGCACA GCAACGGCACGGTGGCCCCGGACTCTCCCGCCTCGCCGGCCTCCGACGGCCCCGGCT GCCCTCGCCCGCATCCCGCGTGGCGGCTTCGCGCTCAGCCTCCTTGGCCAATGCCGAG GCGGCGCGCGGGCGCCCAAGGGCGGCGGCTCTTCCAGCGGGGCGCGCTGCTGGGCA AGCTGCGGCGCGCAGAGTCGCGCACGTCCGTGGGTAGCCAGCGCAGCGTGTCTCAGCTT CCTTAAGAGCGACCTCAGCTCGGGCGCCAGCGACGCGCGTCCACCGCGCTGGGA GAGGCGCGCGAGGGCGCGACGAGGGCCGACCTTCGAGGCCGATATCGACGCCACCA CCACCGAGACCTACATGGGCGAGTGAAGAAGCACAAACGCTCGGGCTTCGGCGTGAG CGAACGCTCCAGTGGCTCCGCTACGAGGGCGAGTGGCTGGACAACCTGCGCCACGGC TATGGCTGCACCACGCTGCCCGACGGCCACCGCGAGGAGGGCAAGTACCGCCACAACG TGCTGGTCAAGGACACCAAGCGCCGATGCTGCAGCTCAAGAGCAACAAGGTCCGCCA GAAAGTGGAGCAGTGTGGAGGGTGCCACGCGCGCGCTGCTATCGCGCGCCAGAAG GCCGAGATTGCCGCTCCAGGACAAGCCAGCCAAAGGCTGAGGCAGCGGAAC AGGCCGCGCTGGCTGCCAACAGGAGTCCAACATTGCTCGCACTTTGGCCAGGGAGCT GGCTCCCGACTTCTACAGCCAGGTCCGGAATATCAGAAGCGCGGCTGCTGCAGGAG ATCCTGGAGAACTCGGAGAGCTGCTGGAGCCCCCGACCGGGGCGCGCGCAGCGG GCCTCCCAAGCGCGCCCGGAGAGCCCGAGCTGCACAGCGGTGAGACCGCTCGGCC CGAGGGTGGCTCCCCGTACCGGCGGGACGCCCCGAGCCCAAGCGGCCAGGGCCC GGGTGTCCAAGGACGGCTGCTGAGCCAGGCGCTTGAACGGCGAGCCAGCGGTG AGGGCAGCGGTCACTCACTCCGTCCGAGGGCGGGGCGCGCAGCCCGCGCGCTCC AGCCACCGAGCGCATGGCCATCGAGGCTCTGCAGGCACCGCTCGCGCGTCCGGGAG CCGAGGTGGCGCTTACCAGGGCTACCAAGCTATGCTGTGTCGCGACCAACCGCCG AGCCCCACCTTTGAGGACCAAGCCGAGCCCGAGGTCTCCGGGTCCGAGTCCGCGCC CTCGTCCCGGGCACCGCCCCGCTGCAGGCCCCACGCTCCGAGGCCCGAGCGCTGCA CGCGAGACCCCCGCAAGCTGGAGCCCAAGCCCATCATCCCCAAGCCGAGCCAGGG CCAAGGCCGCAAGACTGAGGCTCGAGGGCTGACCAAGGCGGGGCCAAGAAGAAGGC GCGGAAGGAGGCGCACTGGCGGCAGAGGCGGAGGTGGAGGTGGAAGAGGTCCCCAAC ACCATCCTCATCTGCAATGGTGATCCTGCTGAACATCGGCCTGGCCATCTCTTTGTTC ACCTCCTGACCTGACCGTCGTTACCAGGTGCAGCCAGCTGGCTGGAGGAGGGGTGG GGGCGAGGAGCCCTGGGG		
	ORF Start: ATG at 70	ORF Stop: TGA at 2158	
	SEQ ID NO: 272	696 aa	MW at 74220.7kD

NOV95a, CG59756-01 Protein Sequence	MSGGRFDFFDDGGAYCGGWEGGKAHGHGLCTGPKQGQGEYSGSWNFGFEVAGVYTWPSSGN TFEGYWSQGRHGLGIETKGRWLYKGEWTHGFKGRYGIQSSSSGAKYEGTWNGLQD GYGTETYADGGTYQGQFTNGMRHGYGVRQSVPYGMVVVRSPLRTSLSSLRSEHSNGT VAPDSPASPASDGPALPSAIPRGGFALSLANAEAAARAPKGGGLFORGALLGKLRR AESRTSVGSQRSRVSLKSDLSSGASDAASTASLGEAAEGADEAAPFEADIDATTET YMGWKNDRSGFGVSRSSGLRYEGEWLDNLRHGYGCTTLPDGHREEGKYRHNVLVK DTKRRLQLKSNKVRQKVEHSVEGAQRAAAIARQKAEIAASRTSHAKAKAEAAEQAL AANQESNIARTLARELAPDFYQPGPEYQKRRLQEI LENSESLEPPDRGAGAAGLPQ PPRESPQLHERETPRPEGGSPSPAGTTPQPKRPRPGVSKDGLLSPGAWNGEPSGEGSR SVTPSEGAGRRSPARPATERMAIEALQAPPAPSREPEVALYQGYHSYAVRTTPPEPPP FEDQPEPEVSGSESAPSPATAPLQAPTLCRGPEPARETPAKLEPKPIIPKAEPRAKAR KTEARGLTKAGAKKARKEAALAAEAEEVEVEVPNTILICMVI LLNIGLAILFVHLIT
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Further analysis of the NOV95a protein yielded the following properties shown in Table 95B.

Table 95B. Protein Sequence Properties NOV95a	
PSort analysis:	0.8000 probability located in nucleus; 0.7000 probability located in plasma membrane; 0.3133 probability located in microbody (peroxisome); 0.2000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV95a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 95C.

Table 95C. Geneseq Results for NOV95a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV95a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79123	Human protein SEQ ID NO 1785 - Homo sapiens, 628 aa. [WO200157190-A2, 09-AUG-2001]	3..696 4..628	293/704 (41%) 377/704 (52%)	e-127
AAM80107	Human protein SEQ ID NO 3753 - Homo sapiens, 378 aa. [WO200157190-A2, 09-AUG-2001]	283..696 24..378	146/421 (34%) 194/421 (45%)	2e-43
ABB21683	Protein #3682 encoded by probe for measuring heart cell gene expression - Homo sapiens, 135 aa. [WO200157274-A2, 09-AUG-2001]	257..389 6..135	78/133 (58%) 104/133 (77%)	7e-42
AAM57089	Human brain expressed single exon probe encoded protein SEQ ID NO: 29194 - Homo sapiens, 135 aa. [WO200157275-A2, 09-AUG-2001]	257..389 6..135	78/133 (58%) 104/133 (77%)	7e-42

AAM17323	Peptide #3757 encoded by probe for measuring cervical gene expression - Homo sapiens, 135 aa. [WO200157278-A2, 09-AUG-2001]	257..389 6..135	78/133 (58%) 104/133 (77%)	7e-42
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In a BLAST search of public sequence databases, the NOV95a protein was found to have homology to the proteins shown in the BLASTP data in Table 95D.

Table 95D. Public BLASTP Results for NOV95a				
Protein Accession Number	Protein/Organism/Length	NOV95a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9GKY7	JUNCTOPHILIN TYPE 2 - Oryctolagus cuniculus (Rabbit), 694 aa.	1..696 1..694	644/701 (91%) 662/701 (93%)	0.0
Q9ET79	JUNCTOPHILIN TYPE 2 - Mus musculus (Mouse), 696 aa.	1..696 1..696	608/706 (86%) 644/706 (91%)	0.0
Q9BR39	DJ1108D11.1 (NOVEL PROTEIN SIMILAR TO C. ELEGANS T22C1.7) - Homo sapiens (Human), 552 aa (fragment).	128..672 1..545	544/545 (99%) 544/545 (99%)	0.0
Q9GKY8	MITSUGUMIN72/JUNCTOPHILIN TYPE1 - Oryctolagus cuniculus (Rabbit), 662 aa.	1..696 1..662	364/704 (51%) 468/704 (65%)	0.0
Q9ET80	JUNCTOPHILIN TYPE 1 - Mus musculus (Mouse), 660 aa.	1..696 1..660	371/707 (52%) 469/707 (65%)	0.0

PFam analysis predicts that the NOV95a protein contains the domains shown in the Table 95E.

Table 95E. Domain Analysis of NOV95a			
Pfam Domain	NOV95a Match Region	Identities/ Similarities for the Matched Region	Expect Value
MORN: domain 1 of 7	14..36	10/23 (43%) 13/23 (57%)	1.1
MORN: domain 2 of 7	38..59	9/23 (39%) 15/23 (65%)	0.31
MORN: domain 3 of 7	60..77	8/23 (35%) 15/23 (65%)	3
MORN: domain 4 of 7	106..128	11/23 (48%) 20/23 (87%)	3.7e-06
MORN: domain 5 of 7	129..151	8/23 (35%) 15/23 (65%)	0.027
MORN: domain 6 of 7	291..313	12/23 (52%) 19/23 (83%)	0.00056
MORN: domain 7 of 7	314..336	11/23 (48%) 19/23 (83%)	0.00022

Example 96.

The NOV96 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 96A.

Table 96A. NOV96 Sequence Analysis		
	SEQ ID NO: 273	3257 bp
NOV96a, CG59708-01 DNA Sequence	CGTAGGCGCTTCGGCCATGACTGCGGAGCTGCAGCAGGACGACGCGGCCGCGCGGCA GACGGCCACGGCTCGAGCTGCCAAATGCTGTTAAATCAACTGAGAGAAATCACAGGCA TTCAGGACCCTTCCTTTCTCCATGAAGCTCTGAAGGCCAGTAATGGTGACATTACTCA GGCAGTCAGCCTTCTCACTGATGAGAGAGTTAAGGAGCCAGTCAAGACACTGTTGCT ACAGAACCATCTGAAGTAGAGGGGAGTGCTGCCAACAAGGAAGTATTAGCAAAAGTTA TAGACCTTACTCATGATAACAAAGATGATCTTCAGGCTGCCATTGCTTTGAGTCTACT GGAGTCTCCCAAATTCAAGCTGATGGAAGAGATCTTAACAGGATGCATGAAGCAACC TCTGCAGAACTAAACGCTCAAAGAGAAAACGCTGTGAAGTCTGGGGAGAAAACCCCA ATCCCAATGACTGGAGGAGAGTTGATGGTTGGCCAGTTGGGCTGAAAATGTTGGCAA TACATGTTGGTTTGTGCTGTTATTTCAGTCTCTCTTTCAATTGCCTGAATTTCAAGA CTTGTCTCAGTTATAGTCTGCCAATAATGTACTTGAAAATGTGCGAAGTCATACAG AAAAGAGAAATATCATGTTTATGCAAGAGCTTCAGTATTTGTTGCTCTAATGATGGG ATCAAAATAGAAAATTTGTAGACCCGCTCTGCAGCCCTGGATCTATTAAAGGGAGCATTC CGATCATCTGAGGAACAGCAGCAAGATGTGAGTGAATTCACACACAAGCTCCTGGATT GGCTAGAGGACGCATTCCAGCTAGCTGTTAATGTTAACAGTCCAGGAACAATCTGA AAATCCAATGGTGCAGCTGTTCTATGGTACTTTCTGACTGAAGGGGTTCTGTGAAGGA AAACCCCTTTGTAACAATGAGACCTTCGGCCAGTATCCTCTTCAGGTAACCGGTTATC GCAACTTAGACGAGTGTGGAAGGGGCCATGGTGGAGGTGATGTTGAGCTTCTTCC CTCCGATCACTCGGTGAAGTATGGACAAGAGCGTTGGTTTACAAAGCTACCTCCAGTG TTGACCTTTGAACTCTCAAGATTTGAGTTTAATCAGTCCCTTGGGCGAGCCAGAGAAAA TTCACAATAAGCTGGAATTTCTCAGATTATTTATATGGACAGGTACATGTACAGGAG CAAGGAGCTTATTTCGAAATAAGAGAGAGTGTATTGAAAAGTTGAAGAGGAAATAAAA ATTCTGCAGCAAAAATTGGAAGGTATGTGAAATATGGCTCAGGCCAGCTCGGTTCC CGCTCCCGGACATGCTGAAATATGTTATTGAATTTGCTAGTACAAAACCTGCCTCAGA AAGCTGTCCACCTGAAAGTGACACACATATGACATTACCACTTTCTTCAGTGCACTGC TCGGTTTCTGACCAGACATCCAAGGAAAGTACAAGTACAGAAGCTCTTCTCAGGATG TTGAAAGTACCTTTTCTTCTCCTGAAGATTCTTTACCAAGTCTAAACCACTGACATC	

	<p>TTCTCGGTCTTCCATGGAAATGCCTTCACAGCCAGCTCCACGAACAGTCACAGATGAG GAGATAAAATTTGTGAAGACCTGTCTCAGAGATGGAGGAGTGAAGATGAACAGATA TACAAGATTTAAAGACTTGTATTGCAAGTACTACTCAGACTATTGAACAGATGTACTG CGATCCTCTCCTTCGTGAGGTGCCTTATCGCTTGCATGCAGTTCTTGTTCATGAAGGA CAAGCAAATGCTGGACACTATTGGGCCTATATCTATAATCAACCCCGACAGAGCTGGC TCAAGTACAATGACATCTCTGTACTGAATCTTCTGGGAAGAGTGAAGAGATTCT CTATGGAGGCTGAGAAATGTTAGTGCTTACTGTCTGATGTACATTAATGCCAACTA CCCTACTTCAATGCAGAGGCGAGCCCAACTGAATCAGATCAAAATGTCAGAAGTGAAG CCCTATCTGTGGAATCAAGCATTACATTAGGAGGATAACTGGCGGTTTGAGCAGGA AGTAGAGGAGTGGGAAGAAGAGCAGTCTTGCAAAATCCCTCAAAATGGAGTCTCCCCC AACTCCTCATCAGGGCTACTCTACATCACAAGAGCCTTCAGTAGCCTCTTCTCATG GGGTTGCTGCTGTCTGATCTGAGCATGCTGTGATTGTAAGGAGCAAACTGCCAGGC TATTGCAACACAGCCGCTGCTATGAGAAGAGCGGTGTAGAAGCGGCATGAGTGAG GCATTCCATGAAGAATACTCCAGGCTCTATCAGCTTGCCAAAGAGACCCCACTCTC ACAGTGATCCTCGACTTCAGCATGTCTTGTCTACTTTTCCAAATGAAGCACCCAA AAGGGTAGTAGAACCAACCTTCTGGAACAGTTTGCAGATAAAATCTTAGCTATGAT GAAAGATCAATCAGCATTATGAAGGTGGCTCAAGCGAACTGAAGAAATTTGTCAG ATGACATGAATATGGAAGAGTACAAGAGGTGGCATGAAGATTATAGTTTGTCCGAAA AGTGTCTGTGATCTCTAACAGGCTAGAACTCTATCAAAAAGGAAAGTACCAAGAG GCACTTCTCTACCTGGTATATGCCTACCAGAGCAATGCTGCCCTGCTGATGAAGGGGC CCCGCCGGGGGTCAAAGAATCCGTGATTGCTTTATACCGAAGAAATGCTTCTGGA GCTGAATGCCAAGCAGCTTCTCTTTTGAACAAATGATGATCACTCCGTAACCTGAG GGCATTAAATGTGATGAATGAATGATCATCCCCTGCATTACCTTATCATTAAATG ACATTTCAAGGATGATCTGGATGCCATTGAGGTGATGAGAAACCATTTGGTGCTCTTA CCTTGGGCAAGATATTGCAGAAAATCTGCAGCTGTGCTAGGGGAGTTTCTACCCAGA CTTCTAGATCCTTCTGCAGAAATCATCGTCTTGAAGAGCCTCCAATATTGACCCA ATTCTCCCTATGACCTATGTAGCCGATTTCAGAGCTGTATGGAGTCAATTACAGGAGT TTCAACTGTGACAGTGAATAAGCTCCACATGTTCAAGGCCATTCTGGTTCTGGC TGCCTGCTCTTGACAGAAAGTTCTGTTGTCATAGTGCTCACCTTGGGAAAAGGATTAG GTGGGCACA</p>
	<p>ORF Start: ATG at 17 ORF Stop: TAA at 3152</p>
	<p>SEQ ID NO: 274 1045 aa MW at 119041.7kD</p>
<p>NOV96a, CG59708-01 Protein Sequence</p>	<p>MTAELQQDDAAGAADGHSSQMLLNQLEITGIQDPSFLHEALKASNGDITQAVSLL TDERVKEPSQDVTATEPSEVEGSAANKEVLAKVIDLTHDNKDDLQAAIALSLLESPI QADGRDLNRMHEATSATKRSKRKRCEVWGENPNPNDRWDGWPVLKNGVNTGWS AVIQSLFQLPEFRRLVLSYSLPQNVLENCRSHTEKRNIMFMQELQYLFALMMSNRKF VDPAAALDLLKGAFRSSEEQQDVSEFTHKLDDLEDAFLAVNVNSPRNKSENPMVQ LFYGTFLTEGVREGKPFENNETFGQYPLQVNGYRNLDCELEGAMVEGDVELLPDSHSV KYGQERWFTKLPVLTFFELSRFEFNQSLGQPEKIHNLKLEFPQIIMYDRMYRSKELIR NKRECIRKLKEEIKILQOKLERYVKYSGPARFPLPDLMLKYVIEFASTKPASESCPPE SDTHMTLPLSSVHCSVSDQTSKESTSTESSQDVSTFSSPEDSLPKSKPLTSSRSSM EMPSQAPARTVTDEEINFVKTCQWRSEIEQDIQDLKTCIASTTQTIEQMYCDPLL QVPYRLHAVLVHEGQANAGHYWAYIYNQPRQSWLKYNDISVTESSWEEVERDSYGLR NVSAICYLMYINAKLPYFNAEAPTESDQMSVEALSVELKHYIQEDNWRFEQVEEWE EEQSKIPQMESSPNSSSQYSTSQEPSVASSHGVRCLSEHAVIVKEQTAQRIANTA RAYEKSGVEAALSEAFHEEYSRLYQLAKETPTSHSDPRLQHLVVFQNEAPKRVVER TLLEQFADKNLSYDERSISIMKVAQAKLKEIGPDDMMMEYKRWHEDEYSLFRKVSYYL LTGLELYQKGYQEALSYLVYAYQNAALLMKGPRRGVKESVIALYRRKCLLELNKA ASLFETNDHDSVTEGINVMNELIIPCIHLIINNDISKDDLDAIEVMRNHWCSYLGQDI AENLQLCLGEFLPRLDPSAEIIVLKEPPTIRPNSPYDLCSRFAVMESIQGVSTVT K</p>
	<p>SEQ ID NO: 275 3044 bp</p>
<p>NOV96b, CG59708-02 DNA Sequence</p>	<p>CGTAGGCGCTTCGGCCATGACTGCGGAGCTGCAGCAGGACGACGCGGCGCGCGGCA GACGGCCACGGCTCGAGCTGCCAAATGCTGTTAAATCAACTGAGAGAAATCACAGGCA TTCAGGACCTTCTCTTCTCCATGAAGCTCTGAAGGCCAGTAATGGTGACATTACTCA GGCAGTCAGCCTTCTCACTGATGAGAGAGTTAAGGAGCCAGTCAAGACACTGTTGCT ACAGAACCATCTGAAGTAGAGGGGAGTGCTGCCAACAGGAAGTATTAGCAAAAGTTA TAGACCTTACTCATGATAACAAAGATGATCTTCAGGCTGCCATTGCTTGTAGTCTACT GGAGTCTCCCAAATTCAGCTGATGGAAGAGATCTTAACAGGATGCATGAAGCAACC TCTGCAGAACTAAACGCTCAAAGAGAAATATCATGTTATGCAAGAGCTTCAGTATT TGTTTGCTCTAATGATGGGATCAAATAGAAAATTTGTAGACCCCTKCGAGCCCTGGA TCTATTAAAGGAGCATTCCGATCATCTGAGGAACAGCAGCAAGATGTGAGTGAATTC ACACACAAGCTCCTGGATTGGCTAGAGGACGCATTCCAGCTAGCTGTTAATGTTAACA GTCCAGGAACAATCTGAAAATCCAATGGTGCAGCTGTTCTATGGTACTTTCCTGAC TGAAGGGGTTCTGTAAGGAAAACCTTTTGTAAATGAGACCTTCCGCCAGTATCCT CTTCAGGTAAACGGTTATCGCACTTAGACGAGTGTGGAAGGGGCCATGGTGGAGG GTGATGTTGAGCTTCTTCCCTCCGATCACTCGGTGAAGTATGGACAAGAGCGTTGGTT TACAAAGCTACCTCCAGTGTGACCTTTGAACTCTCAAGATTGAGTTAATCAGTCC CTTGGGCGAGCCAGAGAAAATTCACAAATAGCTGGAATTTCTCAGATTATTATATGG ACAGGTACATGTACAGGAGCAAGGAGCTTATTCGAAATAAGAGAGAGTGATTGAAA GTTGAAGGAGGAAAATAAAATTCGAGCAAAAATGGAAAGGATGTGAAATATGGC TCAGGCCAGCTCGGTTCCCGCTCCCGACATGCTGAAATATGTTATTGAATTTGCTA GTACAAAACCTGCCTCAGAAAGCTGTCCACCTGAAAGTGACACACATATGACATTACC</p>

	<p>ACTTTCCTCAGTGCAGTCTCGGTTTCTGACCAGACATCCAAGGAAAGTACAAGTACA GAAAGCTCTTCTCAGGATGTTGAAAGTACCTTTTCTTCTCTGAAGATTCTTTACCCA AGTCTAAACCACTGACATCTTCTCGGTCTTCCATGGAAATGCCTTACAGCCAGCTCC ACGAACAGTCAAGATGAGGAGATAAATTTGTAAAGACTGTCTTACAGATGGAGG AGTGAGATTGAACAAGATATACAAGATTTAAAGACTTGTATTGCAAGTACTACTCAGA CTATTGAACAGATGTACTGCGATCCTCTCCTTCTGTCAGGTGCTTATGCTGTGATGC AGTTCCTGTTTCATGAAGGACAAGCAAAATGCTGGACACTATTGGGCCTATATCTATAAT CAACCCCGACAGAGCTGGCTCAAGTACAATGACATCTCTGTTACTGAATCTTCTCTGGG AAGAAGTTGAAAGAGATTCTCTATGGAGGCTGAGAAATGTTAGTGCTTACTGTCTGAT GTACATTAATGCCAACTACCTACTTCAATGCAGAGGAGCCCACTGAATCAGAT CAAAATGTCAGAAGTGAAGCCCTATCTGTGGAAGTCAAGCATTACATTCAGGAGGATA ACTGGCGGTTTGAGCAGGAAGTAGAGGAGTGGGAAGAAGAGCAGTCTTGCAAAATCCC TCAATGGAGTCTCTCCCACTCTCATCACAGGGCTACTCTACATCACAAGAGCCT TCAGTAGCCTCTTCTCATGGGTTTCGCTGCTTGTCTATCTGAGCATGCTGTGATTGTAA AGGAGCAAACTGCCAGGCTATTGCAAAACAGCCCGTGCCTATGAGAAGAGCGGTGT AGAAGCGGCACTGAGTGAGGCATTCCATGAAGAATACTCCAGGCTCTATCAGCTTGCC AAAGAGACCCCACTCTCACAGTGATCCTCGACTTCAAGTGTCTTGTCTACTTTT TCCAAATGAAGCACCAAAAGGGTAGTAGAACGAACCTTCTGGAACAGTTTGCAGA TAAAAATCTTAGCTATGATGAAAGATCAATCAGCATTATGAAGGTGGCTCAAGCGAAA CTGAAGGAAATTTGGTCCAGATGACATGAATATGGAAGAGTACAAGAGGTGGCATGAAG ATTATAGTTTGTTCGAAAAGTGTCTGTGTATCTCCTAACAGGCTAGAACTCTATCA AAAAGGAAAGTACCAAGAGGCATTTCTTACCTGGTATATGCCTACCAGAGCAATGCT GCCCTGCTGATGAAGGGGCCCGCGGGGGGTCAAAGAATCCGTGATTGCTTTATACC GAAGAAATGCCTTCTGAGCTGAATGCCAAAGCAGCTTCTCTTTTGAACAAATGA TGATCACTCCGTAACAGGAGGATTAATGTGATGAATGAATCACTGATCACTGCAAT CACCTTATCATTAAATGACATTTCCAAGGATGATCTGGATGCCATTGAGGTGATGA GAAACCATTTGGTGCTCTTACCTGGGCAAGATATTGCAGAAAATCTGCAGCTGTGCT AGGGGAGTTTCTACCAAGCTTCTAGATCCTTCTGCAGAAATCATCGTCTTGAAGAG CCTCCAATATTGACCCCAATTCTCCTATGACCTATGTAGCCGATTGTCAGCTGTCA TGGAGTCAATTGAGGAGTTCAACTGTGACAGTGAAATAAGTCCACATGTTCAAG GCCCATTTCTGGTTCTGGCTGCCTCTTGACAGAAAGTTCGTTGTATAGTGCTC ACCTTGGGAAAAGGATTAGTGGGCACA</p>
	<p>ORF Start: ATG at 17 ORF Stop: TAA at 2939</p>
	<p>SEQ ID NO: 276 974 aa MW at 110687.3kD</p>
<p>NOV96b, CG59708-02 Protein Sequence</p>	<p>MTAELQQDDAAGAADGHSSCQMLLNQLREITGIQDPSFLHEALKASNGDITQAVSL TDERVKEPSQDVTATPSEVEGSAANKEVLAKVIDLTHDNKDDLQAAIALSLLESFPI QADGRDLNRMHEATSATKRSKRNMFMQELQYLFALMMGSNRKFVDPFSAALDLLKGA FRSSEEQQDVSEFTHKLLDWLEDAFQLAVNVNPNRNSKSNPMVQLFYGTFLTEGVRE GKPFENNETFGYPLQVNGYRNLDCELEGAMVEGDVELLPDSHSVKYQERLHVLPP VLTFFELSRFEPNQLQPEKIHNLKLEFPQIIYMDRYMYRSKELIRNKRERIKLKEEI KILQQKLERIVKYGGSPARFPLPDLMLKYVIEFASTKPASESCPESDTHMTLPLSSVH CSVSDQTSKESTSTESSQDVESTFSSPEDSLPKSKPLTSSRSSMEMPSQAPRTVTD EENFVKTCLQRWRSEIEQDIQDLKTCIASTTQIEQMYCDPLLRQVYRHLHVLVHE GQANAGHYWAYIYNQPRQSWLKYNDISVTESSWEEVERDSYGLLRNVSAYCLMYINAK LPYFNAEAAPTESDQMSVEALSVELKHYIQEDNWRFEQEVEWEVEEQSCKIPQMESS PNSSSQGYSTSQEPSVASSHGVRCLSSHAVIVKEQTAQAIANTARAYEKSGVEAALS EAFHEEYRLYLAKETPTSHSDPRLQHLVLYFFQNEAPKRVVVERTLLEQFADKNLSY DERSISIMKVAQAKLEIGPDDMNMEYKRWHEDESLFRKVSVYLLTGLELYQKGYQ EALSILVYAYQSNALLMKGPRRGVKEVIALYRRKCLLELNAKAASLFETNDDHSVT EGINVMNELIIPCIHLIINNDISKDDLDAIEVMRNHWC SYLGDQIAENLQLCLGELFLP RLLDPSAEIIVLKEPPTIRPNSPYDLCSRFAVMESIQGVSTVTVK</p>
	<p>SEQ ID NO: 277 3231 bp</p>
<p>NOV96c, CG59708-03 DNA Sequence</p>	<p>GCGCTTCGGCCATGACTGCGGAGCTGCAGCAGGACGACGCGGCGCGCGCAGACGG CCACGGCTCGAGCTGCAAAATGCTGTTAAATCAACTGAGAGAAATCAGGCATTCAG GACCCCTTCTTTCTCCATGAAGCTCTGAGGGCCAGTAATGGTGACATTACTCAGCAG TCAGCCTTCTCACTGATGAGAGAGTTAAGGAGCCAGTCAAGACACTGTTGCTACAGA ACCATCTGAAGTAGAGGGGAGTGCTGCCAACAGGAAGTATTAGCAAAAGTTATAGAC CTTACTCATGATAACAAAGATGATCTTCAGGCTGCCATTGCTTTGAGTCTACTGGAGT CTCCCAAAATTCAGCTGATGGAAGAGATCTTAACAGGATGCATGAAGCAACCTCTGC AGAAACTAAACGCTCAAAGAGAAAACGCTGTGAAGTCTGGGGAGAAAACCCCAATCCC AATGACTGGAGGAGAGTTGATGGTTGGCCAGTTGGGCTGAAAAATGTTGGCAATACAT GTTGGTTTAGTGCTGTTATTCACTCTCTCTTCAATTGCTGAAATTTGCGAAGATTGT TCTCAGTTATAGTCTGCCACAAATGTACTTGAATTTGTGCAAGTATACAGAAAAG AGAAATATCATGTTTATGCAAGAGCTTCAATATTGTTTGTCTTAATGATGGGATCAA ATAGAAAATTTGAGACCCGCTCTGCAGCCCTGGATCTATTAAGAGGGAGCTTCGATC ATCTGAGGAACAGCAGCAAGATGTGAGTGAATTCACACACAAGCTCCTGGATTGGCTA GAGGACGCATTCCAGCTAGCTGTTAATGTTAAGTCCAGGAACAAATTTGAAAATC CAATGGTGACGCTGTTCTATGGTACTTTCTGACTGAAGGGGTTTCGTAAGGAAAAC CTTTTGTAACAATGAGACCTTCGGCCAGTATCCTCTTCAGGTAAACGGTATCGCAAC TTAGACGAGTGTGGAAGGGGCCATGGTGGAGGGTGTGTTGAGCTTCTTCCCTCCG ATCACTCGGTGAAGTATGGACAAGAGCGTTGGTTTACAAAGCTACCTCCAGTGTGAC CTTTGAACTCTCAAGATTGAGTTAATCAGTCCCTTGGGCAGCCAGAGAAAATTCAC AATAAGCTGGAATTTCTCAGATTATTTATATGGACAGGTACATGTACAGGAGCAAGG</p>

	AGCTTATTGCAAAATAAGAGAGAGTGTATTGCAAAAGTTGAAGGAGGAAATAAAATCTT GCAGCAAAAATTTGGAAGGGTATGTGAAATATGGCTCAGGCCAGCTCGGTTCCCGCTC CCGGACATGCTGAAATATGTTATTGAATTTGCTAGTACAAAACCTGCCTCAGAAAGCT GTCCACCTGAAAGTGACACACATATGACATTACCACTTTCTTCAGTGCAGTGTCTCGGT TTCTAACGACACATCCAAGGAAAGTACAAGTACAGAAAGCTCTTCTCAGGATGTTGAA AGTACCTTTTCTTCTCCTGAAGATTCTTTACCCAAGTCTAAACCACTGACATCTTCTC GGTCTTCCATGGAAATGCCTTCACAGCCAGCTCCACGAACAGTCACAGATGAGGAGAT AAATTTTGTAAAGACCTGTCTTCAGAGATGGAGGAGTGAGATTGAACAAGATATACAA GATTAAAGACTTGTATTGCAAGTACTACTCAGACTATTGAACAGATGTACTGCGATC CTCTCCTTCGTGAGGTGCCTTATCGCTTGCATGCAGTCTTGTTCATGAAGGACAAGC AAATGCTGGACACTATTGGGCTATATCTATAATCAACCCGACAGAGCTGGCTCAAG TACAATGACATCTCTGTTACTGAATCTTCTGGGAAGAGTTGAAAGAGATTCTCTATG GAGGCTGAGAAATGTAGTGCTTACTGTCTGATGTACATTAAAGCAAACTACCCCTA CTTCAATGCAGAGGCAGCCCCAACTGAATCAGATCAAATGTCAGAAGTGGAAGCCCTA TCTGTGGAATCAAGCATTACATTAGGAGGATAACTGGCGGTTTGAAGCAGGAAGTAG AGGAGTGGGAAGAAGAGCAGTCTTGCAAAATCCCTCAAATGGAGTCTCCACCAACTC CTCATCAGAGGACTACTCTACATCACAAGAGCCTTCAGTAGCTCTTCTCATGGGGTT CGCTGCTGTCTGAGCATGCTGTGATTGTAAAGGAGCAAACTGCCAGGCTATTG CAACACAGCCCGTGCCTATGAGAAGAGCGGTGTAGAAGCGGCACTGAGTGAGGCATT CCATGAAGAATACTCCAGGCTCTATCAGCTTGCCAAAGAGACCCCACTCTCAGAGT GATCCTCGACTTCAGCATGTCCTTGTCTACTTTTCCAAAATGAAGCAACCCAAAGGG TAGTAGAACGAACCTTCTGGAACAGTTTGCAGATAAAAATCTTAGCTATGATGAAAG ATCAATCAGCATTATGAAGTGGCTCAAGCGAACTGAAGGAAATTTGTCAGATGAC ATGAATATGGAAGAGTACAAGAAGTGGCATGAAGATTATAGTTTGTCCGAAAAGTGT CTGTGTATCTCTAACAGGCTAGAACTCTATCAAAAAGGAAAGTACCAAGAGGCACT TTCTACCTGGTATATGCCTACCAGAGCAATGCTGCCCTGCTGATGAAGGGGCCCCGC CGGGGGGTCAAAGAATCCGTGATTGCTTTATACCGAAGAAAATGCCTTCTGGAGCTGA ATGCCAAAGCAGCTTCTCTTTTGAACAATAATGATGATCACTCCGTAACCTGAGGCT TAATGTGATGAATGAATGATCATCCCCTGCATTACCTTATCATTAAATGACATT TCCAAGGATGATCTGGATGCCATTGAGGTGATGAGAAACCATTTGGTGTCTTACCTTG GGCAAGATATTGCAGAAAATCTGCAGCTGTGCCTAGGGGAGTTTCTACCCAGACTTCT AGATCCTTCTGCAGAAATCATCGTCTTGAAGAGCCTCCAACATTCCGACCAATCTCT CCCTATGACCTATGTAGCCGATTGTCAGCTGTCTGAGTCAATTAGGGAGTTTCAA CTGTGACAGTGAATAAGCTCCCATGTTCAAGGCCCATTTGGTTCTGGCTGCCT GCCTCTGCACAGAAGTTCTGTTGTCATAGTGCTCACCTTGG		
	ORF Start: ATG at 12 ORF Stop: TAA at 3147		
	SEQ ID NO: 278	1045 aa	MW at 119107.7kD
NOV96c, CG59708-03 Protein Sequence	MTAELQDDAAGAADGHSSQMLLNQLREITGIQDPSFLHEALRASNGDITQAVSL TDERVKEPSQDTVATEPSEVEGSAANKEVLAKVIDLTHDNKDDLQAAIALSLLESPI QADGRDLNRMHEATSATKRSKRKRCEVWGENPNPNDWRRVDGWVGLKNVNTWFS AVIQSLFQLPEFRRLVLSYSLPQNVLENCRSHTEKRNIMFMQELQYLFALMMSNRKF VDPSAALDLLKGAFRSSEEQQDVSEFTHKLLDWLEDAFLAVNVNPNRKNFENPMVQ LFYGTFLTEGVREGKPFNNETFGQYPLQVNGYRNLDCELEGAMVEGDVELLPDSHSV KYGQERWFTKLPPVLTFFELSRFEFNQSLGQPEKIHNKLEFPQIIYMDRMYRSKELIR NKRECIRKLKEEIKILQQLLEGYVKYSGSPARFPLPDLMLKYVIEFASTKPASESCPPE SDTHMTLPSSVHCSVSNQTSKESTSTESSSQDVESTFSSPEDSLPKSKPLTSSRSSM EMPSQPAPRTVTDEEINFVKTCLOQRWRSEIEQDIQDLKTCIASTTQTIEQMYCDPLLR QVPYRLHAVLVHEGQANAGHYWAYIYNQPRQSWLYNDISVTESSEWEVERDSYGLLR NVSAYCLMYINDKLPHYNAEAPTESDQMSEVEALSVELKHYIQEDNWRFEQEVEEWE EEQSKIPQMESSTNSSSQDYSTSQEPSVASSHGVRCLSEHAVIVKEQTAQAIAANTA RAYEKSGVEAALSEAFHEEYSRLYLAKETPTSHSDPRLQHLVVFQNEAPKRVER TLLEQFADKNLSYDERSISIMKVAQAKLKEIGPDDMNMEYKKWHEDEYSLFRKVSYYL LTGLELYQKGKYEALSYLVYAYQSNAALLMKGPRRGVKESVIALYRKCKLLELNAKA ASLFETNDHDSVTEGINVMNELIIPCIHLIINNDISKDDLDAIEVMRNHWSYLGQDI AENLQCLGFLPRLLDPSAEIIVLKEPPTIRPNSPYDLCSRFAAVMESIQGVSTVTV K		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 96B.

Table 96B. Comparison of NOV96a against NOV96b through NOV96c.		
Protein Sequence	NOV96a Residues/ Match Residues	Identities/ Similarities for the Matched Region

NOV96b	209..1045 138..974	805/837 (96%) 805/837 (96%)
NOV96c	1..1045 1..1045	979/1045 (93%) 981/1045 (93%)

Further analysis of the NOV96a protein yielded the following properties shown in Table 96C.

Table 96C. Protein Sequence Properties NOV96a	
PSort analysis:	0.8800 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV96a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 96D.

Table 96D. Geneseq Results for NOV96a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV96a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE04874	Human protease protein-1 (PRTS-1) - Homo sapiens, 1055 aa. [WO200146443-A2, 28-JUN-2001]	22..1036 18..1047	524/1035 (50%) 713/1035 (68%)	0.0
AAB31552	A human ubiquitin specific protease 25 (USP25) - Homo sapiens, 1055 aa. [WO200079267-A2, 28-DEC-2000]	22..1036 18..1047	524/1035 (50%) 713/1035 (68%)	0.0
AAB31546	A human ubiquitin specific protease 25 (USP25) - Homo sapiens, 1055 aa. [WO200078934-A2, 28-DEC-2000]	22..1036 18..1047	524/1035 (50%) 713/1035 (68%)	0.0
AAB74491	Human SYK kinase binding protein SYK-UBP isoform 1 - Homo sapiens, 1055 aa. [WO200121654-A2, 29-MAR-2001]	22..1036 18..1047	522/1035 (50%) 710/1035 (68%)	0.0
AAB31556	A human ubiquitin specific protease (USP) - Homo sapiens, 1087 aa. [WO200079267-A2, 28-DEC-2000]	22..1036 18..1079	525/1067 (49%) 717/1067 (66%)	0.0

In a BLAST search of public sequence databases, the NOV96a protein was found to have homology to the proteins shown in the BLASTP data in Table 96E.

Table 96E. Public BLASTP Results for NOV96a				
Protein Accession Number	Protein/Organism/Length	NOV96a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96RU2	UBIQUITIN SPECIFIC PROTEASE - Homo sapiens (Human), 1077 aa.	1..1045 1..1077	1041/1077 (96%) 1042/1077 (96%)	0.0
Q9P213	KIAA1515 PROTEIN - Homo sapiens (Human), 757 aa (fragment).	304..1045 16..757	738/742 (99%) 739/742 (99%)	0.0
P57080	Ubiquitin carboxyl-terminal hydrolase 25 (EC 3.1.2.15) (Ubiquitin thiolesterase 25) (Ubiquitin-specific processing protease 25) (Deubiquitinating enzyme 25) (mUSP25) - Mus musculus (Mouse), 1055 aa.	22..1036 18..1047	527/1033 (51%) 710/1033 (68%)	0.0
Q9UHP3	Ubiquitin carboxyl-terminal hydrolase 25 (EC 3.1.2.15) (Ubiquitin thiolesterase 25) (Ubiquitin-specific processing protease 25) (Deubiquitinating enzyme 25) (USP on chromosome 21) - Homo sapiens (Human), 1087 aa.	22..1036 18..1079	525/1067 (49%) 717/1067 (66%)	0.0
Q9H9W1	CDNA FLJ12512 FIS, CLONE NT2RM2001730, WEAKLY SIMILAR TO PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) - Homo sapiens (Human), 737 aa.	313..1036 2..729	363/733 (49%) 510/733 (69%)	0.0

PFam analysis predicts that the NOV96a protein contains the domains shown in the Table 96F.

Table 96F. Domain Analysis of NOV96a			
Pfam Domain	NOV96a Match Region	Identities/ Similarities for the Matched Region	Expect Value

UIM: domain 1 of 1	96..113	9/18 (50%) 14/18 (78%)	8.4
UCH-1: domain 1 of 1	162..193	14/32 (44%) 28/32 (88%)	2.6e-11
UCH-2: domain 1 of 1	580..649	26/72 (36%) 56/72 (78%)	1.5e-19

Example 97.

The NOV97 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 97A.

Table 97A. NOV97 Sequence Analysis			
	SEQ ID NO: 279	1601 bp	
NOV97a, CG59559-01 DNA Sequence	AGGGCAGAGGCCACAGCGCCATCCCCTTCCCCATGGTCTCCCTACCCCCAACCTGCAC TGGGCGCTCCGCCCAGAGGTGAGTCCCTCCCAGCCCTTCTCTCCTTCTGTCTTAGCCA TCCGCAGAGCCATCCTGTGCAAAGGAAGGAGCTAGGCTGTGCGCCCTGGGCGTCATGA TCCTTCTGCGGGCCTCCGAAGTGCGGCAGCTGCTTCACAATAAGTTCGTGGTCATCCT GGGGGACTCTGTGCATAGGGCAGTATACAAGGACCTGGTGCTTCTGTCTGCAGAAGGAC CGCTGCTCACTCCCGGCAGCTTAGAGCAAGGGGGAGCTGAACCTCGAACAAAGATG AGCTGGTGGACGGAGGCCAGCGGGGCCACATGCACAACGGCCTTAACTACCGTGAGGT CCGCGAGTTCGCTCCGACCACCATCTGGTACGTTTTTACTTCCTCACC CGGTGTAC TCCGATTACCTCCAGACCATTCTGAAAGAGCTGCAGTCGGGCGAGCAGCCCCCGACC TGGTCATCATGAATTCCTGCCTCTGGGACATCTCCAGGTATGGTCCGAACCTCTGGAG AAGCTACCTGGAGAACCTGGAGAACCTGTTCCAGTGCCTGGGCCAGGTGCTGCCCGAG TCTTGCCTCCTGGTGTGGAACACGGCCATGCCTGTGGGCGAGGAAGTCACCGGGGGTT TTCTTCCGCCAAGCTCCGGCGGCAGAAGGCCACCTTCTGAAAAACGAAGTGGTCAA AGCCAACCTTCCACAGCGCCACCGAGGCACGTAAACATAACTTCGATGTACTGGACTTG CATTTCACTTCCGCCACGCGAGGGAGAACCTGCAGTGGGACGGGGTGCACTGGAATG GACGTGTGACACCGCTGCCTCTCCAGCTGCTGCTGGCCACGTGGCCGACGCGCTGGGG TGTGGAGCTGCCCCACGCCACCCCGTGGGCGAGTGGATCAAGAAGAAAAACCTGGC CCGAGAGTCGAAGGGCCGCCCCAGGCCAACAGAAATCACCCGGCCTTACCTCTGTCCC CACCTTACCTTCCCCACATACCGCCCCCTGCTTGGGTTCACCCACCGCAGCTTGCC GCTGCTCCCGTCTCCTGTCCCAACAGCTCCTCCTCCATTCTCCATCACCAGGGAATG CCCGGTTCCCAAGGGTCCCCAGATGCCTGTTTTCTCAGACCATACTTTCAGT CGGATCAATTCTATTGCCATTAGATGTCCCCTCATCAGCCCATGACAGTTTCTTCTCGT CGAAGACAATTTATGGTTGGTCTCAGCTGCCTATGCCCTTCTTCCCAACACCCCGT TATCAGCGGCTGCCCAAGTGGTACATAGGGGTTTTTGGCAGGTATCGTCCCGTGGCC CCTATACGCCCTGGGGACAGCGGCTCGACCTTCAAAGAGAGGGCCCCAGCCAATCC TGAGCCAAGGCCTCAATAGACGGACCTAGGCCTTATTTCTCTTTATGAACATGGATT GGACAGATCTGACACTTCCTTTCATTGCTTGGCCTGAACAGACTGACCTTGTTAACT TAAGCCTGGAGTCCATGCCTCGTCTTCTTTTGT		
	ORF Start: ATG at 171	ORF Stop: TAG at 1467	
	SEQ ID NO: 280	432 aa	MW at 49726.6kD
NOV97a, CG59559-01 Protein Sequence	MILLRASEVRQLLHNKFVVLGDSVHRAVYKDLVLLQKDRLLTPGQLRARGELNFEQ DELVDGGQRGHMHNGLNRYREVREFRSDHHLVRFYFLTRVYSYDLQTLKELQSGEHAP DLVIMNSCLWDISRYGPNSWRSYLENLENLFQCLGQVLPESCLLVWNTAMPVGEVVG GFLPPKLRQKATFLKNEVVKANFHSATEARKHNFVDLDLHFHFRHARENLHWDGVHW NGRVHRCLSQLLAHVADAWGVELPHRHPVGEWIKKKKPGPRVEGPPQANRNHPALPL SPPLSPPTYRPLLGFPQRLPLPLSPQPPPIILHHQGMPPRFPQGPDPACFSSDHTF QSDQFYCHSDVPSSAHAGFFVEDNFMVGPQLPMPFFPTPRYQRPAPVVRHGFGRYRPR GPYTPWQQRPRPSKRRAPANPEPRPQ		

Further analysis of the NOV97a protein yielded the following properties shown in Table 97B.

Table 97B. Protein Sequence Properties NOV97a

PSort analysis:	0.5937 probability located in mitochondrial matrix space; 0.5103 probability located in microbody (peroxisome); 0.4900 probability located in nucleus; 0.3252 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV97a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 97C.

Table 97C. Geneseq Results for NOV97a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV97a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG74241	Human colon cancer antigen protein SEQ ID NO:5005 - Homo sapiens, 281 aa. [WO200122920-A2, 05-APR-2001]	34..294 1..266	162/268 (60%) 191/268 (70%)	1e-82
AAE03639	Human extracellular matrix and cell adhesion molecule-3 (XMAD-3) - Homo sapiens, 386 aa. [WO200142285-A2, 14-JUN-2001]	1..421 1..366	197/435 (45%) 231/435 (52%)	2e-82

In a BLAST search of public sequence databases, the NOV97a protein was found to have homology to the proteins shown in the BLASTP data in Table 97D.

Table 97D. Public BLASTP Results for NOV97a				
Protein Accession Number	Protein/Organism/Length	NOV97a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96HM7	SIMILAR TO HYPOTHETICAL PROTEIN FLJ22376 - Homo sapiens (Human), 432 aa.	1..432 1..432	432/432 (100%) 432/432 (100%)	0.0
Q96B20	HYPOTHETICAL 31.4 KDA PROTEIN - Homo sapiens (Human), 279 aa.	121..310 1..190	190/190 (100%) 190/190 (100%)	e-116
Q9H1Q7	BA12M19.1.3 (NOVEL PROTEIN) (CDNA FLJ31791 FIS, CLONE NT2RI2008749, WEAKLY SIMILAR TO SPLICEOSOME ASSOCIATED PROTEIN 49) - Homo sapiens (Human), 454 aa.	1..421 18..434	234/437 (53%) 273/437 (61%)	e-111
Q9H1Q6	BA12M19.1.1 (NOVEL PROTEIN) - Homo sapiens (Human), 403 aa.	1..421 18..383	197/435 (45%) 231/435 (52%)	7e-82
Q9H6D1	CDNA: FLJ22376 FIS, CLONE HRC07327 - Homo sapiens (Human), 403 aa.	1..421 18..383	196/435 (45%) 231/435 (53%)	1e-81

PFam analysis predicts that the NOV97a protein contains the domains shown in the Table 97E.

Table 97E. Domain Analysis of NOV97a			
Pfam Domain	NOV97a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 98.

The NOV98 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 98A.

Table 98A. NOV98 Sequence Analysis			
	SEQ ID NO: 281	981 bp	
NOV98a, CG59669-01 DNA Sequence	GCGCCGGGTCCCAGAATCTAGTCTACGCCACGGTTTTGACCACGCGTGACCCGCTGC CCAGCCGGCCCGGCCATCAGGTGGTCCGTGTGTCCTCTGACATGTCGTCTGCAGCC GCGTGGCCCTGGTAAC TGGGGCTAACAAAGGCATCGGCTTTGCGATCACGCGTGACCT GTGTGCGAAATTCTCCGGGGACGTGGTGCTCACGGCGCGGGACGAGGCGCGGGGCCGC GCGGCGGTGCAGCAGCTGCAGGCGGAGGGCTGAGCCCACGCTTCCACCAGCTGGACA TCGACGACCCGAGAGCATCCGTGCGCTGCGCGACTTTCTGCGCAAGGAGTACGGGGG ACTTAACGTGCTGGTCAACAACGCGGGCATCGCCTTTAGAAGTACTGATCTCACCCAC TTTCACATTCTAAGAGAAGCTGCAATGAAAATACTTTTGGTACCAGGCCGTCT GCACAGAGCTACTCCCTCTAATAAAAAACCAAGGTAGAGTGGTGAATATATCAAGCCT AATAAGTCTAGAGGCCCTGAAAACTGCAGCCTGGAGCTACAGCAGAAGTTTCGAAGT GAGACCATCACAGAGGAGGAGCTGGTGGGGCTCATGAACAAGTTTGTGGAGGATACAA AGAAAGGAGTCCATGCAAAAGAAGCTGGCCTAATAGTGCATACGGGGTGTCTAAGAT TGGAGTGACAGTCCCTGTCCAGAATCCTTGCCAGGAACTCAATGAGCAGAGGAGAGGG GACAAGATCCTTCTGAATGCCTGCTGCCCTGGCTGGGTGAGAACCGACATGGCAGGAC CACAAAGCCACCAAAGCCCAGAAGAAGGAGCAGAGACCCCTGTGTACTTGGCCCTTTT GCCTCCAGATGCAGAGGGACCTCATGGGCAGTTTGTTCAAGATAAAAAAGTGGAAACA TGGTGAATCAGCTCTTTGTACAGCTCCCATCTGTAGCCTGTCTAAAGGGGA		
	ORF Start: ATG at 101	ORF Stop: TGA at 932	
	SEQ ID NO: 282	277 aa	MW at 30547.7kD
NOV98a, CG59669-01 Protein Sequence	MSSCSRVALVTGANKGIGFAITRDLCRKFSGDVLTARDEARGRAAVQQLQAEGLSPR FHQLDIDDPQSIRALRDLRKEYGGLNVLVNNAGIAFRSTD LTHFHILREAA MKNTFF GTQAVCTELLPLIKTQGRVNVISLISLEALKNCSLELQQKFRSETITEELVGLMKN FVEDTKKGVHAKEGWPNSAYGVSKIGVTVLSRILARKLNEQRRGDKILLNACCPGWR TDMAGPQATKSPEEGAETPVYLALLPPDAEGPHGQFVQDKKVEQW		

Further analysis of the NOV98a protein yielded the following properties shown in Table 98B.

Table 98B. Protein Sequence Properties NOV98a	
PSort analysis:	0.4766 probability located in mitochondrial matrix space; 0.4500 probability located in cytoplasm; 0.1822 probability located in mitochondrial inner membrane; 0.1822 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV98a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 98C.

Table 98C. Geneseq Results for NOV98a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV98a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW51011	Human liver carbonyl reductase - Homo sapiens, 277 aa. [US5756299-A, 26-MAY-1998]	1..277 1..277	236/277 (85%) 252/277 (90%)	e-134

AAU33100	Novel human secreted protein #3591 - Homo sapiens, 175 aa. [WO200179449-A2, 25-OCT-2001]	142..277 39..174	119/136 (87%) 128/136 (93%)	2e-66
AAM73641	Human bone marrow expressed probe encoded protein SEQ ID NO: 33947 - Homo sapiens, 123 aa. [WO200157276-A2, 09-AUG-2001]	1..97 1..97	86/97 (88%) 92/97 (94%)	7e-43
AAM60948	Human brain expressed single exon probe encoded protein SEQ ID NO: 33053 - Homo sapiens, 123 aa. [WO200157275-A2, 09-AUG-2001]	1..97 1..97	86/97 (88%) 92/97 (94%)	7e-43
AAM33832	Peptide #7869 encoded by probe for measuring placental gene expression - Homo sapiens, 123 aa. [WO200157272-A2, 09-AUG-2001]	1..97 1..97	86/97 (88%) 92/97 (94%)	7e-43

In a BLAST search of public sequence databases, the NOV98a protein was found to have homology to the proteins shown in the BLASTP data in Table 98D.

Table 98D. Public BLASTP Results for NOV98a				
Protein Accession Number	Protein/Organism/Length	NOV98a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q924V2	CARBONYL REDUCTASE 2 - Cricetulus griseus (Chinese hamster), 277 aa.	1..277 1..277	243/277 (87%) 260/277 (93%)	e-139
Q91X28	SIMILAR TO CARBONYL REDUCTASE 1 - Mus musculus (Mouse), 277 aa.	1..277 1..277	244/277 (88%) 256/277 (92%)	e-139
Q924V3	CARBONYL REDUCTASE 1 - Cricetulus griseus (Chinese hamster), 277 aa.	1..277 1..277	241/277 (87%) 256/277 (92%)	e-137
P48758	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1) - Mus musculus (Mouse), 276 aa.	2..277 1..276	240/276 (86%) 253/276 (90%)	e-136
JC5284	carbonyl reductase (NADPH) (EC 1.1.1.184), inducible - rat, 277 aa.	1..277 1..277	236/277 (85%) 249/277 (89%)	e-134

PFam analysis predicts that the NOV98a protein contains the domains shown in the Table 98E.

Table 98E. Domain Analysis of NOV98a			
Pfam Domain	NOV98a Match Region	Identities/ Similarities for the Matched Region	Expect Value
adh_short: domain 1 of 1	4..274	67/286 (23%) 185/286 (65%)	1.6e-38

Example 99.

The NOV99 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 99A.

Table 99A. NOV99 Sequence Analysis			
	SEQ ID NO: 283	1001 bp	
NOV99a, CG58624-01 DNA Sequence	CTTGGTATAAGTAAGTGCTCGTCAATGTTGGCTACTCTCAATGTGTCAGAGCCGAGCCGCGGGCGCAGAGCGCGATCTCTACCGGGACACGTGGGTGCGATACCTGGGCTATGCCATGAGAGTGGGCGAGGCTTTCCGCTCTCTTGTGCCAGCGCGGTGGTGTGGCTGAGCTATGGCGTGGCCAGCTCTCTACGTGCTGGCGGATGCCATTGACAAAGGCAAGAAGGCTGGAGAGGTGCCAGCCCTGAAGCAGGCCGAGCGCCAGGGTGACTGTGGCTGTGGTGGACACTCTTTGTATGGCAGGCTCTAGCCTCTGTGGCCATTCCGGGCTTCACCATCAACCGCGTGTGTGCTGCCTCTCTCTATGTCTGGGCACTGCCACCCGCTGGCCCTTGGCTGTCCGTAAGTGGACCACCACCGCCTTGGGCTGTTGACCATCCCCATCATTATCCACCCATTACAGGGATCATCCACTCTCCAGTGATGAGAGTGGATCATCCAGTCTCCAGCACGAAGGCCAGGGGTCCACAGGTGAGTGGAGCCCCAGCAGCCCCCTCAGCTCTGCGTGCCCATGTACTGGTCTTCTCCCTGGCTCTATACTCAGTGTTCAAGGGGTTGGACGGGGCTTGGCCGCGGAGCTGCGCCTGGCTTTGCTGCTCCACAAGGGCACCGTGGCTGTGAGCCTGTGCTGCACTGTGTCAGAGCCACGTAGGGTTACAGGTGGTGGCTGGCTGTGGGATCCACTTCTTGTGCATGACACTTCTAGGCATCCGGCTGGGTGCGGCTCTGGCACAGTCAGCACGGCCTCTGCACAGCTGGCCAGTCTGTGCTAGAGGGCATGGTGGCTGGCACCTTCTCTATACCACCTTTCTGAAATCTTTCCACAGGAGCTGGCGACTTCTGAGCAAAGGATCTCAAGGTCAATTCTGCTCTAGAAGGGTGTGCCCTGCTCACTGGCCTGCTCTTCATCCATATCTAGGGGGCTT		
	ORF Start: ATG at 41	ORF Stop: TAG at 992	
	SEQ ID NO: 284	317 aa	MW at 33737.8kD
NOV99a, CG58624-01 Protein Sequence	MSEPQPRGAERDLYRDTWVRYLGYANEVGEAPRSLVPAVVWLSYGVASSYVLADAIDKGGKAGEVPSPEAGRSARVTAVVDTFVWQALASVAIPGFTINRVCAASLYVLGTATRWPLAVRKWTTTALGLLTIPIIIHPIDRDHPLSSDESGSSSLQHEGPGVPQVSGAPAAPALSALRAHVLVFSALYSVFKGLDGAWAAELRLALLLHKGTAVVSLSLQLLQSHVGLQVQVAGCGIHFCLMTLLGIRLGAALAQSAQPLHQLAQSVLEGMVAGTFLYTTFFLEIFPQELATSEQRILKVILLLEGCALLTGLLFIHI		

Further analysis of the NOV99a protein yielded the following properties shown in Table 99B.

Table 99B. Protein Sequence Properties NOV99a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 55 and 56

A search of the NOV99a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 99C.

Table 99C. Geneseq Results for NOV99a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV99a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM93835	Human polypeptide, SEQ ID NO: 3905 - Homo sapiens, 324 aa. [EP1130094-A2, 05-SEP-2001]	140..317 141..324	134/184 (72%) 145/184 (77%)	3e-63
AAY52394	Human transmembrane protein HP10528 - Homo sapiens, 324 aa. [WO9955862-A2, 04-NOV-1999]	140..317 141..324	134/184 (72%) 145/184 (77%)	3e-63
AAY84895	A human proliferation and apoptosis related protein - Homo sapiens, 324 aa. [WO200023589-A2, 27-APR-2000]	140..317 141..324	134/184 (72%) 145/184 (77%)	3e-63
AAB43291	Human ORFX ORF3055 polypeptide sequence SEQ ID NO:6110 - Homo sapiens, 323 aa. [WO200058473-A2, 05-OCT-2000]	140..317 140..323	134/184 (72%) 145/184 (77%)	3e-63
AAM93650	Human polypeptide, SEQ ID NO: 3514 - Homo sapiens, 324 aa. [EP1130094-A2, 05-SEP-2001]	140..317 141..324	133/184 (72%) 144/184 (77%)	2e-62

In a BLAST search of public sequence databases, the NOV99a protein was found to have homology to the proteins shown in the BLASTP data in Table 99D.

Table 99D. Public BLASTP Results for NOV99a				
Protein Accession Number	Protein/Organism/Length	NOV99a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9UDX5	WUGSC:H_DJ0539M06.2 PROTEIN - Homo sapiens (Human), 166 aa.	1..152 1..152	145/152 (95%) 145/152 (95%)	6e-78
Q9CRB8	2610507A21RIK PROTEIN (1700020C11RIK PROTEIN) - Mus musculus (Mouse), 166 aa.	1..168 1..164	133/168 (79%) 143/168 (84%)	8e-69

Q9CZX4	2610507A21RIK PROTEIN - Mus musculus (Mouse), 166 aa.	1..143 1..143	125/143 (87%) 133/143 (92%)	2e-68
Q9NY26	IRT1 PROTEIN (SIMILAR TO ZINC/IRON REGULATED TRANSPORTER-LIKE) (HYPOTHETICAL 34.2 KDA PROTEIN) (UNKNOWN) (PROTEIN FOR MGC:14180) - Homo sapiens (Human), 324 aa.	140..317 141..324	134/184 (72%) 145/184 (77%)	1e-62
Q9Y380	CGI-71 PROTEIN - Homo sapiens (Human), 324 aa.	140..317 141..324	134/184 (72%) 145/184 (77%)	1e-62

PFam analysis predicts that the NOV99a protein contains the domains shown in the Table 99E.

Table 99E. Domain Analysis of NOV99a			
Pfam Domain	NOV99a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Syndecan: domain 1 of 1	235..255	9/21 (43%) 16/21 (76%)	6.9
Zip: domain 1 of 1	174..313	52/178 (29%) 108/178 (61%)	2.3e-15

Example 100.

The NOV100 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 100A.

Table 100A. NOV100 Sequence Analysis		
	SEQ ID NO: 285	987 bp
NOV100a, CG59679-01 DNA Sequence	AGACGCTCACACAGACAACCTCAAGTCCAGCAACATCTTAGTAGCCCAAAATCGACTG CTTTAGTTCTTCTGGTGGGTGCCTCTCACTGTCCACTCGGCTATGCCATCCTGCAGTC GCATTGCACTGGTGAAGTGAAGTAATAAGGGCATTGGCTTTGCGATCACTCGTGACCT GTGTCAAGCAATCTCAGGGGATGTGGTGTCTCACTGCACGGGACGAGGCACGGGGCCTT GCGGCAGTGCAGAGCTGCAGGCTGAGGGCCTGATTCTCGCTTCCACCACTGGACA TCAATGACCCCTCAGAGCATCCATGCACTTCGCAACTTTCTGTCTCAAGGAGTACGGAGG CCTGGATGTGCTGGTCAACAACGCGGGCATTGGCGTGCTTTTCAAAGTGGATGACCCA ACACCCCTTCGACATTCAAGCTGAGGTGACACTGAAGACGAACCTTTTGGCCACTAGAA ATGTCTGCACTGAGTTACTGCCTATAATGAAACACATGGTAGAGTGGTGAAACATCAG CAGTCTGCAGGGGTTAAAGCCCTTGAGAACTGCAGGGAAGATCTTCAGGAAAAGTTC CGATGTGACACACTTACCGAGGTGGACCTGGTGCACCTCATGAAAAAGTTTGTGGAGG ATACAAAAATGAAGTCCATGAGAGGGAAGGTTGGCCAGACTCGGCTTACGGGGTGTC GAAGCTGGGGGTGACAGTCTTACGAGGATCCTGGCCCGGCAGCTGGATGAAAAGAGG AAAGCGGACAGGATTCTGCTCAATGCCTGCTGCCCGGATGGGTGAAGACCGACATGG CGAGGGACAGGGCTCCCGGACCGTGGAAAGAGGGGGCCGAAACCCCGCTTACTTGGC TCTCTGCCTCCAGATGCCACTGAACCTCACGGCCAGTAGTCCGTGACAAAGTTGTG CAAACCTGGTGAACGCTGCTCTGGGGCTTAATTGTTTGATAAACGTTAGCGGGAGAG A	
	ORF Start: ATG at 101	ORF Stop: TGA at 938

	SEQ ID NO: 286	279 aa	MW at 31007.2kD
NOV100a, CG59679-01 Protein Sequence	MPSCSRIALVTGANKGIGFAITRDLCQQFSGDVVLTARDEARGLAQVQKLQAEGLIPR FHQLDINDPQSIHALRNFLKEYGGDLVNNAGIGVLFKVDPTPFDIQAEVTLKTN FFATRNVCTELLPIMKPHGRVNNISLQGLKALENCREDLQEKFRCDTLTEVDLVLDLM KKFVEDTKNEVHEREGWPD SAYGVSKLGVTVLTRILARQLDEKRKADRILLNACCPGW VKTDMARDQGSRTVEEGAETPVYLLALLPPDATEPHGQLVRDKVVQTW		

Further analysis of the NOV100a protein yielded the following properties shown in Table 100B.

Table 100B. Protein Sequence Properties NOV100a	
PSort analysis:	0.3600 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1808 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV100a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 100C.

Table 100C. Geneseq Results for NOV100a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV100a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW51011	Human liver carbonyl reductase - Homo sapiens, 277 aa. [US5756299-A, 26-MAY-1998]	1..279 1..277	198/279 (70%) 233/279 (82%)	e-112
AAU33100	Novel human secreted protein #3591 - Homo sapiens, 175 aa. [WO200179449-A2, 25-OCT-2001]	145..279 40..174	88/135 (65%) 110/135 (81%)	2e-48
AAG46601	Arabidopsis thaliana protein fragment SEQ ID NO: 58644 - Arabidopsis thaliana, 302 aa. [EP1033405-A2, 06-SEP-2000]	3..259 20..283	106/268 (39%) 157/268 (58%)	6e-43
AAG46600	Arabidopsis thaliana protein fragment SEQ ID NO: 58643 - Arabidopsis thaliana, 316 aa. [EP1033405-A2, 06-SEP-2000]	3..259 34..297	106/268 (39%) 157/268 (58%)	6e-43
AAG46599	Arabidopsis thaliana protein fragment SEQ ID NO: 58642 - Arabidopsis	3..259 45..308	106/268 (39%) 157/268 (58%)	6e-43

	SEP-2000]			
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In a BLAST search of public sequence databases, the NOV100a protein was found to have homology to the proteins shown in the BLASTP data in Table 100D.

Table 100D. Public BLASTP Results for NOV100a				
Protein Accession Number	Protein/Organism/Length	NOV100a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JJN7	CARBONYL REDUCTASE (EC 1.1.1.184) (CARBONYL REDUCTASE 3) - Cricetus griseus (Chinese hamster), 277 aa.	1..279 1..277	246/279 (88%) 262/279 (93%)	e-140
AAH02812	CARBONYL REDUCTASE 3 - Homo sapiens (Human), 277 aa.	1..279 1..277	227/279 (81%) 246/279 (87%)	e-126
O75828	Carbonyl reductase [NADPH] 3 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 3) - Homo sapiens (Human), 276 aa.	3..279 2..276	226/277 (81%) 245/277 (87%)	e-126
Q924V2	CARBONYL REDUCTASE 2 - Cricetus griseus (Chinese hamster), 277 aa.	1..279 1..277	206/279 (73%) 244/279 (86%)	e-119
Q91X28	SIMILAR TO CARBONYL REDUCTASE 1 - Mus musculus (Mouse), 277 aa.	1..279 1..277	204/279 (73%) 240/279 (85%)	e-116

PFam analysis predicts that the NOV100a protein contains the domains shown in the Table 100E.

Table 100E. Domain Analysis of NOV100a			
Pfam Domain	NOV100a Match Region	Identities/ Similarities for the Matched Region	Expect Value
adh_short: domain 1 of 1	4..277	77/316 (24%) 186/316 (59%)	5.2e-31

Example 101.

The NOV101 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 101A.

Table 101A. NOV101 Sequence Analysis			
	SEQ ID NO: 287	1011 bp	
NOV101a, CG59644-01 DNA Sequence	CTCCTCGGGGGGGCGGCGGCGGCGATGTTCTCGGTCTCTCGTACGGGCGGCTGGTGG CCCGCGCGGTGCTCGGCGGCTCTCGCAGACCGACCCAGGGCCGGCGGCGGCGGCGG CGGCGCGGTGCTCGGCGGCTCTCGCAGACCGACCCAGGGCCGGCGGCGGCGGCGGCGG GGCGACTACGGAAGGCGGTGCTACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG TCCTCAAGAAGGGCGGCGGTGCTACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG CGCGGACGTGCTCGGTGTTGCAGATGGTGTAGGAGGCTGGAGAGACTATGGAGTTGAT CCATCTCAATTCTCAGGACTTTAATGCGGACGTGTGAACGTTTATGATAAAGAAGGAC GGTTCGTACCTAGTAATCCCATTTGGAATTCTCACCACAAGCTACTGTGAGTTGCTGCA AAATAAAGTCCCTTTGCTCGGTAGCAGCACCGCTGCATTGTGGTGTGGACAGAACC AGCCACCGCTTACACAGCAAACCTGGGCGGATTCAAGGCTTCCTGGTTGTGTCAGGGGTG GTGAAGTCGTGCACCGATCAGATGAGCAGCAGCATTACTTCAACACTCCATTCCAGCT CTCAATCGCTCCCCCTGAAGCCGAGGGAGTCGTCTTGAGCGCAGCTCCGGATGCTGCTG GATAGCACGTCTTTCGATGTCCAGCTAGGAGACATTATCCTGACGGCAACAGATGGAC TCTTTGACAACATGCCTGATTATATGATTCTTCAGGAGCTAAAAAAGTTAAAGAATTTC AAATTATGAGAGTATACAACAGACTGCCAGAAGCATTGCTGAGCAAGCTCATGAGCTG GCCTATGACCCAAATTATATGTACCTTTTGCACAGTTTGCATGTGACAATGGATTGA ATGTGAGAGGTGGTGGAAAGCCAGATGACATCACCGTCCTTCTTCAATAGTGGCTGA GTATACAGACTAGCTGAGGTGTCAA		
	ORF Start: ATG at 25	ORF Stop: TAG at 997	
	SEQ ID NO: 288	324 aa	MW at 34311.1kD
NOV101a, CG59644-01 Protein Sequence	MFSVLSYGRIVARAVLGGLSQTDPRAGGGGGGAVLGGLSQTDPRAGGGGGGGLVLT GCGFGKDFRKGLLKKGACYGDDACFVARHRSADVLGVADGVGGWRDYGVDPSQFSGL MRTCERLVKEGRFVPSNPILGILTSYCELLQNKVPLLSSTACIVVLDRSTHRLHTAN LGDSGFLVVRGGEVVHRSDEQHYFNTPFQLSIAPPEAEGVVLSDSPAADSTSFVQ LGDIILTATDGLFDNMPDYMILQELKKLKNSNYESIQTARSIAEQAHAYDPNYMS PFAQFACDNLNVRGGKPDITVLLSIVAETD		

Further analysis of the NOV101a protein yielded the following properties shown in Table 101B.

Table 101B. Protein Sequence Properties NOV101a	
PSort analysis:	0.5708 probability located in mitochondrial matrix space; 0.4996 probability located in mitochondrial intermembrane space; 0.2852 probability located in mitochondrial inner membrane; 0.2852 probability located in mitochondrial outer membrane
SignalP analysis:	Likely cleavage site between residues 23 and 24

A search of the NOV101a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 101C.

Table 101C. Geneseq Results for NOV101a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV101a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB85357	Human phosphatase (PP) (clone ID 3402521CD1) - Homo sapiens, 304 aa. [WO200153469-A2, 26-JUL-2001]	1..324 1..304	304/324 (93%) 304/324 (93%)	e-173
AAU32112	Novel human secreted protein #2603 - Homo sapiens, 304 aa. [WO200179449-A2, 25-OCT-2001]	25..324 6..304	272/300 (90%) 274/300 (90%)	e-156
AAG52267	Arabidopsis thaliana protein fragment SEQ ID NO: 66421 - Arabidopsis thaliana, 348 aa. [EP1033405-A2, 06-SEP-2000]	71..320 99..340	101/261 (38%) 133/261 (50%)	4e-33
AAG52266	Arabidopsis thaliana protein fragment SEQ ID NO: 66420 - Arabidopsis thaliana, 374 aa. [EP1033405-A2, 06-SEP-2000]	71..320 125..366	101/261 (38%) 133/261 (50%)	4e-33
AAG52265	Arabidopsis thaliana protein fragment SEQ ID NO: 66419 - Arabidopsis thaliana, 467 aa. [EP1033405-A2, 06-SEP-2000]	71..320 218..459	101/261 (38%) 133/261 (50%)	4e-33

In a BLAST search of public sequence databases, the NOV101a protein was found to have homology to the proteins shown in the BLASTP data in Table 101D.

Table 101D. Public BLASTP Results for NOV101a

Protein Accession Number	Protein/Organism/Length	NOV101a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9W0E2	CG12091 PROTEIN - Drosophila melanogaster (Fruit fly), 321 aa.	1..320 1..320	163/322 (50%) 218/322 (67%)	1e-83
Q9W3R1	CG15035 PROTEIN - Drosophila melanogaster (Fruit fly), 374 aa.	55..319 109..373	127/266 (47%) 178/266 (66%)	1e-64
O18183	W09D10.4 PROTEIN - Caenorhabditis elegans, 330 aa.	4..320 7..330	136/331 (41%) 198/331 (59%)	2e-60
Q9VAH4				2e-56

	melanogaster (Fruit fly), 314 aa.	26..309	168/285 (58%)	
Q9SUK9	HYPOTHETICAL 36.2 KDA PROTEIN - Arabidopsis thaliana (Mouse-ear cress), 335 aa.	71..320 86..327	101/261 (38%) 133/261 (50%)	1e-32

PFam analysis predicts that the NOV101a protein contains the domains shown in the Table 101E.

Table 101E. Domain Analysis of NOV101a			
Pfam Domain	NOV101a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PP2C: domain 1 of 1	147..191	13/48 (27%) 36/48 (75%)	0.26

Example 102.

The NOV102 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 102A.

Table 102A. NOV102 Sequence Analysis			
	SEQ ID NO: 289	523 bp	
NOV102a, CG59662-01 DNA Sequence	AGTCCCAGTACTATCAGCCATGGTCAACCACACCATGTTCTTCGACGTTGCTGTCGAC AGTGAGCCCTTGGACCACGTCCTCTTGGAGCTGTTTGACAGAAAAGTTTCCAAAGACAG CAGAAAACGTTTCGTGCTCTGAGCACTGAAGAGAAAGGATTTGGTTATAAGGGTCCCTG CTTTCACAGAATTATACCAGCATTATGTGTGTCAGGGTGGTGACTTCACGCACCATAAT GGCACTGGTGGCAAGTCCATCTACGGGGAGAAAATTGAAGATGAGAAATTTATCCTAA AGCGTACAGGTCTTGGCATCTTGTCATGGCAAATTTCTGGACCCAACACAAACTGTTTC CGTTTTTTTCATCTGCACTGCCAAGACGGGGTGGTTGGATGGCAAGCATGTAGTCTTT GGCAAGGTGAAAGAAGGCATGAATATTTGGAGGCCATAGAGCAATTTGGGTCCAGGA ATGGCAAGACCAGCAAGAAGACCACCATTGCTGACTGTGGACAGCTCTGGTAAGTTTG A		
	ORF Start: ATG at 20	ORF Stop: TAA at 515	
	SEQ ID NO: 290	165 aa	MW at 18237.7kD
NOV102a, CG59662-01 Protein Sequence	MVNHTMFFDVAVDSEPLDHVSFELFAEKFPKTAENVRLSTEKGFGYKGPCHRIIP AFMCQGGDFTHHNGTGGKSIYGEKFEDEKFIKRTGPGILSMANSGPNTNCSVFFICT AKTGWLDGKHVVFQKVKEGMNILEAIEQFGSRNGKTSKKTITADCGQLW		

Further analysis of the NOV102a protein yielded the following properties shown in Table 102B.

Table 102B. Protein Sequence Properties NOV102a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
	No Known Signal Sequence Predicted

analysis:	
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A search of the NOV102a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 102C.

Table 102C. Geneseq Results for NOV102a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV102a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU01195	Human cyclophilin A protein - Homo sapiens, 165 aa. [WO200132876-A2, 10-MAY-2001]	1..164 1..164	141/164 (85%) 148/164 (89%)	1e-80
AAW56028	Calcineurin protein - Mammalia, 165 aa. [WO9808956-A2, 05-MAR-1998]	1..164 1..164	141/164 (85%) 148/164 (89%)	1e-80
AAG65275	Haematopoietic stem cell proliferation agent related human protein #2 - Homo sapiens, 164 aa. [JP2001163798-A, 19-JUN-2001]	2..164 1..163	140/163 (85%) 147/163 (89%)	5e-80
AAP90431	Cyclophilin - Homo sapiens (human), 164 aa. [EP326067-A, 02-AUG-1989]	2..164 1..163	140/163 (85%) 147/163 (89%)	5e-80
AAG03831	Human secreted protein, SEQ ID NO: 7912 - Homo sapiens, 165 aa. [EP1033401-A2, 06-SEP-2000]	1..164 1..164	140/164 (85%) 147/164 (89%)	8e-80

In a BLAST search of public sequence databases, the NOV102a protein was found to have homology to the proteins shown in the BLASTP data in Table 102D.

Table 102D. Public BLASTP Results for NOV102a				
Protein Accession Number	Protein/Organism/Length	NOV102a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC39529	SEQUENCE 26 FROM PATENT WO0132876 - Homo sapiens (Human), 165 aa.	1..164 1..164	141/164 (85%) 148/164 (89%)	4e-80
Q9BRU4	PEPTIDYLPROLYL ISOMERASE A	1..164 1..164	140/164 (85%) 147/164 (89%)	2e-79

	(Human), 165 aa.			
P05092	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) - Homo sapiens (Human), 164 aa.	2..164 1..163	140/163 (85%) 147/163 (89%)	2e-79
Q96IX3	PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A) - Homo sapiens (Human), 165 aa.	1..164 1..164	140/164 (85%) 147/164 (89%)	5e-79
P04374	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) - Bos taurus (Bovine), and, 163 aa.	2..164 1..163	138/163 (84%) 147/163 (89%)	7e-79

PFam analysis predicts that the NOV102a protein contains the domains shown in the Table 102E.

Table 102E. Domain Analysis of NOV102a			
Pfam Domain	NOV102a Match Region	Identities/ Similarities for the Matched Region	Expect Value
pro_isomerase: domain 1 of 1	5..165	105/180 (58%) 141/180 (78%)	4.2e-91

Example 103.

The NOV103 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 103A.

Table 103A. NOV103 Sequence Analysis		
	SEQ ID NO: 291	8860 bp
NOV103a, CG59773-01 DNA Sequence	GGATCCTTGAGGGCACTGGTGCGACTTTCAGGTGAGGTCTTAGCAGATGAAAGCGGCT GGCTGTGGCCCGCGCCAGTAGTGCTTTCTGCTCCGCACTCGCCGTGAGCCAGGTGTGC AACC GGATTGGGGCGAGGGTCGCGCTGGCTACCTCGCATGCGCAGAGCCGGAAGCCC GCTGACCGGACTACAGTCTCCAGAAGAGCCTTGTGGAGGCCGAGACGCGAAGCCGCT GGCGCCATCTTGAAATCTGATCCTCCATCCCGAGGCTTTGCGTCTGCGCGGCCGGCC GCTGCTGCTCCGGGAGCCAGTCTGCTAAAGGGGAGGACGTTGAGGACGCGCGGCT GGCGGGAGAGACAGCTGGGGAGAGACATGGCAGGTCGGAGCGCGGCTGCGCCTCTG TCACTCAGCATCCTCTTAGGCGTTTCCACGCCCGCCCCCTGCCGAGGGGCGGGGCTG ACGGCTCTGGTACCCGAGTCGGCGCGCGGGGAGGGGCGCGCCCTGCAGAGTGGGG ACCCCACTGGGCTGTGCCATGCTGACCGGAGACCACCGAGGCGGGAGACAGCGCGG CGAAGAGCCATTGAGTGGTCACCCAGTAGCCGCGCGCGCGCCGCTCGGGAAGCTTG CCACCCGCTAGGAGGGGAAGATGAAGGAGATTGACAGGATCTGTGCCCGAGAGCTGTGT GGAAACCAGCGCGCTGGATCTTCCACACGGCGTCCAAGCTCAATCTCCAGGTTCTGC TTTCGCACGTCTTGGGCAAGGATGTCCCCGCGATGGCAAAGCGAGTTCGCTTGAG CAAGTGTGCTTTCATGCTTGATCGAATCTATCGATTGACACAGTTATTGCCCGGATT GAAGCGCTTTCTATTGAGCGCTTGCAAAAGCTGCTACTGGAGAGGATCGCCTCAAGT TCTGCATTGCCAGTATGTATCGGAAGAATAACGATGACTGTGGCGCGGAGATCAAGGC GGGGAATGGGACGGTTGACATGTCCGTCTTACCCGATGCGAGATACTGTGCACTGTCTC	

CAGGAGGACTTCGCCTATTTCAGGGTTTGAGTGCTGGGTGGAGAAATGAGGATCAGATCC
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 TGGTTGTGCCGCTTTCGGGGTTGCTGATTCTGACTATGAAGCCATTTGTAAAGTACCT
 CGAAAGGTGGCCAGAAATATCTCTGCGGCCCTTCTAGCAGGTGGTCAGCCAGCATTT
 GCACTGAAGAACCAGCGTTGTCTGAGGTTGGGCCACCCGACTTAGCAAGCACAAGGT
 ACCCCAGATGGAGAAAGCATGGAGGAAGAGACGCTGGTTCTCTGTGGAAATCTTTG
 GATGCAAGCGTCCAGGCTAGCCCTCCACAACAGAAAGATGAGGAGACTGAGAGAAGTG
 CAAAGGAACCTTGGAAAGTGTGACTGTTGTTTCAGATGATCAGGCTCCCGCAGCATGGGTG
 TAATCACAAGCTGGAATTAGCTCTTAGCATGATTAAAGTCTTGATTATAAGCCATC
 CAGAGCCCCCGAGGAGCAGGCTTCCGATTCCAGTGAAATCCAGCCTTCCGCTGGAGCCA
 AGCCTGGCCCTAGCATGACAGATGGAGTTAGTTCCCGTTTCTTAAACAGGTCTTTGAA
 ACCCCTTTACAAGACACCTGTGAGTTATCCCTTGGAGCTTTCAGACCTGCAGGAGCTG
 TGGGATGATCTCTGTGAAGATTATTGCGCTCCGGGTCCAGCCATGAGTGAAGAT
 TGCTGAAACAACAAAAGCTGAATTCACATGAGACCACTATAACTCAGCAGTCTGTATC
 TGATTCCTCACTTGGCAGAACTCCAGGAAAAATCCAGCAACAGAGGCCACCAACAG
 ATTCCTCAAGAGAACTTAATGAAATGAGCTATGAACTAAAGTGTGCTCAGGAGTCGT
 CTCAAAAGCAAGATGGTACAATTCAAGAACTCAAGGAACTCTGAAAGCAGGGAACG
 TGAGACTGAGGAGTTGTACCAGGTAATTGAAGGTCAAAATGACACAATGGCAAAGCTT
 CGAGAAATGCTGCACCAAGCCAGCTTGGACAACCTTCAGAGCTCAGAGGGTACTTCTC
 CAGCTCAGCAACAGGTAGCTCTGCTTGATCTTCAGAGTGCTTTATTCTGCAGCCAACT
 TGAATAACAGAACTCCAGAGGGTGGTACGACAGAAAGAGCGCAACTGGCTGATGCC
 AAACAATGTGTGAATTTGTAGAGGCTGCAGCACACGAGAGTGAACAGCAGAAAGAGG
 CTTCTTGGAAACATAACAGGAATTGCGAAAAGCCTTGACAGCAGCTACAAGAAAGATT
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 ACCCAGGAACAAAACATCCAGCACCTAAACCATAGTCTGAGTCACAAGGAGCAGTTGC
 TTCAAGAAATTTCCGGAGCTCCTACAGTATCGAGATAACTCAGCAAAACCCCTTGAAGC
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 GAGCGGGCTATAGATGAAAAATTTCTGCTCTAGAAGAGAAAGAACTGCGCTGCGCC
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 CTCTCCAAATGAAGCTACTATGCAAGTATGGAGAGTCTCTGAGGGCCAAAGGCCCTG
 GAAGTGGAAACAGTTATCTACTACCTGTCAAAACCTCCAGTGGCTGAAAGAAGAAATGG
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 AGTCTCTGACCAGGAACATACAGATTAAAGAAGATCTCATAAAGGACCTGCAATGCA
 ACTGGTTGATCTTGAAGACATACCAGCTATGGAACGCTGACCCAGGAAGTCTTACTT
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 GGCCTTACAAGCAGAGAGACAGCTCTATAGCAGTCTGGTGAAGTTCCATGCCCATCCA
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 GCTGAGTTCACCAGCACTTAGAAGAGAAGAGGAAAGCTGAGGAGGAAGTGAAGGAGC
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 GCTGAGCCTTTGCCTTGAGAAATGCGGAGCTGAAAGAGCAGATGGGAGAAGCAATGTCT
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 GAGGGGTGGCTGTCTGATGGCACTGGGGCTTCTACTCTCCAGGGCTCAGGCCAAAA
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	<p>TGGACTAGAAGAGAAGCTGGCTGAGGAGCTGAGATCAGCCTCGTGGCCTGGGAAATAT GATTCCCTGATTGAGGATCAGGCCCGGGAACGTCTTACCTACGGCAAAAAATACGAG AAGGGAGAGGTATTGTTATCTTATCACCCGGCATGCAAAAGATACAGTAAATCTTT TGAGGATCTCCTAAGGAGCAATGACATTGACTACTACCTGGGACAGAGCTTCCGGGAG CAACTCGCCAGGAAGCCAGCTGACAGAGAGGCTCACCAGCAAACTCAGCACCAGG ATCATAAAAGTGAGAAAGATCAAGCTGGACTTGAGCCACTGGCCCTCAGGCTCAGCAG GGAGCTGCAGGAGAAGGAGAAAGTGATTGAAGTCTGCAGGCCAAGCTGGATGCTCGG TCCCTCACACCTCCAGCAGCCATGCCTTGTCTGACTCCACCCGCTCTCCAGCAGCA CCTCTTCTGTCTGATGAAGTGAAGCCTGCTCTGACATGGACATAGTCAGCGAGTA CACACACTATGAAGAGAAGAAAGCTTCTCCAGTCACTCAGATTCCATCCATCTCG AGTCATTCTGCTGTGTCTTCTAAACCATCATCAACCAGTGCATCTCAGGGGGCTA AGGCCGAATCCACAGCAACCCCATCAGCTTGCCAACCTCCCAAGATACCCCAAGGA GGCCAACCAGGCCCATTCAGGCTTTCATTTTCACTCCATACCAAGCTGGCTAGCCTT CCTCAGGCCCATTTGCCCTCAGCTCCATCCAGCTTCTGCTCTTCAGGCTCAGGCTG CTCTCTCTCTGCTGTGTGAGACACCAAGTGGTCTCCTTGGCTGAGGCTCAGCAGGA GCTACAGATGCTGCAGAGCAGTTGGGAGAAAGTCCAGCAGCTTCTCTCTGCTTCC ACAGCTACATTGCTGAGCAACGACTTGGAAGCCGACTTCTCTACTCACTCACTCTG CCCAGCCTCACTCTCTCCAAGGGGCACCATAGAACTGGGAAGAAATCTAGAGCCTGG GTACTGGGAGCAGTGGCAAGTGGGATGTGATGAGGCCCTCAGAAAGGGAGTGTATCT GGGGACCTATCTCAGGCTCCTCTGTGTACCAAGCTTAACTCCAAACCCACAGGGGCTG ACCTGCTGGAAGAGCATCTTGGTGAAATCCGGAACCTGCGCCAGCGCTGGAGGATC CATCTGCATCAATGACCGCTACGGGAGCAACTGGAACACCGGCTGACCTCTACTGCT CGTGAAGGGGATCCACTTCTAACTTCTACAGTCAGGGCTGGAGTCCATACCTCAGC TCTGCAATGAGAACAGAGTCTCAGGGAAGACAATCGAAGACTTCAGGCTCACTGAG TCATGTTTCCAGAGAGCACTCCAGGAAACAGAAAGCCTGAGGAGGCTCTCCTGTCC TCTCGATCCACCTTCAAGAGCTGGAAAGGAGCTGGAGCACCAGAAGGTGGAAGGC AGCAGCTTTTGAAGACTTGAGGGAGAAGCAGCAAGAGGTCTTGCATTTACAGGAGGA ACGCTTTTCCCTCCAGGAAACGACTCCAGACTGCAGCACAAGCTGGTCTCTCTGAG CAACAGTGTGAAGAGAAACAGCAGCTCTTTGAGTCCCTCCAGTCAGAGCTACAAATCT ACGAGGCACTTTATGGCAATCCAAGAAGGGGCTGAAAGGCTTGGGTTTGGATACTTC TCCAGTAATGAAGACCCCTCCCAAGCTAGAGGGTGATGCTACTGATGGCTCCTTTGCC AATAAGCATGGCCCGCATGTCTTGGCCACATTGATGACTACAGTCCCTAAGACAGC AGATTGCGGAGGGCAAGCTGCTGGTCAAAAGATAGTGTCTCTGTGAGATCAGCGTG CAGCTTCCCTGGCCTTGAAGCCCAAGGCACAGAGGTGCTAGGAGCAAGGTATTATCAT GAGCTTCGGAGCAGCACCAGTGCCTGCACCATGCCCTAGAGAGCTCGGCTTCCCTCC TCACCATGTTCTGGAGAGCAGCCCTGCCAAGCACCCACATCCCTGTGCTGCCCTGGCAA AGTGGGAGAATCAACAGAAAGGGAACCTTCTGGAAGTGAAGACCAAGTATCCAACAG GAGCGGCTCCTTCAGAGCACAACCTGAGCATCTGAAGAACGCCAACCAGCAGAAGGAGA GCATGGAGCAGTTCATCGTCAGCCAGCTAACCCAGAACATGATGTTTTAAAGAAGGC AAGGACTAACTTAGAGGTGAAATCCCTAAGGGCTCTGCCATGTACTCAGGCTTGTGA CCCTTGCCCTCCAGGAACCATGCAAGAAGCGCAGCCACCAGAAGTCTTAAACAGCA GGAAAGGTGGGCTGTCCCTCTTTGTGTCAGTACCTATCTGCTGAGGAGCATCTGGG CCTCATCTCTCAAGTCCAGGGAGGGTCCAGAAGAGGGAGTCAGAGATGTATCTTGG TGGAGCTGGGAGAAAGGCAGAAAGCCTTCTGACAGCTATGGAATACGATTAGCCAG GTCCACTTGGCCAGCACTAAGAAAAAGATGCGTAGTTTGCACAGAAGGTTTGTGAT CCTGCCTCTCAACAGCCCGCAGCCTTGGGAAGTAGCAAGAGCACATTTCTTGCTCA TCAGCTGTCTGAGATGGAAGAACTCAGTGGATATAGGACCTGATTCCGATGAAGGG GCACGTGGTCCCAATGCTGGAGCTCCTCTGGCAGGTTCTAAAAGCACACTACTGAGCA GCGGTGCCCTGCGGACACTGCTGGCGGGGGCTCAGTGAGCACTACTCACAGATCCAC ACCTGACCCTGTGGGTGAGTCAAGCTGGGCTTGGTCTGCTGCTAGCAGCTGTGT TCTTTGAGTTCACATGAATGTGGTGACTTCCAGATACCATCTCAGGCTTAACT AGCAGATCTATTTCTTTCTTCTATGATATCCAAATTGGACTGACCTCACTTCAAAG TTGCTGTCCATTTGTACCTATCTTATCTCGGGGAAATTGACAGCTGATGGCCAG ACCAACTCTGTGAAATCTTGCATAGAGCAAACTGTGCTCACTTTTAAAGTCAAGT GGAGAGGCCCCAGCCTAGTAAAGCCTAGTCTGTGTCTTACAGTGTGTTAGAAATGT GTTTGTGTATATAATATATATATAGATTATATATGTGTGAACCCATATATTGA AGGCCAACAATACTGGTGGACAGGGTGGGTGACAGAAATGAAAGCCTTTTGGTGAT TGTTAAAGCAAGATGTGTATAAAGAAATAAATAGTTTTTCTTTC</p>
	<p>ORF Start: ATG at 658 ORF Stop: TGA at 7828</p>
	<p>SEQ ID NO: 292 2390 aa MW at 268843.7kD</p>
<p>NOV103a, CG59773-01 Protein Sequence</p>	<p>MKEICRICARELCGNQRRWIFHTASKLNLQVLLSHVLGKDVPRDGKAEFACSKCAFML DRIYRFDTVIARIEALSIERLQKLLLEKDRLEKFIASMYRKNNDSDGAEIKAGNGTVD MSVLPDARYSALLQEDFAYSGFEWVENEDQIQEPHSCHGSEPGNRRRCRGCAALR VADSDYEAIKCVPRKVARISICGPPSSRWSTSICTEPPALSEVGPPDLASTKVPDPGES MEETPGSSVESLDAVQASPPQKDEETERSAKELGKDCDDQAPQHCNHLKLEL ALSMIKGLDYKPIQSPRGSRLPIPVKSSLPKAKPGPSMTDGVSSGFLNRSKLPLYKTP VSYPLELSDQLQELWDDLCEDYLPLRVQPMTEELLKQKQLNSHETTTTQSSVSDSLAE LQEKIQTEATNKLQEKLNEMSYELKCAQESSQKQDGTIQNLKETLSRERETEELY QVIEGQNDTMAKLEMLHQSQLGLHSSSEGTSPAQQQVALLDLQSAIFCSQLEIQKLQ RVVRQKERQLADAKQCVQFVEAAAHESSEQKEASWKNHQLERKALQQLQELQNKSSQ LRAWAEKYNEIRTEQNIQHLNHSLSHKEQLLQEFRELLQYRDNSDKTLEANEMLLE KLQRIRIHDKAVALERAIDEKFSALEEKEKELRQLRLAVRERDHLRLRDLVLSNEAT MQSMESLLRAKGLEVEQLSTTCQNLQWLKEEMETKFSRWQKEQESIQQQLQTSLHNRN KEVEDLSATLLCKLPGQSEIAEELCQRLQRKERMLQDLLSDRNKQVLEHMEIQGLL</p>

	<p>QSVSTREQESQAAAEKLVQALMERNSELQALRQYLGGDRSLMSQAPISNQQAEEVTPPTG RLGKQTDQGSQMIIPSRDDSTSLTAKEDVSI PRSTLGDLDTVAGLEKELSNKAELELM AKKERESQMELSALQSMMAVQEEELQVQAADMESLTRNTQIKEDLIKDLQMQLVDPED I PAMERLTQEVLLREKVASVESQGGQEISGNRRQQLLLMLEGLVDERSRRLNEALQAER QLYSSLVKFHAPHESSEDRDLTQVELEGAQVLRSLRLEEVLGRSLERLNRLETAAIIGG AAAGDDTDTSTEDTDSIEEEAAHSHQQLVKVALEKSLATVETQNPSPSPSPMGGD SNRCLQEEMHLHRAEFHQHLEEKRAEEELKELKAQIEEAGFSSVSHIRNTMLSLCLE NAELKEQMGEMS DGEI BEDKEKGEVMVETVVTKEGLESSESLQAEFRKLQGLKKNNAH NI INLLKEQLVLSKKEGNSKLTPELLVHLTSTIERINTELVGSPGKHQHQEEGNVTVR PFPRLQSLDLGATFTVDAHQLDNQSQPRDPGPQSAFSLPGSTQHLRSQLSQCKORYQD LQEKLLSEATVFAQANELEKYRVMLTGESLVKQDSKQIQVDLQDLGYETCGRSENEA EREETTSPECEEHNSLKEMVLMLEGLCSEQGRRGSTLASSSERKPLENLGKQEEFRVY GKSENI LVLKDIKDLKAQLQANKVIONLKSRRVSLSVTSYSSSLERPRKLRAVGT LEGSSPHSVPEDEGLSDGTGAFYSPGLQAKKDLES LIQRVLEAQLPKNGLEEKL AEELRSASWPGKYDSLQDQARELSYLRQKIREGRGICYLITRHAQDVKVSPEDLLRS NDIDYYLGQSFRQLAQGSQSLTERLTSKLTSDHKSEKQAGLEPLALRLSRELQEK KVIEVLQAKLDARSLTPSSSHALSDSHRSPSSTFSLSDELEACSDMDIVSEYTHYEEK KASPSHSDSIHSSSHSAVLSSKPSSTSASQGAESNSNPISLPTPQNTPEKANQAH GFHFSI PKLASLPQAPLPSPSSFLPFSPGTGPLLGCCTPVVSLAAQQLQMLQK QLGESASTVPPASTATLLSNDLEADSSYYLNSAQPHSPRGITELGRILEPGYLGSSG KWDVMRPQKGSVSGDLSSGSVYQLNSKPTGADLLEEHLGEIRNLQRLEES I CINDR LREQLEHRLTSTARGRGSTSNFYSSQGLSIPQLCNENRVLRREDNRRLQAQLSHVSRH SQETESLREALLSSRSHLQELEKELEHVKVERQQLLEDLREKQQEVLFREERLSLQ NDSRLQHKLVLLQQCEEKQQLFESLQSELQIYEALYGNSSKGLKGLGLDTSFVMKTP PKLEGDATDGSFANKHGRHVIGHIDDYSALRQQAEGKLLVKIIVSLVRSACISFPGLE AQGTEVLGSKGIHELRSSTALHHALESASLLTMFWRAALPSTHIVPLPGKVGESTE RELLELRKTVSKQERLLQSTTEHLKNANQOKESMEQFIVSQLTRTHDVLKKARTNLEV KSLRALPCTPAL</p>
	<div>SEQ ID NO: 293</div> <div>7161 bp</div>
<p>NOV103b, CG59773-02 DNA Sequence</p>	<p>GTTGAGGGGGCAATCGGGCAGGCTCCTCCCATGGGTTGCCCATCATGTCTAATGGAT ATCGCACTCTGTCCAGCACCTCAATGACCTGAAGAAGGAGAACTCAGCCCTCAAGCT GCGCATCTACTTCTGGAGGAGCGCATGCAACAGAAGTATGAGGCCAGCCGGGAGGAC ATCTACAAGCGGAACATTGAGCTGAAGGTTGAAGTGGAGAGCTTGAACGAGAACTCC AGGACAAGAAACAGCATCTGGATAAAACATGGGCTGATGTGGAGAATCTCAACAGTCA GAATGAAGCTGAGCTCCGACGCCAGTTTGGAGGCGCAGCAGGAGACGGAGCATGTT TATGAGCTCTGGAGAATAAGATCCAGCTTCTGCAGGAGGAATCCAGGCTCAAGAAGA ATGAAGCTGCGCGGATGGCAGCTCTGGTGAAGCAGAGAAGGAGTGTAACCTGGAGCT CTCAGAGAAACTGAAGGGAGTCACCAAAACTGGGAAGATGTACCAGGAGACCAGGTC AAGCCCGACCAATACACTGAGGCCCTGGCCAGAGGGCAGGAGAAATTGAAGAAGTGA ATCAGAGCTGGCTGCCAGGAGAGGCTTGTAAGAACAGCTATCTCGGAGAGAAACA ACTGCTACATCTGTTGGAGGAGCCAACTAGCATGGAAGTGCAGCCCATGACTGAAGAG TTGCTGAAACAAACAAAGCTGAATTCACATGAGACCCTATAACTCAGCAGTCTGTAT CTGATTCCCACTTGGCAGAACTCCAGGAAAAATCCAGCAACAGAGGCCACCAACAA GATTCTTCAAGAGAACTTAATGAAATGAGCTATGAACCTAAAGTGTGCTCAGGAGTCG TCTCAAAAGCAAGATGGTACAATTCAGAACCTCAAGGAACTCTGAAAGCAGGGGAA GTGAGACTGAGGAGTTGTACCAGGTAATGAAGGTCAAAATGACACAACTGGCAAGCT TCGAGAAATGTGCAACCAAGCCAGCTTGACCAACTTCAGAGCTCAGAGGTAATCTCT CCAGCTCAGCAACAGGAGTCTGCTTGATCTTCAGAGTGTCTTATCTGCAGCCAA TTGAAATACAGAAGCTCCAGAGGGTGGTACGACAGAAAGAGCGCAACTGGCTGATGC CAACAATGTGTGCAATTTGTAGAGGCTGCAGCACACGAGAGTGAACAGCAGAAAGAG GCTTCTTGGAACATAACAGGAATTGCGAAAAGCCTTGACAGAGCTACAAGAGAAAT TGCAGAATAAGAGCCAAAGCTTCTGCTGGGAGGCTGAAAAATACAATGAGATTG AACCAGGAACAAAACATCCAGCACCTAAACCATAGTCTGAGTCAACAGGAGCAGTTG CTTCAGGAATTTGGGAGCTCCTACAGTATCGAGATAACTCAGACAAAACCTTGAAG CAATGAAATGTGCTTGAGAAACTTCGCCAGCGAATACATGATAAGCTGTGTGCTCT GGAGCGGGCTATAGATGAAAAATCTCTGCTCTAGAAGAGAAAGAAAAAGAACTGCGC CAGCTTCGTCCTGTGTGAGAGAGCGAGATCATGACTTAGAGAGACTGCGCGATGTCC TCTCTCCAATGAAGTACTATGCAAGATGGAGAGTCTCTGAGGGCCAAAGGCT GGAAGTGAACAGTTATCTACTACCTGTCAAACTCCAGTGGCTGAAAGAAGAAATG GAAACCAATTTAGCCGTTGGCAGAAGGAACAAGAGAGTATCATTACAGCAGTTACAGA CGTCTCTTCATGATAGGAACAAAGAAGTGGAGGATCTTAGTGCAACACTGCTCTGCAA ACTTGGACACGGGAGAGTGAATAGCAGAGGAGCTGTGCCAGCTCTACAGCGAAAG GAAAGGATGCTGCAGGACCTTCTAAGTATCGAAATAAACAAGTGTGGAACATGAAA TGGAGATTCAAGGCCTGCTTCAGTCTGTGAGCACCAGGAGCAGGAAAGCCAGCTGC TGCAGAGAAGTTGGTCAAGCCTTAATGGAAAGAAATTCAGAAATTCAGGCCCTGCGC CAATATTTAGGAGGGAGAGACTCCCTGATGTCCCAAGCACCATCTCTAACCAACAG CTGAAGTTACCCCACTGGCCGTCTTGAAAAACAGACTGATCAAGGTTCAATGCAGAT ACCTTCAGAGATGATAGCACTTCATTGACTGCCAAAGAGGATGTGAGCATACCCAGA TCCACATTAGGAGATTGGACACAGTTGAGGGCTGAAAAAGAACTGAGTAATGCCA AAGAGGAACCTGAACTCATGGCTAAAAAGAAAGAGAATCAGAGATGGAACCTTTCTGC TCTACAGTCCATGATGGCTGTGCAGGAAGAAGAGCTGCAGGTGCAGGCTGTGATATG GAGTCTGTGACCAGGAACATACAGATTAAAGAGATCTCATAAAGGACCTGCAATGC AAGTCTGTGACCTGAAGACATACAGCTATGGAACGCTGACCCAGGAAGTCTTACT TCTTCGGGAAAAAGTTGCTTCACTAGAAATCCAGGGTCAAGAAATTCAGGAAACCGA AGACAACAGCAGTTGCTGCTGATGCTAGAAGGACTAGTAGATGAACGAGTGGGCTCA</p>

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GCTGAGCAACGACTTGGAAAGCCGACTCTTCTACTACCTCAACTCTGCCAGCCTCAC
TCTCTCCAAGGGGCACCATAGAAGTGGGAAGAAATCTAGAGCCTGGGTACCTGGGCA
GCAGTGGCAAGTGATGTGATGAGGCTCAGAAAGGAGTGATCTGTGGGAGCACTATC
CTCAGGCTCTCTGTGTACAGCTTAACCTCAAACCCACAGGGGCTGACCTGTGGAA
GAGCATCTTGGTGAATCTGGAACCTGCGCCAGCGCTGGAGGAGTCCATCTGCATCA
ATGACTGCTACGGGAGCAACTGGAACACCGGCTGACCTCTACTGCTGTTGAAGGGG
ATCCACTTCTAACTTCTACAGTCAGGGCTGGAGTCCATACCTCAGCTCTGCAATGAG
AACAGAGTCTCAGGAAGAAAATCGAAGACTTCAGGCTCACTGAGTCATGTTTCCA
GAGGTCACTCCAGGAAACAGAAAGCCTGAGGGAGGCTGTGCTGTCTCTCGATCCCA
CCTTCAAGAGCTGGAAAGGAGCTGGAGCACCAGAAGGTGGAAGGAGCAGCACTTTG
GAAGACTTGAAGGAGAAGCAGCAAGAGGTCTTGCAATTCAGGGAGGAACTCTTTCC
TCCAGGAAAACGACTCCAGACTGCAGCACAAGCTGGTCTCTGTCAGCAACAGTGGA
AGAGAAACAGCAGCTCTTTGAGTCCCTCAGTCAGAGCTACAAATCTACAGGCACTT
TATGGCAATTCCAAGAGGGGCTGAAAGCTTACAGCCTGGATGCTGTGCTGACCAATCC
CTTTGAGCAGTGACCTGAGCCACTGGTGGCAGAGGTACAAGCTCTGAGAGGGCAGCT

	GGAGCAGAGCATTAGGGGAACAATTGTCTGCGACTGCAGCTGCAACAGCAGCTGGAG AGCGGTGCTGGCAAAGCCAGCCTCAGCCCTCCTCCATTAAACAGAACTTCCAGCCA GACTGACCCTGGAAACAAGCAGCTGCTCCTCAAGGTTAGCTGTGTCCCTCCAGT CCGGGATGTTGGTATGAATCCCCAGCTCTGGTCTTCCCAGCTCTGCTTCTCTACT CCTGGCTCAGATTAGTTGTGTGTCATTTCTTTTCAGGCTTGGGTTTGGATCTT CTCCAGTAATGAAGACCCCTCCCAAGCTAGAGGGTGATGCTACTGATGGCTCCTTTGC CAATAAGCATGGCCGCATGTCATTGGCCACATTGATGACTACAGTGCCTTAAGACAG CAGATTGCGGAGGGCAAGCTGCTGGTCAAAAAGATAGTGTCTCTTGTGAGTACAGCT GCAGCTTCCCTGGCCTTGAAGCCCAAGGCACAGAGGGCAGCAAAGGCATTATGAGCT TCGGAGCAGCACCAGTGCCTTGCACCATGCCCTAGAGGAGTCCGCTTCCCTCTCACC ATGTTCTGGAGAGCGGCTTCCAAGCACCACATCCCTGTGTGCTGGCAAACAGG GAGAATCAACAGAAAGGGAACCTTCTGGAAGTGAAGAACCAAGTATCCAAACAGGAGCA GCTCCTTACAGACCAACTGAGCATCTGAAGAACGCCAACCAAGAGAGCATG GAACAGTTCATTGTGAGCGTAACAGAACACATGATGTTTTAAAGAAGGCAAGGACTA ACTTAGAGGTGAATCCCTAAGGGCTCTGCGGTGTACTCCAGCCTTGTGACCCCTTGCC TTCCAGGAACCATGCAAGAAGCGCAGCCACCAGAAGTCTTAAACAGCAGGAAAGGT GAGCCTGTCCCTTTTGTGAGCTACCTATCTGCTGAGGAGCATCTGGGCTCATTCT CTCCAAGT		
	ORF Start: ATG at 155	ORF Stop: TGA at 6950	
	SEQ ID NO: 296	2265 aa	MW at 255081.5kD
NOV103c, CG59773-03 Protein Sequence	MRPAGRTSTSGDVENLNSQNEABLRQFEERQQETEHVYELLENKIQLLQESRLAK NEAARMAALVEAEKCNLESEKLKGVTKNWEDVPGDQVKPDQYTETLAQRDKRIEEL NQSLAAQERLVEQLSREKQQLLHLEPTSMVEQPMTEELLKQKQLNSHETTITQSV SDSHLAELQEKIQTEATNKILQELKNEMSYELKCAQESSQKQDGTIQNLKLTLSKRE RETEELYQVIEGQNDTMAKLREMLHQSOLGQLQSSEGTSPAQQQVALDLQSLFCSQ LEIQKLQVRVVRQKERQLADAKQCVQFVEAAHSESEQQKEASWKHNQELRKLQQLQEE LQNSQQLRAWAEKYNEIRTQEQNIQHLNHSLSHKEQLLQEFRELLQYRDNDSKLTLE ANEMLLEKLQRIRHDKAVALERAIDEKFSALEEKEKELRQLRLAVRERDHDLRLRDV LSSNEATMQSMESLLRAKGLVEQLSTTCQNLQWLKEEMETKFSRWQKEQESIQQQLQ TSLHNRNKEVEDLSATLLCKLPGQSEIAEELCQRLQRKERMQLDLSDRNKQVLEHE MEIQGLLQSVSTREQESQAAAEKLVQALMERNSELQALRQYLGRDLSMSQAPISNQQ AEVTPTRGLGKQTDQGSQMPIPSRDDSTSLTAKEDVSI PRSTLGDLDTVAGLEKELSNA KEEELMAKKERESQMSLSALQSMMAVQEEELQVQAADMESLTRNIQKEDLTKDLQM QLVDPEDIPAMERLTQEVLLREKVASVESQGEISGNRRQQQLLMLLEGLVDESRNL NEALQAERQLYSSLVKFHAHPESSEDRDRLQVELEGAQVLRSLBEVLGRSLERLNL ETLAAIGGAAAGDDTSTSTFTDSIEEEAAHSHQQLVKVALEKSLATVETQNPFSFS PPSPMGDSNRCLQEENHLRAEIQHLEEKRAEEELKELKQAEIIEAGFSSVSHIRN TMSLCLENAELKEQMETSDGWEIEEDKEKEGVMVETVVTKEGLSESSLQAEFRKL QGKLNANHNIINLLKEQLVLSSEKGNKSLTPELLVHLTSTIERINTELVGSPGKHQHQ EEGNVTVRPFPRPQSLDLGATFTVDAHQQLDNQSQPRDPGPQPAFSLPGSTQHLRSQ SQCKQRYQDLQEKLLSEATVFAQANELEKYRVMLESIVKQDSKQIQVDFQDLGYET CGRSENEAEREETTSPECEEHNSLKEMVLMEGLCSEQGRRGSTLASSERKPLENLG KQEEFRVYKSENILVLRKDIEDLKAQLQANKVIQNLKSRVRSLSVTSYSSSLERP RKLRAVGTLEGSSPHSVPDEDEGWLSDGTGAFYSPGLQAKKDLESILQVRSQLEAQLP ENGLEEKLAEEELRSASWPGKYDSLQDQARELSYLQKIREGRGICYLITQHKADTVK SFEDLLRSNDIDYILGQSFRQLAQGSQTERLTSKLSTEDHKSEKQAGLEPLALRL SRELQEKKEVIEVLQAKLDARSLTPSSSRALSDSHRSPSSTSFLSDELEACSDMDIVS EYTHYEEKKASPSHSGSSASQGAESNSNPISLPTPQNTPKKANQAHSGFHFHSIPK LASLPQAPLPSPSSFLPFPPTGPPPLGCCETPEVSLAESQELQMLQKLGESSTVP PASTATLLSNDLEADSSYYLNSAQPHSPPRGTIELGRILEPGYLGSSGKVDVMRPQKG SVSGDLSSGSSVYQLNSKPTGADLLEEHLGEIWNLRQRLEESICTINDCLREQLEHRLT STARGRGSTSNFYSGLESIPQLCNENRVLREENRRLQALSHVSRGHSQETESLREA LLSSRSHLQELEKELEHQKVERQQLLEDLREKQEQEVLHFRERLSLQENDSRSLQHLV LLQQQCEEKQQLFESLQSELQIYEALYGNKKGLKAYSIDACHQIPLSSDLHLVAEV QALRGQLEQSIQGNNCRLRLQLQQLESAGAGKASLSPSSINQNPASTDPGNKQLLLQG SAVSPVVRDVGMPALVFPSSASSTPGSDSVVLSFSFSGGLGLDTPVMKTPPKLEGD ATDGSFANKHGRHVIGHIDDYSALRQQAIEGKLLVKKIVSLVRSACSFPGLEAQGTG SKGIHELRSSTALHHALESASLLTMFWRAALPSTHIPVLPKGQGESTERELLELRT KVSKEQLLQSTTEHLKNANQKESMEQFIVSVTRTHDVLKARTNLEVKSLRALPCT PAL		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 103B.

Table 103B. Comparison of NOV103a against NOV103b through NOV103c.		
Protein Sequence	NOV103a Residues/ Match Residues	Identities/ Similarities for the Matched Region

NOV103b	365..2196 202..2016	1510/1834 (82%) 1518/1834 (82%)
NOV103c	365..2196 140..1954	1510/1834 (82%) 1518/1834 (82%)

Further analysis of the NOV103a protein yielded the following properties shown in Table 103C.

Table 103C. Protein Sequence Properties NOV103a	
PSort analysis:	0.5855 probability located in mitochondrial matrix space; 0.4200 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.2957 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 39 and 40

A search of the NOV103a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 103D.

Table 103D. Geneseq Results for NOV103a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV103a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY71159	Human phosphodiesterase interacting protein, myomegalin - Homo sapiens, 2517 aa. [WO200027861-A1, 18-MAY-2000]	1..2196 1..2204	2193/2204 (99%) 2193/2204 (99%)	0.0
AAM40183	Human polypeptide SEQ ID NO 3328 - Homo sapiens, 1883 aa. [WO200153312-A1, 26-JUL-2001]	635..2196 1..1570	1557/1570 (99%) 1559/1570 (99%)	0.0
AAY71158	Rat phosphodiesterase interacting protein, myomegalin - Rattus sp, 2326 aa. [WO200027861-A1, 18-MAY-2000]	365..2197 202..2017	1433/1837 (78%) 1572/1837 (85%)	0.0
AAY67600	Human adipose tissue protein #3 - Homo sapiens, 944 aa. [JP2000037190-A, 08-FEB-2000]	1..934 1..934	925/934 (99%) 927/934 (99%)	0.0
AAU01768				0.0

	sapiens, 934 aa. [WO200123546-A1, 05-APR-2001]	197..934	733/738 (98%)	
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In a BLAST search of public sequence databases, the NOV103a protein was found to have homology to the proteins shown in the BLASTP data in Table 103E.

Table 103E. Public BLASTP Results for NOV103a				
Protein Accession Number	Protein/Organism/Length	NOV103a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O75042	KIAA0454 PROTEIN - Homo sapiens (Human), 1882 aa (fragment).	636..2196 1..1569	1558/1569 (99%) 1558/1569 (99%)	0.0
Q9WUJ3	MYOMEGALIN - Rattus norvegicus (Rat), 2324 aa.	365..2197 202..2015	1444/1838 (78%) 1581/1838 (85%)	0.0
O75065	KIAA0477 PROTEIN - Homo sapiens (Human), 1132 aa.	1..1132 1..1132	1132/1132 (100%) 1132/1132 (100%)	0.0
Q25893	LIVER STAGE ANTIGEN - Plasmodium falciparum (isolate NF54), 1909 aa.	356..1459 605..1651	243/1129 (21%) 488/1129 (42%)	4e-35
Q13439	Golgi autoantigen, golgin subfamily A 4 (Trans-Golgi p230) (256 kDa golgin) (Golgin-245) (72.1 protein) - Homo sapiens (Human), 2230 aa.	229..1749 267..1814	349/1638 (21%) 679/1638 (41%)	4e-34

PFam analysis predicts that the NOV103a protein contains the domains shown in the Table 103F.

Table 103F. Domain Analysis of NOV103a			
Pfam Domain	NOV103a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Somatomedin_B: domain 1 of 1	150..189	14/47 (30%) 25/47 (53%)	7.6
recA: domain 1 of 1	621..650	8/30 (27%) 22/30 (73%)	8.1
Ribosomal_L10: domain 1 of 1	604..695	20/109 (18%) 59/109 (54%)	9.9
Dishevelled: domain 1 of 1	844..914	19/74 (26%) 37/74 (50%)	2.7
Transposase_22: domain 1 of 1	1135..1416	71/376 (19%) 127/376 (34%)	4.6
Phe_tRNA-synt_N: domain 1 of 1	2079..2152	13/79 (16%) 49/79 (62%)	4.9

Example 104.

The NOV104 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 104A.

Table 104A. NOV104 Sequence Analysis			
	SEQ ID NO: 297	736 bp	
NOV104a, CG57460-01 DNA Sequence	AAAGCACCCGAGATGACCCCGGCTCCTCCACCAGGAGCGCGGCCGGCGCGCGTCCC TAGCGGGCTTCGCCGGGGTGGCGTCTCTGGGGCTGGGGACCCCGCGCGCGCTGA CCCGCGCCCTCTGCCCCAGCGCTGTGCTTCGCCGTGAGCCGCTCGCTGCTGTGACG TGCTGGTGCCGGCCGCGTGTCTGGGCTGCGCTACTACTACAGCCGAAGGTGATCC GCGCTACCTGGAGTGGCGCTGCACACGGACATGGCGGACATCGAGCAGTACTACAT GAAGCCGCCCGGTGTGTCCCTGACCGCCCTATCCCTGCAGGCTCCTGCTTCTGGGTG GCCGTGCTGGATGGCAACGTGGTGGGCATTGTGGCTGCACGGGCCACGAGGAGGACA ACACGGTGGAGCTGCTGCGGATGTCTGTGGACTCACGTTTCCGAGGCAAGGGCATCGC CAAGGCGCTGGGCCGGAAGGTGCTGGAGTTTCGCCGTGGTGACAACACTACTCCGCGGTG GTGCTGGGCACGACGGCCGTCAAGGTGGCCGCCACAAGCTCTACGAGTCGCTGGGCT TCAGACACATGGGCGCCAGTGACCACTACGTGCTGCCGGGCATGACCCTCTCGCTGGC TGAGCGCCTCTTCTTCAGGTCCGCTACCACCGCTACCGCCTGCAGCTGCGCGAGGAG <u>TGACCGCGCGCGCTCGCCCGCCCGCCCCCGGCGGCCCT</u>		
	ORF Start: ATG at 13	ORF Stop: TGA at 697	
	SEQ ID NO: 298	228 aa	MW at 24767.5kD
NOV104a, CG57460-01 Protein Sequence	MTPAPPPGARPGAASLAGFAGVASLPGDPRRAADPRPLPPALCFAVSRSLLTCLV AALLGLRYYYSRKVIRAYLECALHTDMADIEQYMKPPGVSLTALSPAGSCFWAVLD GNVVGIVAAARAEEDNTVELLRMSVDSRFRGKGIKALGRKVLFAVHHNYSAVVLGT TAVKVAAHKLYESLGRHMGASDHVYVLPMTLSLAERLFFQVRYHRYRLQLREE		

Further analysis of the NOV104a protein yielded the following properties shown in Table 104B.

Table 104B. Protein Sequence Properties NOV104a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 64 and 65

A search of the NOV104a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 104C.

Table 104C. Geneseq Results for NOV104a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV104a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB19986	Human camello 3 (Hcm13) protein (partial) - Homo sapiens, 144 aa. [WO200077024-A1, 21-DEC-2000]	42..195 1..144	144/154 (93%) 144/154 (93%)	7e-76
AAB19985	Human camello 2 (Hcm12) protein - Homo sapiens, 227 aa. [WO200077024-A1, 21-DEC-2000]	47..200 56..203	63/158 (39%) 92/158 (57%)	1e-21
AAB19984	Human camello 1 (Hcm11) protein - Homo sapiens, 227 aa. [WO200077024-A1, 21-DEC-2000]	41..196 50..199	60/160 (37%) 88/160 (54%)	7e-20
AAY57959	Human TSC501 protein SEQ ID NO:1 - Homo sapiens, 227 aa. [JP11332579-A, 07-DEC-1999]	41..196 50..199	59/160 (36%) 87/160 (53%)	4e-19
AAB19987	Mouse camello 1 (Mcm11) protein - Mus sp, 222 aa. [WO200077024-A1, 21-DEC-2000]	41..194 50..197	63/158 (39%) 87/158 (54%)	1e-18

In a BLAST search of public sequence databases, the NOV104a protein was found to have homology to the proteins shown in the BLASTP data in Table 104D.

Table 104D. Public BLASTP Results for NOV104a				
	Protein/Organism/Length			

Accession Number		Residues/ Match Residues	Similarities for the Matched Portion	Value
Q9UHF3	PUTATIVE N- ACETYLTRANSFERASE CAMELLO 2 - Homo sapiens (Human), 227 aa.	47..200 56..203	63/158 (39%) 92/158 (57%)	5e-21
Q9UHE5	PUTATIVE N- ACETYLTRANSFERASE CML1 - Homo sapiens (Human), 227 aa.	41..196 50..199	60/160 (37%) 88/160 (54%)	3e-19
Q9UQ17	GLA PROTEIN - Homo sapiens (Human), 227 aa.	41..196 50..199	60/160 (37%) 88/160 (54%)	3e-19
Q96QI8	KIDNEY-AND LIVER-SPECIFIC GENE - Homo sapiens (Human), 227 aa.	41..196 50..199	59/160 (36%) 87/160 (53%)	1e-18
O75839	TSC501 PROTEIN - Homo sapiens (Human), 227 aa.	41..196 50..199	59/160 (36%) 87/160 (53%)	1e-18

Pfam analysis predicts that the NOV104a protein contains the domains shown in the Table 104E.

Table 104E. Domain Analysis of NOV104a			
Pfam Domain	NOV104a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Acetyltransf: domain 1 of 1	111..191	28/82 (34%) 64/82 (78%)	2.2e-17

Example 105.

The NOV105 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 105A.

Table 105A. NOV105 Sequence Analysis		
	SEQ ID NO: 299	1230 bp
NOV105a, CG57464-01 DNA Sequence	CTTCCCGCGGGCTGCGCGATGGACAGCCCCGAGGTGACCTTCACTCTCGCCTATCTGG TGTTGCGCGTGTGCTTCGTGTTCACGCCCAACGAGTTCCACGCGGCGGGGCTCACGGT GCAGAACCTGTGTCGGGCTGGCTGGGCGAGGACGCCGCTTCGTGCCCTTCCAC TTGCGCCGACGCGCGCCACGCTGTGTGCCACTCGCTGCTGCCGCTCGGTGAGGCTG CTCGGGCGGCGCGCCGCATCCTCTCCTGCGCAGGGCTTGCTGGGAGGTACAGGAGAG GCCTCCGCGCAGCTCCCCGAGGCCCGAAAGCGCCTGGGCGCAGCTGGGAGAGGCGCC GGTCCTCATCCAGAGGGACCGCGCGTGGGCTGAGCGCGCTTAGGGGTGCCGCGCGCC TGGCCTGGCGGCTCTTCTCTGCTGCTGGCCGTGACCCCTCCCCTCCATCGCCTGCATCCT GATCTACTACTGGTCCCGTGACCGGTGGGCTGCCACCCACTGGCGGCACCTGGCC CTCTACGCCCTCCACAGTCTGGCTGGCAGGCTGTTCCTCTCTGTCAACACTGAGT TCCGCGGATTGACAAGTTTGCCACGGTGACACAGGTGCCCGTGTGATTGTGACAGA CACGTGGGTGATGAAGTAACCACTACCGAGTGACAGTGGCCAGCAGCAGGACGTG	

	CACCTGACTGTGACGGAGTCTCGGCAGCATGAGCTCTCGCCAGACTCGAACTTGCCCG TGCAGCTCCTCACCATCCGTGTGGCCAGCACCAACCCTGCTGTGCAGGCTTTGACAT CAGGCTGAACCTCACTGAGTACGGGAGCTCTGCGAGAAGCTCCGGGACCCATCCGC AGGGCAGCCCATGTGGTCATCCACCAGAGCTGGGCGACCTGTTCTTGAGACATTG CCTCCCTGGTAGAGGTCAACCCGGCCTACTCAGTGCCAGCAGCCAGGTGGGGGGCCT GGAGGCCTGCATAGGCTGCATGCAGACACGTGCCAGCGTGAAGCTGGTGAAGACCTGC CAGGAGGCAGCCACAGGCGAGTGCCAGCAGTGTACTGCCGCCCATGTGGTGCCTCA CCTGCATGGGCAAGTGGTTCGCCAGCCGAGGACCCCTGCGCCCTGACACCTGGCT GGCCAGCCGCGTCCCTGCCCACTGCCGCGCAGCTTCTGCATCCTGGATGTGTGC ACCGTGCGCTGA		
	ORF Start: ATG at 19	ORF Stop: TGA at 1228	
	SEQ ID NO: 300	403 aa	MW at 44585.0kD
NOV105a, CG57464-01 Protein Sequence	MDSPEVTFLLAYLVFVFCVFTPNEFHAAGLTVQNLLSGWLGSDDAFVPPHLLRTAA TLLCHSLPLGEAARAGRPHPLRRACWEVRRRPPAPRGPESAWAQLGRGAGPHPEG PRRGLSALRGAAGLAWRLFLLLAVTLPSIACILIIYWSRDRWACHPLARTLALYALPQ SGWQAVASSVNTFEFRIDKFATGAPGARVIVTDTWVMKVTTYRVHVAQQQDVHLTVTE SRQHELSPDSNLPVQLLTIRVASTNPAVQAFDIRLNSTEYGEKELRAPIRRAHV IHQSLGDLFLETFASLVEVNPAYSVPSQVGGLEACIGCMQTRASVKLVKTCQEAATG ECQQCYCRPMWCLTCMGKWFASRDPLRPDTWLASRVPCPTRARFCILDVCTVR		

Further analysis of the NOV105a protein yielded the following properties shown in Table 105B.

Table 105B. Protein Sequence Properties NOV105a	
PSort analysis:	0.6760 probability located in plasma membrane; 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	Likely cleavage site between residues 29 and 30

A search of the NOV105a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 105C.

Table 105C. Geneseq Results for NOV105a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV105a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG81377	Human AFP protein sequence SEQ ID NO:272 - Homo sapiens, 362 aa. [WO200129221-A2, 26-APR-2001]	1..403 1..362	344/409 (84%) 345/409 (84%)	0.0

In a BLAST search of public sequence databases, the NOV105a protein was found to have homology to the proteins shown in the BLASTP data in Table 105D.

Table 105D. Public BLASTP Results for NOV105a				
Protein Accession Number	Protein/Organism/Length	NOV105a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC38627	SEQUENCE 271 FROM PATENT WO0129221 - Homo sapiens (Human), 362 aa.	1..403 1..362	345/409 (84%) 346/409 (84%)	0.0
Q9DCF3	0610039G24RIK PROTEIN - Mus musculus (Mouse), 362 aa.	1..403 1..362	311/403 (77%) 328/403 (81%)	e-176
Q96GP5	SIMILAR TO RIKEN CDNA 0610039G24 GENE - Homo sapiens (Human), 232 aa.	1..265 1..226	211/271 (77%) 212/271 (77%)	e-109
Q9VN16	CG14646 PROTEIN - Drosophila melanogaster (Fruit fly), 409 aa.	1..399 1..383	123/409 (30%) 202/409 (49%)	1e-55
Q95TM4	LD39811P - Drosophila melanogaster (Fruit fly), 393 aa.	20..399 4..367	117/390 (30%) 192/390 (49%)	1e-51

PFam analysis predicts that the NOV105a protein contains the domains shown in the Table 105E.

Table 105E. Domain Analysis of NOV105a			
Pfam Domain	NOV105a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 106.

The NOV106 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 106A.

Table 106A. NOV106 Sequence Analysis		
	SEQ ID NO: 301	1136 bp
NOV106a, CG57466-01 DNA Sequence	TTTCTGCAATGGGAGCCTCCGCCACCCACCCCTGGAGCCACAGAAGGCCAGAAAGCCAA ATGGACAGCTGGTGAACCCCAACAACTTCTGGAAGAACCCGAAAGATGTGTGCGCCCA CGCCCATGGCCTCTCAGGGCCAGGCCCTGGGACGTGACCACTAACTGCTCAGCCA ATATCAACTTGACCCACAGCCCTGGTTCCAGTCTCTGGAGCCGAGTCCGGCAGTT TCTCTTCTACGCCCACTGCCGCTACTTCCCCATGCTGCTGAACCAACCGGAGAAGTGC AGGGGCGATGTCTACCTGCTGGTGGTTGTCAAGTCGGTCATCACGCAGCAGCAGCGCC GCGAGGCCATCCGCCAGACCTGGGCGGAGCGGCAGTCCGCGGGTGGGGGCCGAGCGC CGTGCGCACCTCTTCTGCTGGGCACGGCCTCCAAGCAGGAGGAGCGCAGCACTAC CAGCAGCTGTGGCCTACGAAGACGCCCTCTACGGCGACATCCTGCAGTGGGGCTTTC TCGACACCTTCTTCAACCTGACCCTCAAGGAGATCCACTTCTCAAGTGGCTGGACAT CTACTGCCCCCAGTCCCCTTCATTTTCAAAGCGCAGATGACGTCTTCGTCAACCCC ACCAACTGTAGAAATTTCTGGCTGACCGGCAGCCACAGGAAAACCTGTTCTGTTGGGCG	

	ATGTCCTGCAGCAGCTCGGCCCATTCGCAGGAAGACAACAATACTACATCCCGGG GGCCCTGTACGGCAAGCCAGCTATCCGCCGTATGCAGGCGGCGGTGGCTTCTCATG GCCGGCAGCCTGGCCCGCGCTGCACCATGCCTGCGACACCCTGGAGCTCTACCCGA TCGACGACGTCTTCTGGGCATGTGCCTGGAGGTGCTGGGCGTGCAGCCACGGCCCA CGAGGGCTTCAAGACTTTCGGCATCTCCCGGAACCGCAACAGCCGCATGAACAAGGAG CCGTGCTTTTTCGCGCCATGCTCGTGGTGCACAAGCTGCTGCCCTGAGCTGCTCG CCATGTGGGGGTGGTGCACAGCAATCTCACCTGCTCCGCAAGCTCCAGGTGCTCTG <u>ACCCAGCCGGGCTACTAGGACAGGCCAGGGCAC</u>		
	ORF Start: ATG at 9	ORF Stop: TGA at 1101	
	SEQ ID NO: 302	364 aa	MW at 41853.8kD
NOV106a, CG57466-01 Protein Sequence	MGASATHPGATEGPEAKWTAGEPQQLLEPERCVRPRPWPLRAQAWDVTTNCSANIN LTHQPFQVLEPQFRQFLFYRHCYFPMLLNHPEKCRGDVYLLVVVKSUITQHDRREA IRQTWARAAVRGWGPSAVRTLFLLGTASKQEERTHYQQLLAYEDALYGDILQWGLDT FPNLTLEIHFLLKWLDIYCPHVPFIFKGGDDVFVNPTNLLEFLADRQPQENLFVGDVL QHARPIRRKDNKYIIPGALYGKASYPPYAGGGGFLMAGSLARRLHHACDTLELYPIDD VFLGMCLEVLGVQPTAHEGFKTFGISRNRNRSRMNKEPCFFRAMLVVHKLLPPELLAMW GLVHSNLTCSRKLQVL		

Further analysis of the NOV106a protein yielded the following properties shown in Table 106B.

Table 106B. Protein Sequence Properties NOV106a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.4500 probability located in cytoplasm; 0.3122 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV106a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 106C.

Table 106C. Geneseq Results for NOV106a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV106a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB24035	Human PRO4397 protein sequence SEQ ID NO:42 - Homo sapiens, 402 aa. [WO200053750-A1, 14-SEP-2000]	72..352 84..380	149/300 (49%) 191/300 (63%)	4e-76
AAU29167	Human PRO polypeptide sequence #144 - Homo sapiens, 372 aa. [WO200168848-A2, 20-SEP-2001]	26..363 27..371	149/348 (42%) 207/348 (58%)	9e-76
AAB88404	Human membrane or secretory protein clone PSEC0159 - Homo	26..363 27..371	149/348 (42%) 207/348 (58%)	9e-76

	JAN-2001]			
AAB49750	Human beta 1,3-N-acetylglucosamine transferase protein G4 - Homo sapiens, 372 aa. [WO200100848-A1, 04-JAN-2001]	26..363 27..371	149/348 (42%) 207/348 (58%)	9e-76
AAB49749	Human beta 1,3-N-acetylglucosamine transferase protein G4 - Homo sapiens, 372 aa. [WO200100848-A1, 04-JAN-2001]	26..363 27..371	149/348 (42%) 207/348 (58%)	9e-76

In a BLAST search of public sequence databases, the NOV106a protein was found to have homology to the proteins shown in the BLASTP data in Table 106D.

Table 106D. Public BLASTP Results for NOV106a				
Protein Accession Number	Protein/Organism/Length	NOV106a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL32295	BETA-3-GALACTOSYLTRANSFERASE - Brachydanio rerio (Zebrafish) (Zebra danio), 418 aa.	46..364 101..417	199/319 (62%) 249/319 (77%)	e-121
AAL32297	BETA-3-GALACTOSYLTRANSFERASE - Brachydanio rerio (Zebrafish) (Zebra danio), 412 aa.	29..360 82..409	180/337 (53%) 244/337 (71%)	e-104
Q96EK0	UNKNOWN (PROTEIN FOR MGC:20513) - Homo sapiens (Human), 377 aa.	60..352 46..355	152/313 (48%) 198/313 (62%)	9e-76
CAC39768	SEQUENCE 175 FROM PATENT EP1067182 - Homo sapiens (Human), 372 aa.	26..363 27..371	149/348 (42%) 207/348 (58%)	3e-75
Q9C0J2	BETA-1,3-N-ACETYLGLUCOSAMINYLTRANSFERASE BGNT-3 - Homo sapiens (Human), 372 aa.	26..363 27..371	149/348 (42%) 207/348 (58%)	3e-75

PFam analysis predicts that the NOV106a protein contains the domains shown in the Table 106E.

Table 106E. Domain Analysis of NOV106a			
Pfam Domain	NOV106a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PI3_PI4_kinase: domain 1 of 1	195..205	8/12 (67%) 10/12 (83%)	8.5
Galactosyl_T: domain 1 of 1	112..308	69/212 (33%) 148/212 (70%)	7.7e-45

Example 107.

The NOV107 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 107A.

Table 107A. NOV107 Sequence Analysis		
	SEQ ID NO: 303	4091 bp
NOV107a, CG57468-01 DNA Sequence	AAGCAAGAGGCTGAGATGGATCTTGAGGCGGCAAAGAACGGAACAGCCTGGCGCCCCA CGAGCGCGGAGGCGGACTTTGAACTGGGCATCAGCAGCAAACAAAAAGGAAAAAAC GAAGACAGTGAAAATGATTGGAGATTAACATTGTTTCGATACTCCGATTGGCAGGAT AAATTGTTTATGTCGCTGGGTACCATCATGGCCATAGCTCAGGATCAGGTTCTCCCC TCATGATGATAGTATTGGAGAGATGACTGACAAATTTGTTGATACTGCAGGAAACTT CTCCTTTCCAGTGAACCTTTCTCTTGTGCTGCTAAATCCAGGCAAATTTCTGGAAGAA GAAATGACTAGATATGCATATTACTACTCAGGATTGGGTGCTGGAGTTCTTGTGTGCTG CCTATATACAAGTTTCATTTTGGACTTTGGCAGCTGGTCGACAGATCAGGAAATTAG GCAGAAGTTTTTCATGCTATTCTACGACAGGAAATAGGATGGTTTGACATCAATGAC ACCACTGAACTCAATACGCGCTAACAGATGACATCTCCAAATCAGTGAAGGAATTG GTGACAAGGTTGGAATGTTCTTTCAAGCAGTAGCCACGTTTTTTGCGAGATTTCATAGT GGGATTCATCAGAGGATGGAAGCTCACCTTGTGATAATGGCCATCAGCCCTATTCTA GGACTCTCTGCAGCCGTTTGGGCAAAGATACTCTCGGCATTTAGTGACAAAGAACTAG CTGCTTATGCAAAGCAGGCGCCGTCGCGAGAGAGGCTCTGGGGGCCATCAGGACTGT GATAGCTTTCTGGGGCCAGAACAAAGAGCTGGAAGGTATCAGAAACATTAGAAAAAT GCCAAAGAGATTGGAATTAAGAAAGCTATTTCAGCAAACTTCCATGGGTATTGGCT TCCTGTTAATATATGCATCATATGCACTGGCCTTCTGGTATGGATCCACTCTAGTCAT ATCAAAAGAATATACTATTGGAATGCAATGACAGTTTTTTTTCAATCCTAATTGGA GCTATGGCTCGGAGAAACGCTCGTTTTGGCTCCTGAATATCCAAAGCCAAATCGG GGGCTGCGCATCTGTTTGCCTTGTGGAAGAAACCAATATAGACAGCCGAGTCA AGAAGGGAAAAAGCCAGTAAGCGACACATGTGAAGGGAATTTAGAGTTTCGAGAAGTC TCTTTCTTCTATCCATGTGCGCCAGATGTTTTTCATCCTCCGTGGCTTATCCCTCAGTA TTGAGCGAGGAAGACAGTAGCATTGTGTTGGGAGCAGCGCTGTGGGAAAGCACTTC TGTTCAACTTCTGCAGAGACTTTATGACCCCGTGCAAGGACAAGTGGATGGTGTGGAT GCAAAGAAATTGAATGTACAGTGGCTCCGTTCCCAAATAGCAATCGTTCTCAAGAGC CTGTGCTCTTCACTGCAGCATTGCTGAGAACATCGCCTATGGTGACAAACGCCGTGT GGTGCCATTAGATGAGATCAAAGAAGCCGAAATGCAGCAAAATCCATTCTTTTATT GAAGGTCTCCCTGAGAAATACACACACAAGTTGGACTGAAAGGAGCAGAGCTTTCTG GCGGCCAGAAACAAAGACTAGCTATTGCAAGGGCTCTTCTCAAAAACCCAAATTTT ATTGTTGGATGAGGCCACTTCAGCCCTCGATAATGACAGTGAATGCGAGGTGGTTCAG CATGCCCTTGATAAAGCCAGGACGGGAAGGACATGCCTAGTGGTCACTCACAGGCTCT CTGCAATTGAGAACGCAGATTGTAGTGGTTCTGCACAAATGGAAGATAAGGAACA AGGAACTCATCAAGAGCTCTGAGAAATCGAGACATATATTTAAGTTAGTGAATGCA CAGTCAGCGAGCAAAGGTCGACTACAATCGTGGTAGCACACAGCATTTCTACTATT GAAGTGCAAGTTGATTGTGACCTAAAGGATGGAATGCTGGCGGAGAAAGGAGCACA TGCTGAACATAATGGCAAACAGGCTATATTATCACTTGTGATGTACAGGTAATG CTTATGGGACTCTTTAGACTGTGGTAATAGTCTTCTGAAGTCTCTCTATTAAAAA TTTTAAAGTTAAACAAGCCTGAATGGCCTTTGTGGTTCTGGGGACATTTCTGTCTGT TCTAAATGGAAGTTCATCCAGTATTTCCATCATCTTGCAAAATTTATAACCGTA ATGTTTGGAATAATGATCTTTGTTTTCTCCTCAAAATTTTTTATATTCTTCTTT	

	<p>TGTTTTCTCAACAAGGTTTCAGCGTAGATTTTGTGTTGCTTTTCAGGGATT ATTTTACGGCAGAGCAGGGGAAATTTTAACGATGAGATTAAGACACTTGGCCTTCAA GCCATGTTATATCAGGATATTGCCTGGTTTGATGAAAAGGAAACAGCACAGGAGGCT TGACAACAATATTAGCCATAGATATAGCACAATTCAGGAGCAACAGGTTCCAGGAT TGGCGTCTTAAACACAAATGCAACTAACATGGGACTTTTCAGTTATCATTTCCTTTATA TATGGATGGGAGATGACATTCCTGATTCTGAGTATTGCTCCAGTACTTGGCGTGACAG GAATGATTGAAACCGCAGCAATGACTGGATTGCGCAACAAAGATAAGCAAGAAGCTTAA GCATGCTGGAAAGGTAAAGATAGCAACTGAAGCTTTGGAGAAATATACGTACTATAGTG TCATTAACAAGGGAAAAAGCCCTTCGAGCAAATGTATGAAGAGATGCTTCAGACTCAAC ACAGGAGAAATACCTCGAAGAAAGCACAGATTATGGAAGCTGTTATGCATTTCAGCCA TGCCTTTATATATTTTGCTATGCGGCAGGTTTCGATTGAGGCTTATTAATTCAA GCTGGACGAATGTCAAATGCTTTATCTTTTGATAGAGTTTACTGCAATTGCATATG GAGCTATGGCCATCGGAGAAACGCTCGTTTGGCTCCTGAATATTCCAAAGCCAAATC GGGGGCTGCGCATCTGTTGCTTGTGGAAAAGAAACCAATATAGCAGCGCGCAGT CAAGAAGGGAAAAAGCCACTTTCACAGGACACATGTGAAGGGAAATTAAGAGTTTCGAG AAGTCTCTTTCTCTATCCATGTGCGCCAGATGTTTTCATCTCCGTGGCTTATCCCT CAGTATTGAGCGGAAAGACAGTAGCATTGTGGGGAGCAGCGCTGGGAAAAGC ACTTCTGTTCAACTTCTGCAGAGACTTTATGACCCCGTCAAGGACAACAGCTGTTTG ATGGTGTGGATGCAAAAGAAATGAATGTACAGTGGCTCCGTTCCCAATAGCAATCGT TCCTCAAGAGCCTGTGCTCTCAACTGCAGCATGTCTGAGAACATCGCCTATGGTGAC AACAGCCGTGTGGTGGCATTAGATGAGATCAAAGAAGCCGCAATGCAGCAAATATCC ATTCTTTTATTGAAGGTCTCCCTAAATACAACACACAAGTTGGACTGAAAGGAGCACA GCTTTCTGGCGGCCAGAAACAAAGACTAGCTATTGCAAGGGCTCTTCTCAAAAACCC AAAATTTTATTGTTGGATGAGGCCACTTCAGCCCTCGATAATGACAGTGAGAAGGTAC AGGTGGTTCAGCATGCCCTTGATAAAGCCAGGACGGGAAGGACGCTAGTGGTCACT TCACAGGCTCTCTGCAATTCAGAACGCAGATTGTATAGTGGTCTGCACAATGGAAG ATAAAGGAACAAGGAATCATCAAGAGCTCCTGAGAAATCGAGACATATATTTAAGT TAGTGAATGCACAGTCAGCGAGCAAGGTGGGACTACAATCGTGTGACACACCGACT TTCTACTATTGGAAGTGCAGATTGATTGTGACCCCTAAAGGATGGAATGCTGGCGGAG AAAGGAGCACATGCTGAACTAATGGCAAACGAGGTCTATATTACTTGTGATGT CACAGGTAATGCTTATGTGACATAATGCTAT</p>		
	ORF Start: ATG at 16 ORF Stop: TGA at 4078		
	SEQ ID NO: 304	1354 aa	MW at 149167.3kD
NOV107a, CG57468-01 Protein Sequence	<p>MDLEAAKNGTAWRPTSAEGDFELGISSKQKRKTKTVKMIGVLTFRYSWDQDKLFMS LGTIMAIAHGSGPLMMIVFGEMTDKFDVTAGNFSFPVNFSLSLNPGKILEEMTRY AYYYSGLGAGVLVAAYIQVSFWTLAAGRQIRKIRQKFFHAILRQEIWFINDTTELN TRLTDDISKISEGIDRVGMFFQAVATFFAGFIVGFIRGWKLTIVIMAIISPILGLSAA VWAKILSAFSDKELAAAYAKAGAVAEALGAIRTVIAFGGQNKELERYQKHLENKEIG IKKALSANISMGI AFLLIYASYALAFWYGSTLVISKEYTIGNAMTVFVSIILGAMAIG ETLVLAPEYSKAKSGAAHLFALLEKKPNIDSRSEQGKKPVSDTCEGNLEFREVSFFYP CRPDVFI LRGLSLSI ERGKTVA FVGSSGCGKSTSVQLLRQLYDPVQGVQVDGDAKELN VQWLRSQLIAI VPQEPVLFNCISIAENIAYGDNRSRVVPLDEIKEAANAANIHSFIEGLPE KYNTQVGLKGAQLSGGQKQLAIARALLQPKILLLDEATSALDNDSEWQVQVHALDK ARTGRTCLVVTTHRLSAIQNADLIVVLHNGKIKEQGTTHQELLNRNDIYFKLVNAQSASK GRTTIVVAHRLSTIRSADLIVTLKDGMLAEKGHAELMAKRGLYSLVMSQVMLMGT SDCGNSLPEVSLKILKLNKPEWPFVVLGTASVLNGTVHPVFSIIFAKIITVMFGNN DLLPFLKIFLYSFLFLFKQGSVDVFLFAFQGLFYGRAGEILTMRLRHLAFKAMLYQ DIAWFDEKENSTGGLTTILADIAIQGATGSRIGVLTQNAATNMGLSVIISFIYGNEM TFLILSIAPVLAVTGMIAETAMTGFANKDKQELKHAGVKIATEALENIRTIVSLTRE KAFEQMYEMLQTHRRNTSKKAQIIIGSCYAFSHAFIYFAYAAGFRFGAYLIQAGRMS NALSFRVFTAIYGAIAGETLVLAPEYSKAKSGAAHLFALLEKKPNIDSRSEQGKK PLSQDTCEGNLEFREVSFFYP CRPDVFI LRGLSLSI ERGKTVA FVGSSGCGKSTSVQL LQRLYDPVQGGQLFDGVDAKELNVQWLRSQLIAI VPQEPVLFNCISIAENIAYGDNRSRV PLDEIKEAANAANIHSFIEGLPKYNTQVGLKGAQLSGGQKQLAIARALLQPKILLL DEATSALDNDSEKVVQVHALDKARTGRTCLVVTTHRLSAIQNADLIVVLHNGKIKEQGT THQELLNRNDIYFKLVNAQSASKGRTTIVVAHRLSTIRSADLIVTLKDGMLAEKGHA ELMAKRGLYSLVMSQVMLM</p>		

Further analysis of the NOV107a protein yielded the following properties shown in Table 107B.

Table 107B. Protein Sequence Properties NOV107a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.3000 probability located in microbody (peroxisome)

SignalP analysis:	No Known Signal Sequence Predicted
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A search of the NOV107a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 107C.

Table 107C. Geneseq Results for NOV107a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV107a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB81064	Cynomologous monkey P-glycoprotein variant 1 - Macaca fascicularis, 1280 aa. [WO200123565-A1, 05-APR-2001]	1..1299 1..1278	750/1312 (57%) 964/1312 (73%)	0.0
AAB81065	Cynomologous monkey P-glycoprotein variant 2 - Macaca fascicularis, 1283 aa. [WO200123565-A1, 05-APR-2001]	1..1299 1..1281	749/1312 (57%) 967/1312 (73%)	0.0
AAB81959	Human MDR1 - Homo sapiens, 1280 aa. [WO200121762-A2, 29-MAR-2001]	1..1299 1..1278	749/1324 (56%) 967/1324 (72%)	0.0
AAY58186	Human wild-type multidrug resistance-1 (MDR-1) protein - Homo sapiens, 1280 aa. [WO9961589-A2, 02-DEC-1999]	1..1299 1..1278	749/1324 (56%) 967/1324 (72%)	0.0
AAW44073	Human multidrug resistance P-glycoprotein MDR1 - Homo sapiens, 1280 aa. [WO9740160-A1, 30-OCT-1997]	1..1299 1..1278	749/1324 (56%) 967/1324 (72%)	0.0

In a BLAST search of public sequence databases, the NOV107a protein was found to have homology to the proteins shown in the BLASTP data in Table 107D.

Table 107D. Public BLASTP Results for NOV107a				
Protein Accession Number	Protein/Organism/Length	NOV107a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P23174	Multidrug resistance protein 3 (P-glycoprotein 3) - <i>Cricetulus griseus</i> (Chinese hamster), 1281 aa.	1..1299 1..1279	818/1303 (62%) 999/1303 (75%)	0.0
P21440	Multidrug resistance protein 2 (P-glycoprotein 2) - <i>Mus musculus</i> (Mouse), 1276 aa.	1..1299 1..1274	823/1306 (63%) 998/1306 (76%)	0.0
Q08201	Multidrug resistance protein 2 (P-glycoprotein 2) - <i>Rattus norvegicus</i> (Rat), 1278 aa.	1..1299 1..1276	823/1309 (62%) 999/1309 (75%)	0.0
CAC37764	SEQUENCE 1 FROM PATENT WO0123565 - <i>Macaca fascicularis</i> (Crab eating macaque) (<i>Cynomolgus</i> monkey), 1280 aa.	1..1299 1..1278	750/1312 (57%) 964/1312 (73%)	0.0
CAC37765	SEQUENCE 3 FROM PATENT WO0123565 - <i>Macaca fascicularis</i> (Crab eating macaque) (<i>Cynomolgus</i> monkey), 1283 aa.	1..1299 1..1281	749/1312 (57%) 967/1312 (73%)	0.0

Pfam analysis predicts that the NOV107a protein contains the domains shown in the Table 107E.

Table 107E. Domain Analysis of NOV107a			
Pfam Domain	NOV107a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ABC_membrane: domain 1 of 2	57..350	115/301 (38%) 252/301 (84%)	3.3e-83
MVIN: domain 1 of 1	57..447	70/531 (13%) 263/531 (50%)	5.8
SAA_proteins: domain 1 of 1	518..524	6/7 (86%) 7/7 (100%)	3
ABC_tran: domain 1 of 2	424..609	76/199 (38%) 150/199 (75%)	3.1e-56
DsbD: domain 1 of 1	722..926		9.6

		126/249 (51%)	
ABC_membrane: domain 2 of 2	722..1008	80/297 (27%) 222/297 (75%)	2.2e-43
ABC_tran: domain 2 of 2	1083..1270	77/202 (38%) 154/202 (76%)	7.1e-54
GidB: domain 1 of 1	1170..1312	29/202 (14%) 97/202 (48%)	6.6

Example 108.

The NOV108 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 108A.

Table 108A. NOV108 Sequence Analysis			
	SEQ ID NO: 305	520 bp	
NOV108a, CG59609-01 DNA Sequence	CCCCGTTCTATCAGCCATGGTCAACCCACCAGGTTCTTAGACATCATCGTGGATGGT GAGCTCTTGGGACGTGTCTCCTTTGAGCTGTTTGCAGACAAGATTCCAAAGACAGCAG AAAATTTTTGTGCTCTAATCATTGGAGAGAAAGGATTTGGTTATAAAGGTTCTTACTT TCACAGAATTGTTCTGGGTTTATGTGTGAGGGTGGTGACTTCACACAGCATAATGGC ACTGGTGGCAAGTCCATCTACGGGAAGAAATTTGATGATGAGAACTTCGTCTTAAATT ATACAGGTCCTGGCATCTTGTCCGTGGAGAATGCTGGACCCAAACAAATGGTTCCCA GTTTTTCATCTGCAC TGCCATGTCTGAGTGGTTGGATGGCATGCAGGTGGTCTTTGGC AAGGGAAGGAAGGTGAGTATTGTGGAAGCCATGGAGTGCTTTGGGTCCACAAATGGCA AGACCAGCAAGAAGATCACCATTGCTGACTGTGGACAACCTCTAAATAGGTTTGACTT		
	ORF Start: ATG at 17	ORF Stop: TAA at 506	
	SEQ ID NO: 306	163 aa	MW at 17734.1kD
NOV108a, CG59609-01 Protein Sequence	MVNPTRFLDIIVDGELLGRVSFELFADKIPKTAENFCALIIGEKGFYKGSYFHRIVE GFMCQGGDFTQHNGTGGKSIYKKFDDENFVLNYTGPGLSVENAGPNTNGSQFFICT AMSEWLDMGMQVVFVGKGRKVSIVEAMECFGSTNGKTSKKITTIADCGQL		

Further analysis of the NOV108a protein yielded the following properties shown in Table 108B.

Table 108B. Protein Sequence Properties NOV108a	
PSort analysis:	0.6400 probability located in microbody (peroxisome); 0.6000 probability located in plasma membrane; 0.4500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV108a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 108C.

Table 108C. Geneseq Results for NOV108a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV108a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU01195	Human cyclophilin A protein - Homo sapiens, 165 aa. [WO200132876-A2, 10-MAY-2001]	1..163 1..164	134/164 (81%) 147/164 (88%)	2e-75
AAW56028	Calcineurin protein - Mammalia, 165 aa. [WO9808956-A2, 05-MAR-1998]	1..163 1..164	134/164 (81%) 147/164 (88%)	2e-75
AAR13726	Bovine cyclophilin - Bos taurus, 163 aa. [US5047512-A, 10-SEP-1991]	2..163 1..163	133/163 (81%) 146/163 (88%)	5e-75
AAG65275	Haematopoietic stem cell proliferation agent related human protein #2 - Homo sapiens, 164 aa. [JP2001163798-A, 19-JUN-2001]	2..163 1..163	133/163 (81%) 146/163 (88%)	9e-75
AAP90431	Cyclophilin - Homo sapiens (human), 164 aa. [EP326067-A, 02-AUG-1989]	2..163 1..163	133/163 (81%) 146/163 (88%)	9e-75

In a BLAST search of public sequence databases, the NOV108a protein was found to have homology to the proteins shown in the BLASTP data in Table 108D.

Table 108D. Public BLASTP Results for NOV108a

Protein Accession Number	Protein/Organism/Length	NOV108a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
CAC39529	SEQUENCE 26 FROM PATENT WO0132876 - Homo sapiens (Human), 165 aa.	1..163 1..164	134/164 (81%) 147/164 (88%)	8e-75
Q9BRU4	PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A) - Homo sapiens (Human), 165 aa.	1..163 1..164	134/164 (81%) 146/164 (88%)	2e-74
P04374	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein) - Bos taurus (Bovine), and, 163 aa.	2..163 1..163	133/163 (81%) 146/163 (88%)	2e-74
P05092	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase)	2..163 1..163	133/163 (81%) 146/163 (88%)	3e-74

	binding protein) - Homo sapiens (Human),, 164 aa.			
Q9TTC6	CYCLOPHILIN 18 - Oryctolagus cuniculus (Rabbit), 164 aa.	1..163 1..164	133/164 (81%) 147/164 (89%)	5e-74

Pfam analysis predicts that the NOV108a protein contains the domains shown in the Table 108E.

Table 108E. Domain Analysis of NOV108a			
Pfam Domain	NOV108a Match Region	Identities/ Similarities for the Matched Region	Expect Value
pro_isomerase: domain 1 of 1	5..163	101/181 (56%) 137/181 (76%)	5.2e-79

Example 109.

The NOV109 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 109A.

Table 109A. NOV109 Sequence Analysis			
	SEQ ID NO: 307	887 bp	
NOV109a, CG59613-01 DNA Sequence	GATATCATTTTTTATGGCAGCCATTGTTAAGCCTCCAGAACCTATACCTTTAAATGG TTAACAGATAAGCCAGTTTGGATAGAACAAATGGCCACTGAGTAAAGAGAACTGGAGG CTTTAGAGGATTTGGTTACTGAACAATTCTCAATAATCATTTTCCAAAAAGTGAACCT ACACAGCATGAAAGTATCACACATTTCTTAGTGACGCTAACCCCTGTGTGACCAGGGC TTCAACACATACCACTGTGACCACAACCTAGCCATGAGCATGAGCCTCACCAGCATGT CCAAAAATGCTAAAAATACAACAATGGCAGTGAAGACATCACTACATGGAGGGCTGAAGG TACTATGGATCTCTTGGTGCTAGAATTTGAAGCACTAAATCAAGAGAACTTTTGTGGAC TGTGAATTGAAGTTAATGACTCTAGATGTTGAGCAACTTGAAATTCAGAACCAAGAGT ACAGCTGTGTAATAAAGATGCATTCTAGTGAATTTGTTTCATATATGCCAAGATCTCAG TCATATTGGAGAGTCTGCTATAATTTCTGTGCAAAAGATGGAGTGAATTTTCTGCA AATGGGAACTTGGACATGGAAACATTGCCACAATTGCCCAACAAAGTAATTACAATA AAGAAGAGGAGGCTGTTGCCATAATGATGAATGGGCCAGTTCAGCTAACTTTTGCACT AAGTTACTTTAAATTTCTTTATAACAGGCACTCCACTCTCTCAGATGCACCCCTTGCTG GAGAGTATAAGATTGCCGATATGGAACATTTAAAGTATTATTGGCTCCCAAAATTG AGGATGAAAAGGATTTTAGAAATTTCTAGAATCCAAGAAAATAAACTAAGCTCTTT GAAAATTGCTTCTGAGA		
	ORF Start: ATG at 14	ORF Stop: TAG at 830	
	SEQ ID NO: 308	272 aa	MW at 30831.1kD
NOV109a, CG59613-01 Protein Sequence	MAAIVKPPEPIPLKWLTDKPVWIEQWPLSKEKLEALEDLVTEQFSIIIFQKVNLSMK VSHISLVQLTLCDDQGFNTYHCDHNLAMSLTSMKMLKYNNGSEDIITWRAEGTMDL LVLEFEALNQENFVDCELKMLTLDVEQLEIPEQEYSCVIKMHSEFVHICQDLSHIGE SAIISCAKDGVNFSANGELGHGNIATIAQTSNYNKEEEAVAIMMNGPVQLTFALSYLN FFITGTPLSQMHPLESIRLPDMEHLKYLLAPKIEDEKGF		

Further analysis of the NOV109a protein yielded the following properties shown in Table 109B.

Table 109B. Protein Sequence Properties NOV109a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen); 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	Likely cleavage site between residues 19 and 20

A search of the NOV109a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 109C.

Table 109C. Geneseq Results for NOV109a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV109a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AA51639	Human PCNA protein fragment - Homo sapiens, 261 aa. [WO200008164-A2, 17-FEB-2000]	25..271 8..260	158/255 (61%) 184/255 (71%)	8e-78
AA52010	Human PCNA protein - Homo sapiens, 261 aa. [DE19840771-A1, 10-FEB-2000]	25..271 8..260	158/255 (61%) 184/255 (71%)	8e-78
AAB43712	Human cancer associated protein sequence SEQ ID NO:1157 - Homo sapiens, 269 aa. [WO200055350-A1, 21-SEP-2000]	25..271 16..268	158/255 (61%) 184/255 (71%)	8e-78
AAG75139	Human colon cancer antigen protein SEQ ID NO:5903 - Homo sapiens, 268 aa. [WO200122920-A2, 05-APR-2001]	25..269 16..266	157/253 (62%) 182/253 (71%)	5e-77
AAW90758	Human PCNA protein fragment #2 - Homo sapiens, 236 aa. [DE19840771-A1, 10-FEB-2000]	39..268 1..236	149/238 (62%) 171/238 (71%)	7e-73

In a BLAST search of public sequence databases, the NOV109a protein was found to have homology to the proteins shown in the BLASTP data in Table 109D.

Table 109D. Public BLASTP Results for NOV109a				
Protein Accession Number	Protein/Organism/Length	NOV109a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P12004	Proliferating cell nuclear antigen (PCNA) (Cyclin) - Homo sapiens (Human), 261 aa.	25..271 8..260	158/255 (61%) 184/255 (71%)	3e-77
P04961	Proliferating cell nuclear antigen (PCNA) (Cyclin) - Rattus norvegicus (Rat), 261 aa.	25..271 8..260	158/255 (61%) 185/255 (71%)	5e-77
P57761	Proliferating cell nuclear antigen (PCNA) - Cricetulus griseus (Chinese hamster), 261 aa.	25..271 8..260	158/255 (61%) 184/255 (71%)	7e-77
Q91ZH2	11 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2700095L20, FULL INSERT SEQUENCE - Mus musculus (Mouse), 261 aa.	25..272 8..261	156/256 (60%) 183/256 (70%)	1e-75
P17918	Proliferating cell nuclear antigen (PCNA) (Cyclin) - Mus musculus (Mouse), 261 aa.	25..270 8..259	155/254 (61%) 182/254 (71%)	5e-75

PFam analysis predicts that the NOV109a protein contains the domains shown in the Table 109E.

Table 109E. Domain Analysis of NOV109a			
Pfam Domain	NOV109a Match Region	Identities/ Similarities for the Matched Region	Expect Value
PCNA: domain 1 of 1	23..143	46/128 (36%) 83/128 (65%)	2.3e-20
PCNA_C: domain 1 of 1	145..265	59/131 (45%) 98/131 (75%)	1.6e-45

Example 110.

The NOV110 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 110A.

Table 110A. NOV110 Sequence Analysis

	SEQ ID NO: 309	1233 bp
NOV110a, CG59619-01 DNA Sequence	<p>TGGCAATGGAAGAAGAGATCCCCGCGCTCTTCATTGACAATGGCTCCGGCATGTGGAA AGCAGCTTTGCTGGGAGACAATGCCCTCCGAGCCATATCCCCTCCATCATCGGGCAC CCCCGGCACCAGGGCGTGATGGTGGGCATGGGCCAGAAGGACTCCTACGTGGGCGACC AGGCCAGAGCAAGTGCGGCATCCTGACCCTGAAGTACCCATCAAGCATGGCATCGT CACAACTGGGACGACATGGAGAAGATCTGGCACCATGTTTTCTACAACGAGCTGTGC GTGGCCCTGGAGGAGCAGGTGGTGTGCTGACCGAGGCCCGCTAAACCCAGGGCCA ATAGGGAGAAGATGACTCAGATCATGTTTAAGACCTTCAACACCCAGGCCATGTACGT GGCCATTTCAGGCCGTGCTGACCCTCCACAGCTCTGGTTGCACCACTGGCATTGTCTATG GACTCTGGAGATGGGGTCACCACACAGTGGCCATCTACGAGCGCCACACCCCTCCCTC ACACCATCTTGCATCTGGACCTGGCTGGCCAGGACCTTACTGACTACCTCATGAAGAT CCCTACCTACCGCAGCTATAGCTTCAACACCATGGCCAAGTGGAAAATCGTGCGCAAC ATCAAGGAGAAGTATGCTATGTGCTGCTGACTTCGAGGAGGAGATGGCCATGTGCTG CATCTCCTCCTCCCTGGAGAAGAGTACGAGCTGCCTGACAGCCAGGCCATCATTAT TAGCAATGAGCGGTTCCGGTGTCCGGAGGCACTGTTCCAGCCTTCCTTCTGGGCATG GAATCCTGTGGCATCCATGAAAGTACCTTCAACTCCATCATGAAGTGTGATATGGACA TCCCCAAGACCTGTAGCCAAACACAGTGTGTCTGGCGTCACCACCATGTACCCTGG CATCCCCAATAGGATGCAGAAGGAGATCACTGCCCTGGCATCCAGCACCATGAAGATC AAGATATCGTGCCCATCGTGCCCCAGAGTGCAAGTACTTTGTGTGGATCGGTGGCT CCATCCTGGCCTCACTGTCCACCTCCAGCAGATGTGGATTAGCAAGCAGGATACAA CGAGTCGGGCCCTCCATCATCCACGCAAATGGACTGCGAGCAGATGCATAGCATTT GCTGCATGGGTTAATTGAGAAGTATAAAATTGCCCTGGCAAATGCATATACCTCATG CTAGCCTCACCATAC</p>	
	ORF Start: ATG at 6	ORF Stop: TAA at 1185
	SEQ ID NO: 310	393 aa MW at 44147.5kD
NOV110a, CG59619-01 Protein Sequence	<p>MEEELPALFIDNGSGMWKAAALLGDNALRAIFPSIIIGHPRHQGVVMGMQKDSYVGDQA QSKCGILTLKYPIKHGIVTNWDDMEKIWHHVYFYNELCVALEEQVLLTEAPLNPRANR EKMTQIMFKTFNTQAMYVAIQAVLTLHSSGCTTGIVMDSGDGVHTVPIYERHTLPHT ILHLDLAGQDLTDYLMKIPTYRSYSFNTMAKWKIVRNIKEKLCYVALDFEEMATAAS SSSLEKSYELPDSQAIISNERFRCPALFQPSFLGMESCGIHSTFNSIMKCDMDIP KDLYANTVLSGVTTMYPGIPNRMQKEITALASSTMKIKISCPVPPECKYFVWIGGSI LASLSTFQQMWISKQYNEGSPSIIHRKWTASRCIAFAAWVNSEV</p>	

Further analysis of the NOV110a protein yielded the following properties shown in Table 110B.

Table 110B. Protein Sequence Properties NOV110a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.1547 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV110a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 110C.

Table 110C. Geneseq Results for NOV110a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV110a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU32060	Novel human secreted protein #2551 - Homo sapiens, 399 aa. [WO200179449-A2, 25-OCT-2001]	1..376 25..397	315/376 (83%) 336/376 (88%)	e-180
AAB43991	Human cancer associated protein sequence SEQ ID NO:1436 - Homo sapiens, 413 aa. [WO200055350-A1, 21-SEP-2000]	1..376 39..411	311/376 (82%) 336/376 (88%)	e-179
AAP61532	Sequence of beta-actin - Homo sapiens, 375 aa. [EP174608-A, 19-MAR-1986]	1..376 1..373	311/376 (82%) 335/376 (88%)	e-179
AAB12985	Human beta-actin protein sequence - Homo sapiens, 374 aa. [US6087398-A, 11-JUL-2000]	2..376 1..372	310/375 (82%) 334/375 (88%)	e-178
AAR50328	Drug resistant structural protein - Homo sapiens, 375 aa. [JP06038773-A, 15-FEB-1994]	1..376 1..373	309/376 (82%) 335/376 (88%)	e-178

In a BLAST search of public sequence databases, the NOV110a protein was found to have homology to the proteins shown in the BLASTP data in Table 110D.

Table 110D. Public BLASTP Results for NOV110a				
Protein Accession Number	Protein/Organism/Length	NOV110a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P02571	Actin, cytoplasmic 2 (Gamma-actin) - Homo sapiens (Human), 375 aa.	1..376 1..373	315/376 (83%) 336/376 (88%)	e-179
ATBOG	actin gamma (tentative sequence) - bovine, 374 aa.	2..376 1..372	314/375 (83%) 335/375 (88%)	e-179
P53505	Actin, cytoplasmic type 5 - Xenopus laevis (African clawed frog), 376 aa.	2..376 3..374	313/375 (83%) 335/375 (88%)	e-178
P29751	Actin, cytoplasmic 1 (Beta-actin) - Oryctolagus cuniculus (Rabbit), 375 aa.	1..376 1..373	311/376 (82%) 337/376 (88%)	e-178

O93400	ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) (CYTOPLASMIC BETA ACTIN) - <i>Xenopus laevis</i> (African clawed frog), 375 aa.	1..376 1..373	311/376 (82%) 336/376 (88%)	e-178
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PFam analysis predicts that the NOV110a protein contains the domains shown in the Table 110E.

Table 110E. Domain Analysis of NOV110a			
Pfam Domain	NOV110a Match Region	Identities/ Similarities for the Matched Region	Expect Value
actin: domain 1 of 1	1..378	284/382 (74%) 336/382 (88%)	2.2e-227

Example 111.

The NOV111 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 111A.

Table 111A. NOV111 Sequence Analysis			
	SEQ ID NO: 311	1197 bp	
NOV111a, CG59621-01 DNA Sequence	AACCATGTCTAAGCGGAGTCCCTTTAACTGGAAAGTTATGAATTGGACAAAAGCTTC TGGCTAACCCAGATTCACTGAACCTGAAGGGCACAGGTTGCAAAAGTGCCCAAGATGTCT TGCAAAAATTGCTGGAATCTTTACAGGAGAACCCTTCCAAGAAGATGAGCAGATTTCT GGGAGCCGTTATGCCAAGGCTTCGCATTGGAATGGATACTTGTGCCATTTCTTTGAGG CATGGTGGGCTTTCTTGGTTCAAACCAAGATTACATTTACCCGATCGTAGACGACC CTTACATGATGGGCAGGATAGCATGTGCCAATGTCCCTCAGTGACCTCTATGCAATGGG GGTCACAGAATGTGACAATATGCTGATGCTCCTTGGAGTCAGTAATAAAATGACCGAC AGGGAAAGGGATAAAGTGATGCCTCTGATTATCCAAAGTTTAAAGATGCAGCTGAGG AAGCAGGAATGTCTGTAATGGTCAGCCAAACAGTACTAAATCCCTGGATTGCTCCTGGG AGGAGTCACTACCACTGTCTTCCAGCCCCAATGAATTTATCATGCCAGACAATGCAGTG CCAGGGGACGTGCTGGTGTGACAAAACCCCTGGGGACACAGGTGGCAGTGGCTGTGC ACCACTGGCTGGATATTCCTTTGAAATGGAATAAGATTAAAGCTAGTGGTCACCGAAGA TGTAAGAGCTGGCCAACAGGAGGCGATGATGAACATGGTGAGGCTCAACAGGACAGCT GCAGGACTCATGCACACGTTCAATGCCACATGGCCACTGACATCACGGGCTTCGGGA TTTGGGCCACGTGCAGAACCTAGCCAAGCAGCAGAGGAACGAGGTGCTGTTGTAAT TCACAACCTCCTGGTGTCTGGCAAGATGGCTGCGGTGAGCAAGGCCTGCGGAAACATG TTCAGCCTCATGCATGGGACCTGCCCGGAGACCTCAGGCGGCCCTTCTGATCTGTTTAC CATGTCAGCAAGCAGCTCGGTTCTGTGCAGAGATAAAGTCCCCCAAATATAGTGAAGG CCACCAAGCATGGATTATTGGGATTGTAGAGAAGGGCAACCACAGCCAGGAATCATA GACAAACCCAGATCATCAAGGTTGCACCACAAGTGGCCACTCAAATGTGAATCTCA CACCGGGGCCACATCTTAATCTAGACAGAAATAGCT		
	ORF Start: ATG at 5	ORF Stop: TAA at 1178	
	SEQ ID NO: 312	391 aa	MW at 43193.9kD
NOV111a, CG59621-01 Protein Sequence	MSKRESFNLESYELDKSFWLRFTELKGTGCKVPQDVLQKLLSLQENHFQDEQFLG AVMPRLRIGMDTCAISLRHGLSLVQTTDYIYPIVDDPYMMGRIACANVLSOLYAMGV TECDNMLMLLGVSNKMTDRERDKVMPLIIQSFKDAEEAGMSVMVSQTVLNPWIVLGG VTTTFVQPNFIMPDNAVPGDVLVLTKPLGTQVAVAVHQWLDIPLKWNKIKLVVTEDEV ELANQEAMNMVRLNRTAAGLMHTFNAHMTDITGFGILGHVQNLAKQQRNEVSFVIH NLLVLAKMAAVSKACGMNFMHGTCPETSGGLLICLPQQAARFCABEIKSPKYSSEGH QAWIIGIVEKGNHTARIIDKPQIIKVA PQVATQNVNLTGATS		

Further analysis of the NOV111a protein yielded the following properties shown in Table 111B.

Table 111B. Protein Sequence Properties NOV111a	
PSort analysis:	0.8500 probability located in endoplasmic reticulum (membrane); 0.4400 probability located in plasma membrane; 0.1000 probability located in mitochondrial inner membrane; 0.1000 probability located in Golgi body
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV111a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 111C.

Table 111C. Geneseq Results for NOV111a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV111a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB58174	Lung cancer associated polypeptide sequence SEQ ID 512 - Homo sapiens, 250 aa. [WO200055180-A2, 21-SEP-2000]	166..391 20..243	168/227 (74%) 189/227 (83%)	2e-88
AAO01161	Human polypeptide SEQ ID NO 15053 - Homo sapiens, 122 aa. [WO200164835-A2, 07-SEP-2001]	147..264 1..118	81/119 (68%) 92/119 (77%)	2e-36
AAB53700	Human colon cancer antigen protein sequence SEQ ID NO:1240 - Homo sapiens, 106 aa. [WO200055351-A1, 21-SEP-2000]	42..99 1..58	53/58 (91%) 54/58 (92%)	1e-24

In a BLAST search of public sequence databases, the NOV111a protein was found to have homology to the proteins shown in the BLASTP data in Table 111D.

Table 111D. Public BLASTP Results for NOV111a				
Protein Accession Number	Protein/Organism/Length	NOV111a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BVT4	SELENOPHOSPHATE SYNTHETASE, HUMAN SELENIUM DONOR PROTEIN - Homo sapiens (Human), 392 aa.	1..391 1..392	364/392 (92%) 367/392 (92%)	0.0
P49903	Selenide,water dikinase 1 (EC 2.7.9.3) (Selenophosphate synthetase 1) (Selenium donor protein 1) - Homo sapiens (Human), 383 aa.	1..375 1..376	348/376 (92%) 351/376 (92%)	0.0
AAC50958	SELENOPHOSPHATE SYNTHETASE 2 - Homo sapiens (Human), 448 aa.	2..391 33..441	272/411 (66%) 313/411 (75%)	e-147
Q99611	Selenide,water dikinase 2 (EC 2.7.9.3) (Selenophosphate synthetase 2) (Selenium donor protein 2) - Homo sapiens (Human), 448 aa.	2..391 33..441	272/411 (66%) 313/411 (75%)	e-147
AAC53024	SELENOPHOSPHATE SYNTHETASE 2 - Mus musculus (Mouse), 452 aa.	2..387 36..441	267/407 (65%) 307/407 (74%)	e-146

Pfam analysis predicts that the NOV111a protein contains the domains shown in the Table 111E.

Table 111E. Domain Analysis of NOV111a			
Pfam Domain	NOV111a Match Region	Identities/ Similarities for the Matched Region	Expect Value
AIRS: domain 1 of 1	32..188	29/180 (16%) 113/180 (63%)	3e-18
AIRS_C: domain 1 of 1	191..367	34/197 (17%) 125/197 (63%)	1.1e-20

Example 112.

The NOV112 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 112A.

Table 112A. NOV112 Sequence Analysis

	SEQ ID NO: 313	1544 bp
NOV112a, CG59625-01 DNA Sequence	CGATGGGACACAGACAGGTCAACCCAGCTCTGATCTTTGCCATCACAGTTGCTACAAT CGGCTCTTTCCAGTTTGGCTACAACACTGGGGTCATCAATGCTCTGAGACGGTGCAG ATCATAAAGGAATTTATCAATAAACTTTGACGGACAAGGCAAATGCCCTCCCTCTG AGGTGCTGCTCAGGAATCTCTGGTCCTTGTCTGTGGCCATATTTCCGTCGGGGGTAT GATCGGCTCCTTTCCGTCGGACTCTTTGTTAACCGCTTTGGCAGGAGGCGCAATTCA ATGCTGATTGTCAACCTGTTGGCTGCCACTGGTGGCTGCTTATGGGACTGTGTAAAA TAGCTGAGTCAGTTGAAATGCTGATCCTGGGCCGCTTGGTTATGGCCTCTTCTGCGG ACTCTGCACAGGTTTGTGCCCATGTACATTGGAGAGATCTCGCTACTGCCCTGAGG GGTGCTTTGGCACTCTCAACCAGCTGGGCATAGTTATGGAATCTGGTGGCCAGG TAATCTTTGGTCTGGAACCTCATCTTGGGTCTGAAGAGCTATGGCCGGTGTATTAGG CTTTACCATCCTTCCAGCTATCCTGCAAAGTGCAGCCCTTCCATGTTGCCCTGAAAGT CCAGATTTTGTCTATTAAACAGAAAAAAGAGGAGAATGCTACGCGGGTCCCTCCAGC GGTTGTGGGGCACCCAGGATGTATCCCAAGACATCCAGGAGATGAAAGATGAGAGTGC AAGGATGTACAGAAAAGCAAGTCAACCGTGTGGAGCTCTTTAGAGTGTCCAGCTAC CGACAGCCCATCATTTCCATTGTGCTCCAGCTCTCTCAGCAGCTCTCTGGGATCA ATGCTGTGGTGTCTATTACTCAACAGGAATCTTCAAGGATGCAGGTGTTCAACAGCC CATCTATGCCACCATCAGCGCGGGTGTGGTTAATACTATCTTCACTTTACTTTCTGTA GTAGCTCAGATGCTGTTTTATGAAAGGAAAACTGAAGTTTCATGTCATAACTGTTT CTTTGTTATTAAAGCTGGGTACACTGTCTTAAATTTAATCTTCTGTGTTCTTCCCT CTTACAGAATCACTATAATGGGATGAGCTTTGTCTGTATTGGGCTATCTTGGTCTTT GTGGCTGTTTTGAAATTGGACAGGCCCATTCCTGGTTTATTGTGGCCGAACTCT TCAGCCAGGGCCCCCGCCAGCTGCGATGGCAGTGGCCGGCTGCTCCAACCTGGACCTC CAACTTCTAGTCGGATTGCTCTTCCCTCTGCTGCTTACTATTAGGAGCCTACGTT TTTATTATCTTACCGGCTTCTCATTACCTTCTTGGCCTTTACCTTCTTCAAAGTCC CTGAGACCCGTGGCAGGACTTTGAGGATATCACACGGGCCTTTGAAGGGCAGGCACA CGGTGCAGATAGATCTGGGAAGGACGGCGTCATGGGGATGAACAGCATCGAGCCTGCT AAGGAGACCACCAATGTCTAAGTCATGCCTCCT	
	ORF Start: ATG at 3	ORF Stop: TAA at 1530
	SEQ ID NO: 314	509 aa MW at 55571.7kD
NOV112a, CG59625-01 Protein Sequence	MGHRQVTPALIFAIVTATIGSFQFGYNTGVINAPETVQIIKEFINKLTLDKANAPPSE VLLTNLWSLSVAIFSVGGMIGSFVGLFVNRFGRRRNSMLIVNLLAATGGCLMGLCKI AESVEMLIILGRVIGLFCGLCTGFVPMYIGEISPTALRGAFGTINQLGIVIGILVAQV IFGLELILGSEELWPVLLGFTILPAILQSAALPCCPESPRFLLINRKEENATRVLQR LWGTQDVSQDIQEMKDESARMSQEKQVTVLELFRVSSYRQPIIISIVLQLSQQLSGIN AVVPYYSTGIFKDAGVQQPIYATISAGVVNTIFTLSSVVAQMLFSWKGLKPFHVITVS LLLLKLGTVTFKFNLLCSFLLQNHYNMGMSFVCIGAILVVFACFEIGPGPIPFIVAELF SQGPRPAAMAVAGCSNWTNLFVGLLFPSAAYLGAIVFIIFTGFLITFLAFTFFKVP ETRGRTFEDITRAFEGQAHGADRSKDGVMGMNSIEPAKETTTNV	

Further analysis of the NOV112a protein yielded the following properties shown in Table 112B.

Table 112B. Protein Sequence Properties NOV112a	
Psort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 22 and 23

A search of the NOV112a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 112C.

Table 112C. Geneseq Results for NOV112a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV112a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY27289	Glucose transporter protein GLUT3 - Homo sapiens, 494 aa. [US5942398-A, 24-AUG-1999]	1..505 1..492	389/505 (77%) 431/505 (85%)	0.0
AAR11360	Glucose Transporter Protein from CHO cells - Cricetulus sp, 492 aa. [WO9103554-A, 21-MAR-1991]	4..491 6..481	289/489 (59%) 364/489 (74%)	e-156
AAW17835	Human glucose transporter GLUT-1 - Homo sapiens, 492 aa. [WO9715668-A2, 01-MAY-1997]	4..491 6..481	287/489 (58%) 362/489 (73%)	e-155
AAW93000	Human GLUT1 protein - Homo sapiens, 492 aa. [WO9618957-A1, 20-JUN-1996]	4..491 6..481	284/489 (58%) 360/489 (73%)	e-153
AAB30522	Amino acid sequence of a consensus GLUT polypeptide - Synthetic, 493 aa. [US6136547-A, 24-OCT-2000]	6..501 10..490	289/496 (58%) 357/496 (71%)	e-151

In a BLAST search of public sequence databases, the NOV112a protein was found to have homology to the proteins shown in the BLASTP data in Table 112D.

Table 112D. Public BLASTP Results for NOV112a				
Protein Accession Number	Protein/Organism/Length	NOV112a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P11169	Solute carrier family 2, facilitated glucose transporter, member 3 (Glucose transporter type 3, brain) - Homo sapiens (Human), 496 aa.	1..509 1..496	446/510 (87%) 468/510 (91%)	0.0
P47842	Solute carrier family 2, facilitated glucose transporter, member 3 (Glucose transporter type 3, brain) - Canis familiaris (Dog), 495 aa.	1..507 1..494	400/507 (78%) 446/507 (87%)	0.0
P47843	Solute carrier family 2, facilitated glucose transporter, member 3 (Glucose transporter type 3, brain) - Ovis aries (Sheep), 494 aa.	1..505 1..492	389/505 (77%) 431/505 (85%)	0.0
P58352	Solute carrier family 2, facilitated	1..505 1..492	390/505 (77%) 431/505 (85%)	0.0

	(Glucose transporter type 3, brain) - Bos taurus (Bovine), 494 aa.			
Q07647	Solute carrier family 2, facilitated glucose transporter, member 3 (Glucose transporter type 3, brain) - Rattus norvegicus (Rat), 493 aa.	1..508 1..492	380/508 (74%) 422/508 (82%)	0.0

PFam analysis predicts that the NOV112a protein contains the domains shown in the Table 112E.

Table 112E. Domain Analysis of NOV112a			
Pfam Domain	NOV112a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Herpes_glycop: domain 1 of 1	1..249	40/417 (10%) 171/417 (41%)	7.2
GntP_permease: domain 1 of 1	65..329	70/478 (15%) 185/478 (39%)	2.5
sugar_tr: domain 1 of 1	12..478	188/503 (37%) 410/503 (82%)	2.2e-158

Example 113.

The NOV113 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 113A.

Table 113A. NOV113 Sequence Analysis		
	SEQ ID NO: 315	1731 bp
NOV113a, CG59887-01 DNA Sequence	<p>ACTACTTCGCCGACACTCGCCAGCCTCGGCTACGAGCAAAAAATGCACCGCACCATGA GCTCGTTACCTCGTTTGCCTTGGCCCTTTTCCATGGTCTCGATCAACACCGCGTGGT CACGCTGTTCCGCCGACCGTTCAACCGCGTCGGGGCATCGGCATCCTCCTGTGGCTG TTGGTGATCCCGCTGGTGTGCTGCATCGTCATGGTCTACTGCCACCTGGCCGGCGCA TTCCGCTCACGGCTACGCCCTACCAATGGTCCAGCCGATTGGCGGGCAATCACTTCGG CTGGTTTACCGGCTGGGTGGCGTTACCTCGTTTGTCCCGGTACAGCCGCCACCTCG GCGGCCATCGGTACGGTGTTCGCACCGGAGATCTGGGCCAACCCGACACAGGGTCAGA TCCAGGGCCTGAGCATCGGCGCCACGCTGGTGGTGGGCTTGCTGAATATCTCGGGAT TCGCCTGGCCACCCGATCAACGACATCGGCGCGATCATCGAAATCATCGGCACGGTA CTGCTGGCGATTGCGTTGTTCTTCGGGGTGTCTTTCTTCTTTGAGCACACCCAGGGCG TGGCGATCCTGACCTCCGCGCAACCAAGTACGCGGCGGCAGCTCAGCTTACCAACCAT CGCCTCGCCACCTTGCTGCCGGTCTCGGTGCTGCTGGGTGGGAAGGCGCCGCCGAC CTGTCCGAGGAAACCAAGGACCAACGCGCGCCGCCCGCGCGCGCGCGCGCGCGCG TGCTGGTGTCCAGCGTATTGGGCTTCGTGGTGTTCGCCTTGCTGAGCATCGGCATCCC GGGCTCGGTGAGCGAATGCTCAGCCACAGCGAAACCCGGTGAATCAATATCGTGCCG TCGCCTGCCTGATCGCCCAACATGGCGGTGGCCACGCGCATGACCTTCGCCCTGTCGG GGACAACATGCTCGCGGCTCCAAGTGCTGGCGAAGATCAACCCGCACTTCGGCAGC CCGGTCGCCGCATCGTGTGATCACCGCCATCGCGTGTGCTGAACCTGGCGAGTG GCGGGTTTGTACGGCGATCTACTCGATGGTCCGCTGACCTACTACTGCACCTTACCT GCTGACGCTGATTGCCGCTACCTGGCCTATAAAACGGCCGGATGCCGGGGCGCCT GCGGCGGTGTTACGCTGGGCGCTGGTTGCTGCCGATGATTATCCTCGGCGCGCTGT</p>	

	GGGCCATCGCGGTGATCCTGACCTGAGCGTGCCGGAAGAAAGCCACTGGCGCTAT CACCACCGGGGTACACTCGGCGTGGGCGTGTGTGGTGGTGTTCACCTGCGCACG CGCCTTAACAATGGCACCGCGGGCCGAGCGGCAAATTGCTCGACCACTAGCCGCTGA TTGCAAGCCAAAAGACAAAACCCGAAACACCGGGGTTTTGTCTTGTCACTCCAAGGAG CTTCCCGATGTTTGAACAGGCCAGCTGGCTCAATCAACCCAGCATTTGGCGCGAGAA GGCGAGCGACTCAAGGTCCGCAACCGATGCCAGTACCGATTCTGGCGTGAACCCACT ATGTTTTGTACGCGACAACGGGCATTTCCTGTTGTGTGAACCGACGCGGACTTTAC CGCCCAAGTCAAATCCACAGTGAGTTTACCCACCTGTATGACCTTCGC		
	ORF Start: ATG at 43	ORF Stop: TAG at 1441	
	SEQ ID NO: 316	466 aa	MW at 49070.4kD
NOV113a, CG59887-01 Protein Sequence	MHRTMSSPSTFALAFSMVSIINTGVVTLFADPFNRVGGIGILLWLLVPLVCCIMVYC HLAGRIPLTGAYAYQWSSRLAGNHFGWFTGWVAFSTFVAGTAATSAAIGTVFAPEIWAN PTQGGIQLSIGATLVVGLLNICGIRLATRINDIGAIIEIIGTVLLAIALFFGVFFFF EHTQGVAILTSAQPVSGGTLSTFTIALATLLPVSVLLGWEAADLSEETKDPRAAPR AMIRAVLVSSVLGFVVFALLSIAIPGSVSELLSHSENPNVINIIRLQLGNAAGVGMIVI AFASILACLIANMAVATRMTPALSRDNMLPGSKVLAKINPHFGTPVAAIVLITAIIVL LNLASGGFVTAIYSMVGLTYCTYLLTLIAAYLAYKNGRMPGAPAGVPSLGRWLLPMI ILGGLWAIIVILTSVPEESHTGAITTGVTLGVGVLWWLFSRLRLNNGTAGPSGKLL DH		
	SEQ ID NO: 317	1433 bp	
NOV113b, CG59887-02 DNA Sequence	AAAAATGCACCGCACCATGAGCTCGTTCACCTCGTTGCCCTGGCCTTTCCATGGTC TCGATCAACACCGGCGTGGTACGCTGTTCCGCGACCCGTTCAACCGCGTCCGGGGCA TCGGCATCCTCCTGTGGCTGTGGTGATCCCGTGGTGTGCTGCATCGTATGGTCTA CTGCCACCTGGCGGGCGCATTCGCTCACCGGCTACGCTACCAATGGTCCAGCCGA TTGGCGGCAATCACTTCGGCTGGTTTACCGGCTGGGTGGCGTTCACCTCGTTGTGCG CCGGTACAGCCGCCACCTCGGCGGCCATCGGTACGGTGTTCGACCGGAGATCTGGGC CAACCCGACACAGGGTCAGATCCAGGGCCTGAGCATCGGCGCCACGCTGGTGGTGGGC TTGCTGAATATCTGCGGGATTGCGCTGGCCACCGGATCAACGACATCGGCGCGATCA TCGAAATCATCGGCACGGTACTGCTGGCGATTGCGTTGTTCTTCGGGGTGTTTTCTT CTTTGAGCACACCCAGGGCGTGGCGATCCTGACCTCCGCGCAACCACTGAGCGGCGGC ACGCTCAGCTTCACCAACATCGCCCTCGCCACCTTGCTGCCGCTCTCGGTGCTGCTGG GTTGGGAAGGCCCGCGACCTGTCCGAGGAAACCAAGGACCAACGCGCGCGCGCC CCGGGCGATGATTCTGTCGGTGTGTTGTTGTCAGCGTATTGGGCTTCGTGGTGTTCGCC TTGCTGAGCATCGCGATCCCGGGCTCGGTGAGCGAACTGCTCAGCCGAGCGAAACCC CGGTGATCAATATCGTGGCCTGCAACTGGGCAATGCCGCGGCGTGGCATGGTGTGCT GATCGCTTTCGCTCGATCCTCGCTGCTGATCGCCAACATGGCGGTGGCCACGCGC ATGACCTTCGCCCTGTCCCGGACAACATGCTGCCGGGCTCCAAGGTGCTGGCGAAGA TCAACCCGCACTTCGGCAGCCGGTTCGCGCCCATCGTGTGATCACCGCATCGCCGT GCTGCTGAACCTGGCGAGTGGCGGGTTTGTACGGCGATCTACTCGATGGTTCGGCCTG ACCTACTACTGCACTTACCTGCTGACGCTGATTGCCGCGTACCTGGCCTATAAAACG GCCGGATGCCGGGGCGCCTGCGGGCGTGTTCAGCCTGGGCGCTGGTGTGCTGCCGAT GATTATCCTCGGCGGCTGTGGGCCATCGCGGTGATCCTGACCCTGAGCGTGCCGGAA GAAAGCCCACTGGCGCTATCACCACCGGGTTACTCGGCGTGGGCGTGTGTGTTGTT GGTTGTTTTCACTGCGCACGCGCTTAACAATGGCACCGCGCGGCGAGCGGCAAAATT GCTCGACCACTAGCCGCTGATTGTCAGCCAAAAGACAAAACC		
	ORF Start: ATG at 5	ORF Stop: TAG at 1403	
	SEQ ID NO: 318	466 aa	MW at 49075.4kD
NOV113b, CG59887-02 Protein Sequence	MHRTMSSPSTFALAFSMVSIINTGVVTLFADPFNRVGGIGILLWLLVPLVCCIMVYC HLAGRIPLTGAYAYQWSSRLAGNHFGWFTGWVAFSTFVAGTAATSAAIGTVFAPEIWAN PTQGGIQLSIGATLVVGLLNICGIRLATRINDIGAIIEIIGTVLLAIALFFGVFFFF EHTQGVAILTSAQPVSGGTLSTFTIALATLLPVSVLLGWEAADLSEETKDPRAAPR AMIRAVLVSSVLGFVVFALLSIAIPGSVSELLSRSENPNVINIIRLQLGNAAGVGMIVI AFASILACLIANMAVATRMTPALSRDNMLPGSKVLAKINPHFGTPVAAIVLITAIIVL LNLASGGFVTAIYSMVGLTYCTYLLTLIAAYLAYKNGRMPGAPAGVPSLGRWLLPMI ILGGLWAIIVILTSVPEESHTGAITTGVTLGVGVLWWLFSRLRLNNGTAGPSGKLL DH		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 113B.

Table 113B. Comparison of NOV113a against NOV113b.

Protein Sequence	NOV113a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV113b	1..466 1..466	343/466 (73%) 344/466 (73%)

Further analysis of the NOV113a protein yielded the following properties shown in Table 113C.

Table 113C. Protein Sequence Properties NOV113a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Likely cleavage site between residues 59 and 60

A search of the NOV113a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 113D.

Table 113D. Geneseq Results for NOV113a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV113a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG49885	Arabidopsis thaliana protein fragment SEQ ID NO: 63155 - Arabidopsis thaliana, 504 aa. [EP1033405-A2, 06-SEP-2000]	1..449 17..492	122/486 (25%) 217/486 (44%)	3e-31
AAG49884	Arabidopsis thaliana protein fragment SEQ ID NO: 63154 - Arabidopsis thaliana, 516 aa. [EP1033405-A2, 06-SEP-2000]	1..449 29..504	122/486 (25%) 217/486 (44%)	3e-31
AAG20282	Arabidopsis thaliana protein fragment SEQ ID NO: 22407 - Arabidopsis thaliana, 504 aa. [EP1033405-A2, 06-SEP-2000]	1..449 17..492	122/486 (25%) 217/486 (44%)	3e-31
AAG20281	Arabidopsis thaliana protein fragment SEQ ID NO: 22406 - Arabidopsis thaliana, 516 aa. [EP1033405-A2, 06-SEP-2000]	1..449 29..504	122/486 (25%) 217/486 (44%)	3e-31
AAG20280				3e-31

SEQ ID NO: 22405 - Arabidopsis thaliana, 528 aa. [EP1033405-A2, 06-SEP-2000]	41..516	217/486 (44%)	
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In a BLAST search of public sequence databases, the NOV113a protein was found to have homology to the proteins shown in the BLASTP data in Table 113E.

Table 113E. Public BLASTP Results for NOV113a				
Protein Accession Number	Protein/Organism/Length	NOV113a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9KZF1	PROBABLE AMINO ACID/METABOLITE PERMEASE - Streptomyces coelicolor, 504 aa.	3..450 27..481	139/469 (29%) 214/469 (44%)	2e-41
Q98H14	AMINO ACID/METABOLITE PERMEASE - Rhizobium loti (Mesorhizobium loti), 518 aa.	1..446 27..485	118/466 (25%) 209/466 (44%)	1e-36
Q92NI8	PUTATIVE AMINO-ACID PERMEASE PROTEIN - Rhizobium meliloti (Sinorhizobium meliloti), 515 aa.	1..449 25..487	122/475 (25%) 204/475 (42%)	1e-32
O22509	PUTATIVE AMINO ACID OR GABA PERMEASE - Arabidopsis thaliana (Mouse-ear cress), 516 aa.	1..449 29..504	122/486 (25%) 217/486 (44%)	1e-30
Q9ZU50	PUTATIVE AMINO ACID PERMEASE - Arabidopsis thaliana (Mouse-ear cress), 517 aa.	1..449 29..505	120/487 (24%) 216/487 (43%)	2e-28

PFam analysis predicts that the NOV113a protein contains the domains shown in the Table 113F.

Table 113F. Domain Analysis of NOV113a			
Pfam Domain	NOV113a Match Region	Identities/ Similarities for the Matched Region	Expect Value
oxidored_q3: domain 1 of 1	162..307	28/182 (15%) 91/182 (50%)	3.7
ISK_Channel: domain 1 of 1	196..326	32/136 (24%) 55/136 (40%)	8.8

ABC2_membrane: domain 1 of 1	122..377	46/273 (17%) 154/273 (56%)	8.3
SSF: domain 1 of 1	7..394	77/470 (16%) 222/470 (47%)	7.8
Aa_trans: domain 1 of 1	29..417	67/483 (14%) 236/483 (49%)	9.7
aa_permeases: domain 1 of 1	1..451	86/516 (17%) 287/516 (56%)	1.1e-05

Example 114.

The NOV114 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 114A.

Table 114A. NOV114 Sequence Analysis			
	SEQ ID NO: 319	876 bp	
NOV114a, CG59861-01 DNA Sequence	<u>AACTTGCTTTTGGGAGCCAGCGGTATGGCGTCGGGCTGCAAGATTGGCCCGTCCATCC</u> TCAACAGCGACCTGGCCAATTTAGGGGCCGAGTGCTCCCGGATGCTAGACTCTGGGGC CGATTATCTGCACCTGGACGTAATGGACGGGCATTTTGTTCCTCAACATCACCTTTGGT CACCTGTGGTGAAGACCTTCGAAAGCAGCTAGGCCAGGACCTTTCTTTGACATGC ACATGATGGTGTCCAAGCCAGAACAGTGGGTAAAGCCAATGGCTGTAGCAGGAGCCAA TCAGTACACCTTTCATCTCGAGGCTACTGAGAACCAGGGGCTTTGATTAAAGACATT CGGGAGAATGGGATGAAGGTTGGCCTTGCCATCAAACCAGGAACCTCAGTTGAGTATT TGGCACCATGGGCTAATCAGATAGATATGGCCTTGGTTATGACAGTGAACCGGGGTT TGGAGGGCAGAAATTCATGGAAGATATGATGCCAAAGGTTCACTGGTTGAGGACCCAG TTCCCATCTTTGGATATAGAGGTCGATGGTGGAGTAGGTCCTGACACTGTCCATAAAT GTGCAGAGGCAGGAGCTAACATGATTGTGTCTGGCAGTGCTATTATGAGGAGTGAAGA CCCCAGATCTGTGATCAATCTATTAAGAAATGTTTGTCTCAGAAGCTGCTCAGAAACGT TCTCTTGATCGGTGA <u>AAACCATAAGGAGCCAGTGTCTCTGTT</u> CATGAATCTCCCTTT TACTGGAAAACAGGAATATTGACTACCAATCACAATGCAATGCAATGCAAGCCGTACTGCTT TTTTGAGCAGTTATTTCATTCAGTGATTA <u>AACTGATTGTGCAGAATAAAAAAAAAA</u> <u>AAAAAA</u>		
	ORF Start: ATG at 25	ORF Stop: TGA at 709	
	SEQ ID NO: 320	228 aa	MW at 24901.4kD
NOV114a, CG59861-01 Protein Sequence	MASGCKIGPSILNSDLANLGAECRMLDSGADYLHLDVMDGHFVFNITFGHPVVESLR KQLGQDPFFDMHMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGMKVG LAIKPGTSVEYLPANQIDMALVMTVEPGFGGQKFMEDMMPKVHWRLTQFPSLDIEV DGGVGPDTVHKCAEAGANMIVSGSAIMRSEDPRSVINLLRNVCSEAAQKRSDDR		
	SEQ ID NO: 321	730 bp	
NOV114b, CG59861-02 DNA Sequence	<u>AACTTGCTTTTGGGAGCCAGCGGTATGGCGTCGGGCTGCAAGATTGGCCCGTCCATCC</u> TCAACAGCGACCTGGCCAATTTAGGGGCCGAGTGCTCCCGGATGCTAGACTCTGGGGC CGATTATCTGCACCTGGACGTAATGGACGGGCATTTGTTCCTCAACATCACCTTTGGT CACCTGTGGTGAAGACCTTCGAAAGCAGCTAGGCCAGGACCTTTCTTTGACATGC ACATGATGGTGTCCAAGCCAGAACAGTGGGTAAAGCCAATGGCTGTAGCAGGAGCCAA TCAGTACACCTTTCATCTCGAGGCTACTGAGAACCAGGGGCTTTGATTAAAGACATT CGGGAGAATGGGATGAAGGTTGGCCTTGCCATCAAACCAGGAACCTCAGTTGAGTATT TGGCACCATGGGCTAATCAGATAGATATGGCCTTGGTTATGACAGTGAACCGGGGTT TGGAGGGCAGAAATTCATGGAAGATATGATGCCAAAGGTTCACTGGTTGAGGACCCAG TTCCCATCTTTGGATATAGAGGTCGATGGTGGAGTAGGTCCTGACACTGTCCATAAAT GTGCAGAGGCAGGAGCTAACATGATTGTGTCTGGCAGTGCTATTATGAGGAGTGAAGA CCCCAGATCTGTGATCAATCTATTAAGAAATGTTTGTCTCAGAAGCTGCTCAGAAACGT TCTCTTGATCGGTGA <u>AAACCATAAGGAGCCAGTG</u>		
	ORF Start: ATG at 25	ORF Stop: TGA at 709	
	SEQ ID NO: 322	228 aa	MW at 24927.5kD
NOV114b, CG59861-02 Protein Sequence	MASGCKIGPSILNSDLANLGAECRLMLDSGADYLHLDVMDGHFVFNITFGHPVVESLR KQLGQDPFFDMHMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGMKVG LAIKPGTSVEYLPANQIDMALVMTVEPGFGGQKFMEDMMPKVHWRLTQFPSLDIEV		

DGGVGPDTVHKCAEAGANMIVSGSAIMRSEDPRSVINLLRNVCSEAAQKRSLDR
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Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 114B.

Table 114B. Comparison of NOV114a against NOV114b.		
Protein Sequence	NOV114a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV114b	1..228	227/228 (99%)
	1..228	227/228 (99%)

Further analysis of the NOV114a protein yielded the following properties shown in Table 114C.

Table 114C. Protein Sequence Properties NOV114a	
PSort analysis:	0.6500 probability located in cytoplasm; 0.1753 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space; 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV114a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 114D.

Table 114D. Geneseq Results for NOV114a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Protein/Organism/Length [Patent #, Date]	NOV114a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41358	Human polypeptide SEQ ID NO 6289 - Homo sapiens, 247 aa. [WO200153312-A1, 26-JUL-2001]	1..228 20..247	227/228 (99%) 227/228 (99%)	e-132
AAM41357	Human polypeptide SEQ ID NO 6288 - Homo sapiens, 247 aa. [WO200153312-A1, 26-JUL-2001]	1..228 20..247	227/228 (99%) 227/228 (99%)	e-132
AAM39571	Human polypeptide SEQ ID NO 2716 - Homo sapiens, 228 aa. [WO200153312-A1, 26-JUL-2001]	1..228 1..228	227/228 (99%) 227/228 (99%)	e-132

AAB71912	Human ISOM-4 - Homo sapiens, 228 aa. [WO200112790-A2, 22-FEB-2001]	1..228 1..228	227/228 (99%) 227/228 (99%)	e-132
AAM39572	Human polypeptide SEQ ID NO 2717 - Homo sapiens, 246 aa. [WO200153312-A1, 26-JUL-2001]	1..228 1..246	227/246 (92%) 227/246 (92%)	e-129

In a BLAST search of public sequence databases, the NOV114a protein was found to have homology to the proteins shown in the BLASTP data in Table 114E.

Table 114E. Public BLASTP Results for NOV114a				
Protein Accession Number	Protein/Organism/Length	NOV114a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96AT9	HYPOTHETICAL 24.9 KDA PROTEIN - Homo sapiens (Human), 228 aa.	1..228 1..228	227/228 (99%) 227/228 (99%)	e-131
Q9BSB5	HYPOTHETICAL 25.3 KDA PROTEIN - Homo sapiens (Human), 232 aa (fragment).	1..228 5..232	227/228 (99%) 227/228 (99%)	e-131
AAH19126	HYPOTHETICAL 24.9 KDA PROTEIN - Mus musculus (Mouse), 228 aa.	1..228 1..228	221/228 (96%) 226/228 (98%)	e-129
O43767	RIBULOSE-5-PHOSPHATE-EPIMERASE - Homo sapiens (Human), 174 aa (fragment).	55..228 1..174	174/174 (100%) 174/174 (100%)	2e-98
Q96N34	CDNA FLJ31466 FIS, CLONE NT2NE2001372, HIGHLY SIMILAR TO HOMO SAPIENS PUTATIVE RIBULOSE-5-PHOSPHATE-EPIMERASE - Homo sapiens (Human), 178 aa.	69..228 1..178	160/178 (89%) 160/178 (89%)	2e-86

Pfam analysis predicts that the NOV114a protein contains the domains shown in the Table 114F.

Table 114F. Domain Analysis of NOV114a			
Pfam Domain	NOV114a Match Region	Identities/ Similarities	Expect Value

		Region	
Ribul_P_3_epim: domain 1 of 1	6..204	95/209 (45%) 174/209 (83%)	1.9e-105
IGPS: domain 1 of 1	179..213	15/35 (43%) 27/35 (77%)	0.02
trp_syntA: domain 1 of 1	34..222	45/273 (16%) 124/273 (45%)	2.9

Example 115.

The NOV115 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 115A.

Table 115A. NOV115 Sequence Analysis			
	SEQ ID NO: 323	1761 bp	
NOV115a, CG59857-01 DNA Sequence	AGTGTGGTACCTATCTGTCCCCCTCTGGAGGGGTTGACAAGGGAAGGGCACCGGGG GGCACAGAGATGCAGGACAGATTGCACATCCTGGAGGACCTGAATATGCTCTACATTC GGCAGATGGCACTCAGCCTGGAGGACACGGAGTTGCAGAGGAAGCTAGACCATGAGAT CCGGATGAGGGAAGGGGCTGTAACTGTCTGGCAGCCTGCTCCAGCGAGAGCAGGCT CTGGAGGCCACCAAGAGCCTGCTAGTGTGCAACAGCCGATCCTCAGTACATGGGCG AGCTGCAGCGGCGCAAGGAGGCGCAGGTGCTGGGGAAGACAAGCCGGCGGCCTTCTGA CAGTGGCCCGCCGCTGAGCGCTCCCCCTGCCGCGGCCGGGTCTGCATCTCTGACCTC CGGATTCCACTCATGTGAAGGACACAGAATATTTCAAGAAACAAGACTTGCACCCGCT GGGCTGTGTTCTCTGCTGCTGAGCTGGGGGAACACATCCAGGACACAGAGATGATCCT AGTGGACAGGACCCTCACAGACATCTCCTTTCAGAGCAATGTGCTCTTCGCTGAGGCG GGGCCAGACTTTGAACTGCGGTTAGAGCTGTATGGGGCCTGTGTGGAAGAAGAGGGGG CCCTGACTGGCGGCCCAAGAGGCTTGCCACCAAACTCAGCAGCTCCCTGGGCCGCTC CTCAGGGAGGCGTGTCCGGGCATCGCTGGACAGTGTGGGGTTTCAGGAGCAGTCCC ATCTTGCTCCCCACCCAGTTGTTGGTGGTCTCTCGTTACCACCTCTTGGCTCACACCA CACTCACCTGGCAGCAGTGAAGATGGATTCCGCACACATGACCTCACCTTGGCAG TCATGAGGAGAACCTGCTGCTGGCTGCCCCTTTATGGTAGCGTGTGTTGCCGTCTGGCA GCTCAGCCTCTCTGCATGACTCAGCCCACTGCAAGTGGTACCTCAGGGTGCAGCAAG CTGGGGAGATGCAGAACTGGGCACAAGTGCATGGAGTTCTGAAAGGCACAAACCTCTT CTGTTACCGGCAACCTGAGGATGCAGACACTGGGGAAGAGCCGCTGCTTACTATTGCT GTCAACAAGGAGACTCGAGTCCGGGCAGGGGAGCTGGACCAGGCTCTAGGACGGCCCT TCACCTTAAGCATCAGTAACAGTATGGGGATGATGAGGTGACACACACCTTCAGAC AGAAAGTCGGGAAGCACTGCAGAGCTGGATGGAGGCTCTGTGGCAGCTTTTCTTTGAC ATGAGCCAAATGGAAGCAGTGTGTGATGAAATCATGAAATTTGAACTCCTCTGCTCCCC GGAAACCAACCCCAAGCACTGGCAAGCAGGGGTCTTGTACCATGAGATGGCTATTGA GCCGCTGGATGACATCGCAGCGGTGACAGACATCTGACCCAGCGGGAGGGCGCAAGG CTGGAGACACCCCCACCTGGCTGGCAATGTTTACAGACCAGCCTGCCTGCCTAACCC CCTGCTCGCCTGCCTCAGTGGCCCCAGCCCCAGACTGGACCCACCCCTGCGCTGGGG GAGACCCGAACCTTTTCCCTGGATGCTGTCCCCCAGACCACTCCCTAGGGCTCGC TCGGTTGCCCCCCCTCCACCTCAGCGATCCCCACGGACCAGAGGCTCTGCAGCAAAG GCCAACCTCGCACTTGGCTCCAGTCACCAAGTGTGAGAGAGAAAGGTGCTGGCATAGGA TCTGCCCAAGAGAAAAATGA		
	ORF Start: ATG at 68	ORF Stop: TGA at 1715	
	SEQ ID NO: 324	549 aa	MW at 61171.0kD
NOV115a, CG59857-01 Protein Sequence	MQDRLHILEDLNLMIYIRQMALESDTELQRKLDHEIRMREGACKLLAACSQREQALEA TKSLLVCNSRILSYMGELQRRKEAQLVGLKTSRRPSDSGPPAERSPCRGRVCISDLRIE LMWKDEYFKNKDLHRWAVFLLQLGEHIQDTEMILVDRITLTDISFQSNVLF AEAGPD FELRLELYGACVEEGALTGGPKRLATKLSLSSGRSSGRRVRASLDSAGSGSSSPIILL PTPVVGGPRYHLAHTLTLLAAVQDGFRTDHLTLASHEENPAWLPYGVSVCCRLAAQF LCMTQPTASGTLRVQQAGEMQNWAVHGVKGTNLFYRQPEDADTGEEPLLTIAVNK ETVRAGELDQALGRPFTLSISNQYGDDEVTHLTQTESREALQSWMEALWQLFFDMSQ WKQCCDEIMKIETPAPRKPPQALAKQGSLYHEMAIEPLDDIAAVTDILTQREGARLET PPPWLAMFTDQPALPNPCSPASVAPAPDWTPLPWGRPRTFSLDAVFPDHSPRARSVA PLPPQRSPRTRGLCSKGQPRTNLQSPV		

Further analysis of the NOV115a protein yielded the following properties shown in Table 115B.

Table 115B. Protein Sequence Properties NOV115a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1707 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV115a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 115C.

Table 115C. Geneseq Results for NOV115a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV115a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB35241	Human rhotekin - Homo sapiens, 563 aa. [US6183990-B1, 06-FEB-2001]	24..549 37..563	526/527 (99%) 526/527 (99%)	0.0
AAY44559	Human Rhotekin protein - Homo sapiens, 563 aa. [WO9958667-A1, 18-NOV-1999]	24..549 37..563	526/527 (99%) 526/527 (99%)	0.0
AAB35242	Human rhotekin EST-derived protein - Homo sapiens, 527 aa. [US6183990-B1, 06-FEB-2001]	24..549 1..527	522/527 (99%) 523/527 (99%)	0.0
AAY44560	Human Rhotekin variant protein - Homo sapiens, 527 aa. [WO9958667-A1, 18-NOV-1999]	24..549 1..527	522/527 (99%) 523/527 (99%)	0.0
AAB26790	Human Ras correlative GTP binding kinase protein sequence - Homo sapiens, 544 aa. [CN1257924-A, 28-JUN-2000]	24..549 18..544	518/527 (98%) 519/527 (98%)	0.0

In a BLAST search of public sequence databases, the NOV115a protein was found to have homology to the proteins shown in the BLASTP data in Table 115D.

Table 115D. Public BLASTP Results for NOV115a
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Protein Accession Number	Protein/Organism/Length	NOV115a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAH17727	SIMILAR TO RHOTEKIN - Homo sapiens (Human), 550 aa.	1..549 1..550	549/550 (99%) 549/550 (99%)	0.0
Q9BST9	SIMILAR TO RHOTEKIN - Homo sapiens (Human), 587 aa (fragment).	24..549 61..587	526/527 (99%) 526/527 (99%)	0.0
Q96PT6	RTKN - Homo sapiens (Human), 544 aa.	24..549 18..544	518/527 (98%) 519/527 (98%)	0.0
Q9HB05	RHOTEKIN - Homo sapiens (Human), 567 aa (fragment).	24..549 41..567	505/527 (95%) 513/527 (96%)	0.0
Q61192	RHOTEKIN - Mus musculus (Mouse), 551 aa.	1..549 1..551	477/551 (86%) 500/551 (90%)	0.0

PFam analysis predicts that the NOV115a protein contains the domains shown in the Table 115E.

Table 115E. Domain Analysis of NOV115a			
Pfam Domain	NOV115a Match Region	Identities/ Similarities for the Matched Region	Expect Value
HR1: domain 1 of 1	23..95	17/87 (20%) 54/87 (62%)	0.27
PH: domain 1 of 1	296..397	19/102 (19%) 72/102 (71%)	1e-06

Example 116.

The NOV116 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 116A.

Table 116A. NOV116 Sequence Analysis			
	SEQ ID NO: 325	450 bp	
NOV116a, CG59855-01 DNA Sequence	<div>CTGGGAGACTGAAAAATGCAGACCACCGGGGTATTACTCATTCTCCAGCTCTGATC TGCTGTTGTACCAGGGGTCTAATCAGGCCTGTGTCTGCCTTCTCCTTGAATAGCCCAG AGAATTTCATCTAAACAGCCTTCTACAGCAGCTCCCCACTCCAGGTGGCCAGACGGGA GTTCCAGACCACTGTTGTCTCCCGGGACACTGACACAGCCGCAAGTTATGGTGCT GGGTCAGCCACAGTTGGTGTGGCTGATTGAGGGGCTGGCATTGGAGCGGTGTTTGGCA GCTTGATTATTGTCTATGCCAGGAAGCTGTCTCTCAAGCAGCAACTCTCTTCTATGC CATTCTGGGCTTTGCCCTGTCTGAGGCCATGGGGCTCTTCTGTTTGATGATCTCCTTC TTCATCCTGTTTCGCATGTGAGGCTCCGTGAGGGTCACCTGCCT</div>		
	ORF Start: ATG at 17	ORF Stop: TGA at 425	
	SEQ ID NO: 326	136 aa	MW at 14384.6kD

NOV116a, CG59855-01 Protein Sequence	MQTTGVLLISPALICCTRGLIRPVSAFSLNSPENSSKQPSYSSSPLQVARREFQTSV VSRD TD TAAKFIGAGSATVGVADSGAGIGAVFGSLIIIVYARKLSLKQQLLFYAILGFA LSEAMGLFCLMISFFILFAM		
	SEQ ID NO: 327	434 bp	
NOV116b, CG59855-02 DNA Sequence	ATGCAGACCACCGGGGATTACTCATTTCTCCAGCTCTGATCTGCTGTTGTACCAGGG GTCTAATCAGGCCTGTGTCTGCCTTCTCCTTGAATAGCCAGAGAATTCATCTAAACA GCCTTCCTACAGCAGCTCCCCACTCCAGGTGGCCAGACGGGAGTTCAGACCAGTGTT GTCTCCCGGGACACTGACACAGCCGCCAAGTTTATTGGTGCTGGGTCAGCCACAGTTG GTGTGGCTGATTAGAGGCTGGCATTGGAGCGGTGTTTGGCAGCTTGATTATTGTCTA TGCCAGGAAGCTGTCTCTCAAGCAGCAACTCCTCTTCTATGCCATTCTGGGCTTTGCC CTGTCTGAGGCCATGGGGCTCTTCTGTTTGATGATCTCCTTCTTCATCCTGTTTCGCA TGTGAGGCTCCGTGAGGGTCACCTGCCT		
	ORF Start: ATG at 1	ORF Stop: TGA at 409	
	SEQ ID NO: 328	136 aa	MW at 14456.7kD
NOV116b, CG59855-02 Protein Sequence	MQTTGVLLISPALICCTRGLIRPVSAFSLNSPENSSKQPSYSSSPLQVARREFQTSV VSRD TD TAAKFIGAGSATVGVADSEAGIGAVFGSLIIIVYARKLSLKQQLLFYAILGFA LSEAMGLFCLMISFFILFAM		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 116B.

Table 116B. Comparison of NOV116a against NOV116b.		
Protein Sequence	NOV116a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV116b	1..136	120/136 (88%)
	1..136	120/136 (88%)

Further analysis of the NOV116a protein yielded the following properties shown in Table 116C.

Table 116C. Protein Sequence Properties NOV116a	
PSort analysis:	0.9190 probability located in plasma membrane; 0.3000 probability located in lysosome (membrane); 0.1888 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	Likely cleavage site between residues 28 and 29

A search of the NOV116a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 116D.

Table 116D. Geneseq Results for NOV116a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV116a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAG75142	Human colon cancer antigen protein SEQ ID NO:5906 - Homo sapiens, 142 aa. [WO200122920-A2, 05-APR-2001]	1..136 7..142	115/136 (84%) 119/136 (86%)	2e-57
AAB43866	Human cancer associated protein sequence SEQ ID NO:1311 - Homo sapiens, 142 aa. [WO200055350-A1, 21-SEP-2000]	1..136 7..142	115/136 (84%) 119/136 (86%)	2e-57
AAU69713	Cell death protective sequence CNI-00730, protein #1 - Homo sapiens, 142 aa. [WO200176532-A2, 18-OCT-2001]	7..136 7..142	85/136 (62%) 98/136 (71%)	2e-36
ABB12016	Human ATP synthase subunit homologue, SEQ ID NO:2386 - Homo sapiens, 187 aa. [WO200157188-A2, 09-AUG-2001]	7..136 52..187	85/136 (62%) 98/136 (71%)	2e-36
AAB53428	Human colon cancer antigen protein sequence SEQ ID NO:968 - Homo sapiens, 212 aa. [WO200055351-A1, 21-SEP-2000]	7..136 77..212	85/136 (62%) 98/136 (71%)	2e-36

In a BLAST search of public sequence databases, the NOV116a protein was found to have homology to the proteins shown in the BLASTP data in Table 116E.

Table 116E. Public BLASTP Results for NOV116a				
Protein Accession Number	Protein/Organism/Length	NOV116a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P05496	ATP synthase lipid-binding protein, mitochondrial precursor (EC 3.6.1.34) (ATP synthase proteolipid P1) (ATPase protein 9) (ATPase subunit C) - Homo sapiens (Human), 136 aa.	1..136 1..136	115/136 (84%) 119/136 (86%)	9e-57
P32876				1e-54

	mitochondrial precursor (EC 3.6.1.34) (ATP synthase proteolipid P1) (ATPase protein 9) (ATPase subunit C) - Bos taurus (Bovine), 136 aa.	1..136	117/136 (85%)	
P17605	ATP synthase lipid-binding protein, mitochondrial precursor (EC 3.6.1.34) (ATP synthase proteolipid P1) (ATPase protein 9) (ATPase subunit C) - Ovis aries (Sheep), 136 aa.	1..136 1..136	113/136 (83%) 117/136 (85%)	2e-54
Q9CR84	ATP SYNTHASE C CHAIN ISOFORM 1 (EC 3.6.1.34) (LIPID-BINDING PROTEIN) (SUBUNIT C) - Mus musculus (Mouse), 136 aa.	1..136 1..136	112/136 (82%) 117/136 (85%)	1e-53
P48202	ATP synthase lipid-binding protein, mitochondrial precursor (EC 3.6.1.34) (ATP synthase proteolipid P1) (ATPase protein 9) (ATPase subunit C) - Mus musculus (Mouse), 136 aa.	1..136 1..136	112/136 (82%) 117/136 (85%)	1e-53

Pfam analysis predicts that the NOV116a protein contains the domains shown in the Table 116F.

Table 116F. Domain Analysis of NOV116a			
Pfam Domain	NOV116a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ATP-synt_C: domain 1 of 1	67..135	31/70 (44%) 57/70 (81%)	2.3e-18

Example 117.

The NOV117 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 117A.

Table 117A. NOV117 Sequence Analysis		
	SEQ ID NO: 329	1769 bp
NOV117a, CG59807-01 DNA Sequence	GAGGTGATGCTGGAGACCTGCGGACTTCTCATGTCTCTGGGCTGTCTTTGTTCAAAC CAGAGCTGATCTACCAGTTGGATCACAGACAGGAGCTATGGATGGCTACAAAAGACCT CTCCCAAAGCTCCTATCCAGGTGACAACACAAAACCCAAGACCACAGAGCCTACCTTT TCTCACCTGGCCTTGCTGAGGAAGTCTTACTCCAGGAACAACCTGACACAGGAGCCT CAAAGAAGTCCCAATTAGGGCAATCCAAGGATCAGGATGGGCCATCTGAAATGCAAGA AGTCCACTTGAAAATAGGGATAGGCCCCAGCGGGGGAAGCTGCTGGAGAAAATGAGT TCTGAACGTGATGGTTTGGGGTCAGATGATGGTGTATGTACAAAGATTACACAGAAAC AAGTTTCAACAGAAGGTGATCTCTATGAATGTGATTACATGGACCAGTTACAGATGC CTTGATTCGCGAAGAGAAAAATTCCTATAAATGTGAGGAATCGGGAAAGTGTTTAAA AAGAATGCCCTCCTTGTTTCAGCATGAACGGATTCACTCAAGTGAAGCCCTATGAAT GCACAGAGTGTGGGAAAACCTTTAGCAAGAGCACTCATCTTTCAGCACCTCATCAT CCCACTGGGGAGAAGCCCTATAAGTGCATGGAGTGTGGGAAGGCTTTTAACCGCAGG	

	TCACACCTCACACGGCACCAGCGGATTCACAGTGGAGAGAAGCCTTATAAGTGCAGTG AATGTGGAAAGGCCTTCACCCACCGCTCCACTTTTGTCTTGTCATCACAGGAGCCACAC TGGAGAAAAACCTTTGTGTGCAAAAGAGTGTGGCAAAGCCTTTGAGATAGGCCAGGT TTCATTGCACTACATCATCCACACGGGAGAGAAGCCCTATGAGTGCATTGAGTGTG GGAAGGCCTTCAACCGCCGGTCATACCTCACGTGGCACCACAGATTACACTGGAGT GAAACCTTTGAATGCAACGAGTGTGGAAAAGCTTTTTCGAGAGTGCAGACCTCATT CAACACTACATTATCCACACTGGGGAGAAGCCCTATAAGTGCATGGAGTGTGGGAAGG CGTTCAACCGTAGGTACACCTCAAGCAGCATCAACGGATTACACTGGGGAGAAGCC TTATGAATGCAGTGAATGTGGAAAGGCCTTCACCCACTGCTCCACTTTTGTCTTGCA AAAAGGACCCACACAGGAGAAAAACCTATGAATGCAAGAATGTGGAAAAGCCTTTA GTGATAGGCAGACCTATTGCGCACTTCAGCATCCACACTGGAGAGAAACCTATGA GTGCGTGGAGTGTGGAAAGGCCTTCAACCGCAGCTCACACCTCACAGGCACCAACAG ATTCACACTGGAGAGAAACCTATGAATGCATCCAGTGTGGAAAGCCTTTTGCCGGA GCGCAAACTTTATTCGACACTCCATCATTACACTGGAGAGAAGCCGTATGAATGCAG TGAGTGTGGAAAGGCCTTTAATCGCGGCTCATCCCTCACACATCATCAAGGATTCAT ACTGGGAGAAACCTTACCATTGTAACAGATGTGGGAAGACCTTTTATGACTGCACAGA CTTCACTCAACATCCAGGAACCTTTATTAGGGAAGAGTTTTTGAATATCACCACTGA AGAAAATCTGTGGTGAAGGGAACATCTTACCATCTGGCCATTACACTGAAGAGAAA CTTCATAAGCATCCTCTCTTTGAGAAAAC		
	ORF Start: ATG at 7	ORF Stop: TGA at 1696	
	SEQ ID NO: 330	563 aa	MW at 64300.6kD
NOV117a, CG59807-01 Protein Sequence	MLETGGLMSLGCPLFKPELIYQLDHRQELWMATKDLSSQSSYPGDNTKPKTTEPTFSH LALPEEVLLQEQLTGAGKNSQLGQSKDQDGPSEMVEVHLKIGIPQRGKLEKMSSE RDGLGSDDGVCCKITQKQVSTEGDLYECDSHGPVTDALIREEKNSYKCECGKVFKKN ALLVQHERIHTQVKPYECTECGKTFKSTHLLQHLIHTGEKPYKCMCEGKAFNRSSH LTRHQRIHSGEKPYKCECGKAFTHRSTFVLHHRSHTEGKPFVCKEKGKAFDRPGFI RHYIHTGEKPYECIECGKAFNRSSYLTHWQIHTGVKPFECNECGKAFCEADLIQH YIIHTGEKPYKCMCEGKAFNRSSHLKQHQRIHTGEKPYECSECGKAFTHCSTFVLHKR THTGEKPYECKEGKAFSDRADLRHFSIHTGEKPYECVECGKAFNRSSHLTRHQQIH TGEKPYECIQCGKAFCRSANLRHSIHTGEKPYECSECGKAFNRSSSLTHHQRIHTG RNPTIVTDVGRPFMTAQTSVNIQELLGKEFLNITTEENLW		

Further analysis of the NOV117a protein yielded the following properties shown in Table 117B.

Table 117B. Protein Sequence Properties NOV117a	
Psort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	Likely cleavage site between residues 19 and 20

A search of the NOV117a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 117C.

Table 117C. Geneseq Results for NOV117a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV117a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79549	Human protein SEQ ID NO 3195 - Homo sapiens, 603 aa. [WO200157190-A2, 09-AUG-2001]	1..563 38..603	563/566 (99%) 563/566 (99%)	0.0
AAM78565	Human protein SEQ ID NO 1227 - Homo sapiens, 603 aa. [WO200157190-A2, 09-AUG-2001]	1..563 38..603	563/566 (99%) 563/566 (99%)	0.0
ABB21767	Protein #3766 encoded by probe for measuring heart cell gene expression - Homo sapiens, 551 aa. [WO200157274-A2, 09-AUG-2001]	44..562 10..527	375/519 (72%) 437/519 (83%)	0.0
AAM69575	Human bone marrow expressed probe encoded protein SEQ ID NO: 29881 - Homo sapiens, 551 aa. [WO200157276-A2, 09-AUG-2001]	44..562 10..527	375/519 (72%) 437/519 (83%)	0.0
AAM57172	Human brain expressed single exon probe encoded protein SEQ ID NO: 29277 - Homo sapiens, 551 aa. [WO200157275-A2, 09-AUG-2001]	44..562 10..527	375/519 (72%) 437/519 (83%)	0.0

In a BLAST search of public sequence databases, the NOV117a protein was found to have homology to the proteins shown in the BLASTP data in Table 117D.

Table 117D. Public BLASTP Results for NOV117a				
Protein Accession Number	Protein/Organism/Length	NOV117a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O43296	Zinc finger protein 264 - Homo sapiens (Human), 627 aa.	1..562 43..603	401/562 (71%) 468/562 (82%)	0.0
Q96NL3	CDNA FLJ30663 FIS, CLONE FCBBF1000598, MODERATELY SIMILAR TO ZINC FINGER PROTEIN 84 - Homo sapiens (Human), 588 aa.	1..535 38..572	299/535 (55%) 369/535 (68%)	0.0
Q99676				e-151

	sapiens (Human), 751 aa.	58..595	355/542 (65%)	
Q96SE7	ZINC FINGER 1111 - Homo sapiens (Human), 839 aa.	151..541 306..694	233/391 (59%) 281/391 (71%)	e-148
Q03923	Zinc finger protein 85 (Zinc finger protein HPF4) (HTF1) - Homo sapiens (Human), 595 aa.	1..535 33..547	266/544 (48%) 328/544 (59%)	e-148

PFam analysis predicts that the NOV117a protein contains the domains shown in the Table 117E.

Table 117E. Domain Analysis of NOV117a			
Pfam Domain	NOV117a Match Region	Identities/ Similarities for the Matched Region	Expect Value
KRAB: domain 1 of 1	1..34	14/66 (21%) 24/66 (36%)	0.15
zf-C2H2: domain 1 of 13	162..184	11/24 (46%) 19/24 (79%)	3.6e-06
zf-C2H2: domain 2 of 13	190..212	11/24 (46%) 19/24 (79%)	7.1e-06
zf-C2H2: domain 3 of 13	218..240	14/24 (58%) 22/24 (92%)	2.3e-07
zf-BED: domain 1 of 3	203..241	13/52 (25%) 25/52 (48%)	2
zf-C2H2: domain 4 of 13	246..268	11/24 (46%) 20/24 (83%)	4.6e-05
LIM: domain 1 of 1	220..284	16/72 (22%) 50/72 (69%)	0.69
zf-C2H2: domain 5 of 13	274..296	8/24 (33%) 18/24 (75%)	7.6e-05
zf-C2H2: domain 6 of 13	302..324	11/24 (46%) 20/24 (83%)	8.4e-05
Zn_carbOpept: domain 1 of 1	312..330	5/19 (26%) 17/19 (89%)	1.2
zf-C2H2: domain 7 of 13	330..352	8/24 (33%) 19/24 (79%)	9.7e-05
zf-C2H2: domain 8 of 13	358..380	14/24 (58%) 22/24 (92%)	5.3e-07

zf-BED: domain 2 of 3	343..381	12/52 (23%) 26/52 (50%)	1.3
zf-C2H2: domain 9 of 13	386..408	11/24 (46%) 20/24 (83%)	9.4e-05
zf-C2H2: domain 10 of 13	414..436	11/24 (46%) 20/24 (83%)	5e-06
zf-C2H2: domain 11 of 13	442..464	12/24 (50%) 22/24 (92%)	3e-07
zf-BED: domain 3 of 3	427..465	14/52 (27%) 27/52 (52%)	0.38
zf-C2H2: domain 12 of 13	470..492	12/24 (50%) 19/24 (79%)	0.00044
zf-C2H2: domain 13 of 13	498..520	12/24 (50%) 22/24 (92%)	9.8e-07

Example 118.

The NOV118 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 118A.

Table 118A. NOV118 Sequence Analysis		
	SEQ ID NO: 331	1899 bp
NOV118a, CG59805-01 DNA Sequence	<p> CAAACTCTACTACCTCTATATGACATTTTCAGGTGTCTGTGACCTTTTGATGATGTGGCT GTGACTTTTACCAGGAGGAGTGGGGCCAGCTGGACCTAGCTCAGCGGACCTGTACC AGGAGGTGATGTGGAAACTGTGGGCTCCTGGTATCTCTGGGTGGGTGTCTGTGCC CAGACCTGAGCTGATCTACCACTAGAGCATGGGCAGGAGCCATGGACCAGGAAGGAA GACCTCTCCCAAGGCACCTGTCCAGGTGACAAAGGAAACCCAGAGCACAGAACCTA CCACCTGTGAGCTAGCTTGTCTGAAGGAATCTCTTTTGGGGACAACCAACAAGG AGCTTCAGGGGACTCCCACTTGGGGCAACCCAGGATCAGGATGGGTTTTCAGAAATG CAGGGAGAACGCTTGAGACCAGGGTTAGATTCCTCAAAAGGAGAAGCTTCCTGGAAAAA TGAGCCCCAAACATGATGGTTTAGGGACAGCTGATAGTGTGTGTTCAAGGATTATACA GGATCGAGTCTCCTTAGGAGATGATGTCCATGACTGTGACTCACATGGATCAGGTA AATCCAGTTATTCAGGAAGAGGAAATATCTTTAAATGCAATGAATGTGAAAAAGTGT TTAACAAGAAACGCTTGTCTCGGCATGAGAGGATTCACTCTGGAGTGAAGCCCTA TGAATGCACAGAGTGTGGAAAAACCTTTAGCAAGAGTACATACCTCCTGCAGCACCAC ATGGTCCACACTGGGGAGAAAGCCCTATAAGTGCATGGAGTGTGGGAAGGCTTTTAAATC GGAAGTCAACCTTACCCAGCACCAGCGGATTCACAGTGGAGAGAAGCCTTATAAGTG CAGTGAATGTGAAAGGCCCTTACCCACCGCTCCACTTTTGTCTGCATAACAGGAGC CACACTGGAGAAAAACCTTTGTGTGCAAGAGTGTGGCAAAGCCTTTCGAGATAGGC CAGGTTTCATTGCACTACATCATCCACAGTGGTGAAGTCCCTACGAGTGTCTCGA ATGTGGCAAGGTCTTCAACACAGATCATACCTCATGTGGCACCAGCAGACTCATACC GGGGAGAAGCCCTATGAGTGCAGTGAATGTGGGAAGGCCTTCTGTGAGAGCGCAGCGC TGATTCACCACTATGTATCCACTGGAGAGAAGCCCTTTGAGTGCCTCGAGTGTGG GAAGGCTTTCAACCACCGATCCTACCTCAAAAGGCACCAGCGGATTCACACTGGGGAG AAGCCATATGTGTGTAGTGAATGCGGAAGGCCCTTCAACCACTGCTCTACTTTTCACT TGCATAAAAGGGCCCACTGGAGAAAAACCTTTGAGTGCAGAGTGTGGGAAAGC CTTTAGCAATAGGGCAGACCTATTGCGCACTTCAGCATCCCACTGGAGAGAAGCCC TATGAGTGCATGGAGTGTGGAAAGGCCCTTCAACCGCAGGTCAGGCTCACAAGGCACC AGCGGATTATAGTGGAGAGAAGCCCTATGAATGCATCGAGTGTGGGAAACATTTTG CTGGAGCAAAACCTTATCGACTCTATCATCCCACTGGAGAGAAGCCGTATGAG TGCAGTGAATGTGGAAAGGCCCTTCACTGCAGCTCGTCCCTCACTCAGCATCAAAGGA TGCATACTGGGAGAAATCCTATCAGTGTAAACAGATGTGGGAAGACCTTTTACAAGTGG GCAGACCTCAGTCAACATCCAAGAACTTTTATGGGGAAAACTTTTGAATGTCAACC ACTGAGGAAAACTTTTGCAGGAAGCATCTTACATGGCATCTGATCGTACATACC AAAGAGAAACCCACAAGTGTCTTCACTGTGAGAAAACCTTCT </p>	
	ORF Start: ATG at 20	ORF Stop: TGA at 1886

	SEQ ID NO: 332	622 aa	MW at 70677.2kD
NOV118a, CG59805-01 Protein Sequence	MTFQVSVTFDDVAVTFTQEEWGQLDLAORTLYQEVMLENCGLLVSLGGCPVPRPELIY HLEHGQEPWTRKEDLSQGTCPGDKGKPKSTEPTTCELALSEGISFWGQLTQGASGDSQ LGQPKDQDGFSEMQGERLRPGLDSSQKEKLPKMSPKHDGLGTADSVCSRIIQDRVSLG DDVHDCDSHSGKNPVIQEEENIFKCNECEKVFNKRLLARHERIHSGVKPYECTECG KTFSKSTYLLQHHMVHTGEKPYKMECGKAFNRKSHLTQHQRHSGEKPYKCECGKA FTHRSTFVLNRSHTGEKPFVCKEKGAFRDRPGFIRHYIIHSGENPYECFECGKVFK HRSYLMWHQQTHTGEKPYECSECGKAFCEAALIHHYVIHTGEKPFECLECGKAFNHR SYLKRHRQRIHTGEKPYVCEGKAFTHCSTFILHKRAHTGEKPFECGKAFSNRAD LIRHFSIHTGEKPYECMECGKAFNRRLTRHQRHSGEKPYECIECGKTFCWSTNLI RHSIIHTGEKPYECSECGKAFSRSSSLTQHQRMTGRNPISVTDVGRPFTSGQTSVNI QELLGKNFLNVTTEENLLQEEASYMASDRTYQRETPQVSSL		

Further analysis of the NOV118a protein yielded the following properties shown in Table 118B.

Table 118B. Protein Sequence Properties NOV118a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3796 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV118a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 118C.

Table 118C. Geneseq Results for NOV118a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV118a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABB22693	Protein #4692 encoded by probe for measuring heart cell gene expression - Homo sapiens, 468 aa. [WO200157274-A2, 09-AUG-2001]	81..548 1..468	468/468 (100%) 468/468 (100%)	0.0
AAM70526	Human bone marrow expressed probe encoded protein SEQ ID NO: 30832 - Homo sapiens, 468 aa. [WO200157276-A2, 09-AUG-2001]	81..548 1..468	468/468 (100%) 468/468 (100%)	0.0
AAM58080	Human brain expressed single exon probe encoded protein SEQ ID NO: 30185 - Homo sapiens, 468 aa. [WO200157275-A2, 09-AUG-2001]	81..548 1..468	468/468 (100%) 468/468 (100%)	0.0
AAM30843				0.0

	measuring placental gene expression - Homo sapiens, 468 aa. [WO200157272-A2, 09-AUG-2001]	1..468	468/468 (100%)	
AAM18364	Peptide #4798 encoded by probe for measuring cervical gene expression - Homo sapiens, 468 aa. [WO200157278-A2, 09-AUG-2001]	81..548 1..468	468/468 (100%) 468/468 (100%)	0.0

In a BLAST search of public sequence databases, the NOV118a protein was found to have homology to the proteins shown in the BLASTP data in Table 118D.

Table 118D. Public BLASTP Results for NOV118a				
Protein Accession Number	Protein/Organism/Length	NOV118a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
O43296	Zinc finger protein 264 - Homo sapiens (Human), 627 aa.	4..622 11..627	530/619 (85%) 567/619 (90%)	0.0
Q96NL3	CDNA FLJ30663 FIS, CLONE FCBBF1000598, MODERATELY SIMILAR TO ZINC FINGER PROTEIN 84 - Homo sapiens (Human), 588 aa.	7..572 9..573	334/566 (59%) 403/566 (71%)	0.0
Q99676	Zinc finger protein 184 - Homo sapiens (Human), 751 aa.	2..571 23..623	280/604 (46%) 377/604 (62%)	e-160
P51523	Zinc finger protein 84 (Zinc finger protein HPF2) - Homo sapiens (Human), 738 aa.	4..617 5..626	286/637 (44%) 368/637 (56%)	e-157
Q9BX82	EZFIT-RELATED PROTEIN 1 - Homo sapiens (Human), 626 aa.	7..617 14..626	278/621 (44%) 364/621 (57%)	e-156

PFam analysis predicts that the NOV118a protein contains the domains shown in the Table 118E.

Table 118E. Domain Analysis of NOV118a

Pfam Domain	NOV118a Match Region	Identities/ Similarities for the Matched Region	Expect Value
KRAB: domain 1 of 1	7..70	41/66 (62%) 54/66 (82%)	2.2e-33
zf-C2H2: domain 1 of 13	198..220	11/24 (46%) 17/24 (71%)	3.9e-05
BolA: domain 1 of 1	161..238	14/88 (16%) 49/88 (56%)	3.4
zf-C2H2: domain 2 of 13	226..248	10/24 (42%) 18/24 (75%)	6.2e-05
zf-C2H2: domain 3 of 13	254..276	14/24 (58%) 22/24 (92%)	5e-07
TFIIS: domain 1 of 1	257..292	12/39 (31%) 21/39 (54%)	5.7
zf-C2H2: domain 4 of 13	282..304	11/24 (46%) 20/24 (83%)	3.7e-05
LIM: domain 1 of 1	256..320	14/71 (20%) 48/71 (68%)	0.38
zf-C2H2: domain 5 of 13	310..332	8/24 (33%) 18/24 (75%)	7.6e-05
zf-C2H2: domain 6 of 13	338..360	11/24 (46%) 19/24 (79%)	1.1e-05
zf-C2H2: domain 7 of 13	366..388	9/24 (38%) 18/24 (75%)	0.00027
zf-C2H2: domain 8 of 13	394..416	12/24 (50%) 21/24 (88%)	7.9e-07
zf-C2H2: domain 9 of 13	422..444	10/24 (42%) 19/24 (79%)	0.00014
zf-C2H2: domain 10 of 13	450..472	10/24 (42%) 20/24 (83%)	8.3e-06
zf-C2H2: domain 11 of 13	478..500	13/24 (54%) 21/24 (88%)	3e-07
zf-BED: domain 1 of 1	463..501	14/52 (27%) 29/52 (56%)	0.1
zf-C2H2: domain 12 of 13	506..528	11/24 (46%) 17/24 (71%)	0.0016

zf-C2H2: domain 13 of 13	534..556	13/24 (54%) 23/24 (96%)	7.2e-08
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Example 119.

The NOV119 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 119A.

Table 119A. NOV119 Sequence Analysis			
	SEQ ID NO: 333	1546 bp	
NOV119a, CG59928-01 DNA Sequence	<div>GCTCAGTAGGCGTCGGGCTGTGATGCCCCAACTGCTCCAGCGTCTGCAGGCGCGCGCG GGCGCGGTAGGCGTACTCGCTGGCCGGATAGCGCGTGATGTAAGTGGTAGGTTCTGC GCCGCATCGACGAACAGGCTCTCGCGCTCCAGGCATTGACCGCGCAGCAGGGAAATCT CCGGCTGCAGGTAATTGCGTGAGCGGCTCTTGCGCTCGGCCCTGCGCAGCTCCAGCGC GACACGGGCGCAATCGCCTTCGTTGTAGGCGCGATAGGCGTTGTTTCAGATGATGGTCG AGCGAGACACGGGTGCAACCGCAGCAACAGGGCCACGGCCAGAATGATCAGGTTAC GCATGGGCAATTCTCTCCAATGAGCAGTGATTCGACAGCCCAGGCAAAAACCTGAACAGC GGCAAGCCGACGACGGTTTTTCTGGCGGCGCCTTGGCATGACGCCACTGCCTCTCATT TTATCAACGCCAGCGCCACGACCGCTCGTCCTCTCGAACCAGCGCTAAATCCCCCTTCT GCGCTGACCCATATCAATGCCGTTTACGCGCAACAGGGTGTGTAATGTAGGTACAGACT CCAGGCGAGGACGCTGCCATGAAACTGCAACGACTGTTGGTCTGTCATCGACGCCGAAC ACCAGCAACAACCGCCCTGCAACGCGCAGCCGATGTGGCAGCAGACCGCGCCGA ATTGCACCTGTTGCAGATCGAATACCACCCAAGCCTGGAAAGCGGCTGCTGGACAGC CATCTGCTCAACCGCGCCCGTGAAACCATCCTGCGACAGAGCCACGAGGCCCTGCGTG CCAGCGTCGCTCACCTGAGCGATGAAGGATTCAGATCGCAGTGGACGTGCGCTGGGG CAAACGTCGTATGAAGAAATCCTCGCCCGCGTCGCGGTGTTGCAACCGGACATCCTG TTCAAGTCGACTCATCCAGCAGTGCCTGCGCGCGCTGTTGTTTCACTGATACCAGTT GGCAGCTGATTGCGCCGAGCCCGGTGCGCTGTGGCTGGTACAGCAGCCGAGCCCCA TGGTCAGAGCCTGTGCGCTGCGCTCGACCCGCTGCACAGCGCGGACAAACCTGCGCCG CTCGATCATCAGTTGATTGATGCCAGCCAGACCCTGCAGGCCGAGCTCGGCTTACAGG CCCAATACCTGCATGCACAGGCGCCTCTGCGCGGTGCTGCTGTTTCGACGCCGAGGT AGCGCAGGAATATGAAGACTACGTGACCCAGTGCAGCCGCGAGCACCGCGAAGCCTTC GACAAGCTGATCGCCAGCAGCCATCGATAGAGCACAGGCCCACTGTTGGACGGTT TTGCCGAGGAAGTCATCCCGCGTTTCGTGCGTGAGCACAATATAGGCTGCTGGTGAT GGGCGCCATCGCCCGCGCCATCTGGACAGCCTGCTGATCGGCCACACCGCAGAACGG GTGCTGGAACGTGTCGAGTGCATCTGCTGGTGATCAAATCGCACGAAGGGTAGT GCACAGGAACAATGACTACAGCCCGACGCCTACTGAGC</div>		
	ORF Start: ATG at 599	ORF Stop: TAG at 1505	
	SEQ ID NO: 334	302 aa	MW at 33922.3kD
NOV119a, CG59928-01 Protein Sequence	<div>MKLQRLLVVIDAEHQQPALQRAADVARKTGAEHLHLQIEYHPSLESGLLDSHLLNRA RETILRQSHALRASVAHLSDEGFKIAVDVRWGRKRHEEILARVAVLQPDILFKSTHP SSALRRLLFSDTSWQLIRRSVPVPLWLVDHAEPHGQSLCAALDPLHSADKPAALDHQLI DASQTLQAEGLQAQYLHAQAPLPRSLLFDAEVAQEYEDYVTQCSREHREAFDKLIAQ HAIDRAQAHLLDGFABEVI PRFVREHNI GLLVMGAIARGHLDSLLIGHTAERVLERVE CDLLVIKSHGKG</div>		

Further analysis of the NOV119a protein yielded the following properties shown in Table 119B.

Table 119B. Protein Sequence Properties NOV119a	
PSort analysis:	0.3000 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.2014 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV119a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 119C.

Table 119C. Geneseq Results for NOV119a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV119a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found				

In a BLAST search of public sequence databases, the NOV119a protein was found to have homology to the proteins shown in the BLASTP data in Table 119D.

Table 119D. Public BLASTP Results for NOV119a				
Protein Accession Number	Protein/Organism/Length	NOV119a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9HW73	HYPOTHETICAL PROTEIN PA4328 - <i>Pseudomonas aeruginosa</i> , 304 aa.	1..297 1..299	156/299 (52%) 200/299 (66%)	1e-79
Q9KS28	HYPOTHETICAL PROTEIN VC1433 - <i>Vibrio cholerae</i> , 315 aa.	5..300 6..304	78/302 (25%) 147/302 (47%)	4e-29
CAC91106	PUTATIVE STRESS PROTEIN - <i>Yersinia pestis</i> , 318 aa.	2..300 3..303	93/310 (30%) 137/310 (44%)	2e-28
AAL20579	PUTATIVE UNIVERSAL STRESS PROTEIN - <i>Salmonella</i> typhimurium LT2, 315 aa.	4..297 5..300	91/305 (29%) 139/305 (44%)	2e-28
CAD01669	CONSERVED HYPOTHETICAL PROTEIN - <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi, 315 aa.	4..297 5..300	91/305 (29%) 139/305 (44%)	3e-28

PFam analysis predicts that the NOV119a protein contains the domains shown in the Table 119E.

Table 119E. Domain Analysis of NOV119a			
Pfam Domain	NOV119a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Usp: domain 1 of 2	2..144	28/153 (18%) 92/153 (60%)	0.0014
Usp: domain 2 of 2	160..297	28/153 (18%) 88/153 (58%)	0.013

Example 120.

The NOV120 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 120A.

Table 120A. NOV120 Sequence Analysis			
	SEQ ID NO: 335	2202 bp	
NOV120a, CG59947-01 DNA Sequence	<p>CACCCTCCCGCCCCCGCCCCCGTCCAATGCTGAGCTCAGTCTGCGTCTCGTCTTCCG CGGGCGCCAGGGGGCCAGCAAGCAGCAGCCGGCGCCACCGCCGACGCCGCCGAGGTC CCCGGTGGCGACAGCGGCAAGATCGTGATCAACGTGGGCGGCGTGCCCATGAGACGT ACCGCTCGACGCTGCGCACCTGCCGGGGACGCGGCTGGCCGGCTGACGGAGCCGA GGCGGCGGACGCTTCGACTACGACCCGGGCGCGACGAGTTCTTCTTGACCGGCAC CCGGGAGTCTTCGCGTACGTGCTCAACTACTACCGCACCGGCAAGCTGCACTGCCAG CCGACGTGTGCGGGCCCTGTTTGGAGGAGGAGCTCGGCTTCTGGGGCATCGACGAGAC CGACGTGGAGGCTGCTGCTGGATGACCTACCGGCAGCATCGGACGCTGAGGAGGCG CTCGACTCTTCGAGGGCGCCGACCCCGGGGCGCGGCCAACGCCGCAACGCCGCGAG GCGCCACGACGAGGAGGCTGGACGACGAGGCGGGCGCGGGCGCGGCGGCTGGACGG AGCGGGCGGCGAGCTCAAGCGCCTCTGCTTCCAGGACGCGGGCGGGCGCGGGGGG CCGCCAGGGGGCGCGGGCGGGCGGGCGGCACATGGTGGCGCGCTGGCAGCCCCGCG TGTGGGCGCTCTTCGAGGACCCCTACTCGTCGCGGGCTGCCAGGTATGTGGCCTTCG CTCCCTCTTCTTCATCTCATCTCCATCACCACTTCTGCCTGGAAACCCATGAGGGC TTTCATCCATATTAGCAACAAGACGGTGACCCAGGCTCCCGCATCCCGGGGACCTC CGGAGAACATCACCAACGTGGAGGTGGAGACGGAGCCCTTCTGACCTACGTGGAGGG GGTGTGCGTGGTCTGGTTCACCTTCGAGTTCTCATGCGCATCACCTTCTGCCAGAC AAGTGGAGTTTCTTAAAGCAGCCTCAACATCATCGACTGTGTGGCCATCTTGCCCT TCTATCTCGAGGTGGGCTCTCGGGCTCAGCTCCAAGGCCGCAAGACGTGCTGGG CTTCTCGGGTGGTCTCGCTTCGTCGCGATCTTCAAGCTGACCGCGCAC TTCTGTGGGCTGCGCGTGTGGGACACAGCTCCGCGCCAGCACCAACGAGTTCTCTG TGCTCATCATCTTCTTGCCCTGGGGGTGCTCATCTTCGCCACCATGATTTACTACGC TGAGCGCATTTGGCGCGACCCGATGACATCTTGGGCTCCAACCACACTTACTTCAAG AACATCCCCATTGGCTTCTGGTGGGCTGTGGTCACCATGACGACCTTGGGCTATGGAG ACATGTACCCCAAGACGTGGTGGGGATGCTGGTGGGGCGCTGTGTGCCCTGGCGGG GGTGCTGACCATCGCATGCCTGTGCCCGTCATTGTCAACAATTTGGCATGTACTAT TCGCTGGCCATGGCCAAGCAGAAGCTGCCAAGAAGAAGAACAAACATCCCCGGGC CCCCGCAACCGGGCTGCCCCAACTACTGCAAGCCTGACCCACCCCGCCACCCCGCC CCACCCGACCACGGACGCGGGGATCAGCCCGCGCCACCCATCACCCACCTCC ATGGGGGTGACTGTGGCCGGGGCTACCCAGCGGGGCCACAGCACCCCGGGCTGC TCAGGGGGGAGCGGGTGGGCTGGGGATCATGGGGCTGCCTCTCTGCGAGCCCCGG CGAGCCTTGCCCGTTGGCTCAGGAGGAGGTGATTGAGATCAACCGGGCAGATCCTCG CCCAATGGGGATCCGGCAGCAGCTGCGCTTGCCACGAGGACTGCCAGCCGATTGACC AGCCTGCCATGTCCCCGAAGACAAGAGCCCCATCAGCCTGGAAGCGGTGGCCGCTA TAGCCGGGACCGAGCCTGCTTCTCTCTCACCGACTATGCCCTTCCCTGATGGCTCC ATCCGAAAAGCCACTGGTGTCTCCCACTGCCCCCCCAAGACTGGCGTAAGCCAGGCC CCCCAAGCTTCTTGCCGACCTCAACGCCAACGCCGCGGCGCTGGATATCCCCCTAGTG GACGAACCCCTCCCCCGGGCTCTGTACCGCTGAGACCTCGCGAGACTTTCG</p>		
	ORF Start: ATG at 27	ORF Stop: TAG at 2142	
	SEQ ID NO: 336	705 aa	MW at 75590.5kD
NOV120a,	<p>MLSSVCVSSFRGRQASKQQPAPPPQPEVPGDSGKIVINVGGVRHETYRSTLRLLP GTRLAAGLTEPEAAARFDYDPGADEFFDRHFGVFAYVLNYYRTGKLHCPADVCGPLFE</p>		

CG59947-01 Protein Sequence	EELGFWGIDETDVEACWMTYRQHRDAEEALDSFEAPDPAGAANAANAAGAHGGLDD EAGAGGGGLDAGGELKRLCFQDAGGGAGGPPGGAGGAGGTWRRWQPRVWALFEDPY SSRAARYVAFASLFFILISITTFCLTHEGFIHISNKTVTQASIPGAPPENITNVEV ETEPFLTYYVEGVCVVWFTFEFLMRITFCPDKVEFLKSSLNIIDCVAILFFYLEVGLSG LSSKAAKDVLGFLRVVRVIRILRIFKLTRHFVGLRVLGHTRLASTNEFLLLIIFLALG VLIIFATMIYYAERIGADPDDILGSNHTYFKNIPIGFWWAVVTMTLGYGDMYPKTWSG MLVGALCALAGVLTIAMPVPIVNNFMYSLAMAKQKLPKKKNKHIPRPQPGSPNY CKPDPPPPPPPHHGGSGGISPPPPITPPSMGVTVAGAYPAGPHTHPGLLRGGAGGLG IMGLPPLPAPGEPCPLAQEEVIEINRADPRNGDPAAALAHEDCPAIDQPAMSPEDK SPITPGSRGRYSRDRACFLLDYAPSPDGSIRKATGAPPLPPQDWRKPGPPSFLPDLN ANAAAWISP
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Further analysis of the NOV120a protein yielded the following properties shown in Table 120B.

Table 120B. Protein Sequence Properties NOV120a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.5071 probability located in mitochondrial inner membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV120a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 120C.

Table 120C. Geneseq Results for NOV120a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV120a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAV34120	Human potassium channel K+Hnov4 - Homo sapiens, 601 aa. [WO9943696-A1, 02-SEP-1999]	32..526 4..476	371/510 (72%) 399/510 (77%)	0.0
AAV32016	Caenorhabditis elegans cation channel protein - Caenorhabditis elegans, 556 aa. [WO9947923-A2, 23-SEP-1999]	33..512 27..465	217/486 (44%) 300/486 (61%)	e-113
AAB86319	Human Kv4.2 protein - Homo sapiens, 629 aa. [DE19963612-A1, 12-JUL-2001]	16..521 22..441	173/511 (33%) 256/511 (49%)	5e-69
AAV13523	Amino acid sequence of KV4.2FL ion channel protein - Mammalia, 630 aa. [WO9923880-A1, 20-MAY-1999]	16..521 23..442	173/511 (33%) 257/511 (49%)	8e-68

AAW42996	Putative mature potassium channel 2 protein - Homo sapiens, 494 aa. [US5710019-A, 20-JAN-1998]	17..510 4..425	171/503 (33%) 240/503 (46%)	2e-66
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In a BLAST search of public sequence databases, the NOV120a protein was found to have homology to the proteins shown in the BLASTP data in Table 120D.

Table 120D. Public BLASTP Results for NOV120a				
Protein Accession Number	Protein/Organism/Length	NOV120a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q14003	Voltage-gated potassium channel protein Kv3.3 (KSHIID) - Homo sapiens (Human), 757 aa.	1..705 1..757	704/757 (92%) 704/757 (92%)	0.0
Q01956	Voltage-gated potassium channel protein Kv3.3 (KSHIID) - Rattus norvegicus (Rat), 889 aa.	1..693 1..756	663/757 (87%) 668/757 (87%)	0.0
Q63959	Voltage-gated potassium channel protein Kv3.3 (KSHIID) - Mus musculus (Mouse), 769 aa.	1..671 1..724	650/725 (89%) 653/725 (89%)	0.0
A42073	potassium channel protein Kv3.3 - mouse, 679 aa.	32..607 8..581	557/576 (96%) 559/576 (96%)	0.0
Q9PVD1	KV3.1 POTASSIUM CHANNEL - Xenopus laevis (African clawed frog), 592 aa.	34..671 6..547	441/640 (68%) 479/640 (73%)	0.0

PFam analysis predicts that the NOV120a protein contains the domains shown in the Table 120E.

Table 120E. Domain Analysis of NOV120a			
Pfam Domain	NOV120a Match Region	Identities/ Similarities for the Matched Region	Expect Value
K_tetra: domain 1 of 1	36..137	50/112 (45%) 86/112 (77%)	1.6e-47
thaumatin: domain 1 of 1	314..319	4/6 (67%) 6/6 (100%)	0.7

ion_trans: domain 1 of 1	295..486	51/231 (22%) 155/231 (67%)	2.1e-29
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Example 121.

The NOV121 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 121A.

Table 121A. NOV121 Sequence Analysis			
	SEQ ID NO: 337	1943 bp	
NOV121a, CG59938-01 DNA Sequence	AGATCCACGTGATCTCCAAAGACCCCTGTTGTGTTGTGTTGGGAGGTGGATCCTGAAT CCACCCAGAGAAGCCTGATACCAATAAAATCCCTGCTTGCTTTCCAGGAGACCCCTGG TCTTCATGTCTTTGGTGTGTGCACTCTTGAACACATGCCAGGCACACAGGGTGCATGA CGACAAGCCTAATATTGTCTTAATCATGGTTGATGACCTGGGTATTGGAGATCTGGGC TGCTACGGCAATGACACCATGAGGACGCCTCACATCGACCGCTTGCCAGGGAAGGCG TGCGACTGACTCAGCACATCTCTGCCGCCTCCCTCTGCAGCCCAAGCCGGTCCGCGTT CTTGACGGGAAGATACCCCATCCGATCAGGTATGGTTTCTAGTGGTAATAGACGTGTC ATCCAAAATCTTGCACTCCCGCAGGCCTCCCTCTTAATGAGACAACACTTGCAGCCT TGCTAAAGAAGCAAGGATACAGCACGGGGCTTATAGGTAAGTTAGGCAAAATGGCACCT GGGTTTGAGCTGCGCCTCTCGGAATGATCACTGTTACCACCGCTCAACCATGGTTTTT CACTACTTTTACGGGGTGCCCTTTTGGACTTTTAAAGCACTGCCAGGCATCCAAGACAC CAGAACTGCACCGCTGGCTCAGGATCAAACTGTGGATCTCCACGGTAGCCCTTGCCCT GGTTCCTTTTCTGCTTCTCATTCCCAAGTTCGCCCGCTGGTCTCAGTGGCATGGAAG GTCATCTTGTCTTTGCTCTCCTCGCCTTTCGTGTTTTCACCTCTCTGGTACTCTAGTT ATGGATTTACTCGACGTTGGAATTGCATCCTTATGAGGAACCATGAAATTATCCAGCA GCCAATGAAAGAGGAGAAAGTAGCTTCCCTCATGCTGAAGGAGGCACCTTGCTTTCATT GAAAGGTACAAAAGGGAACCTTTTCTCCTCTTTTTTTCCTTCTGCACGTACATACTC CACTCATCTCCAAAAGAGTTTGTGGGCGCAGTAAATATGGCAGGTATGGGGACAA TGTAAGAAGAAATGGATTGGATGGTGGGTGGTAAATCCTGGATGCCCTGGACCGAGG CGCCTGGCCAACCAACCTTGGTGTACTTCACCTCTGACAACGGGGGCCACCTGGAGC CCCTGGACGGGGCTGTTTCACTGGGTGGCTGGAACGGGATCTACAAGGTGGCAAAGG AATGGGAGGATGGGAAGGAGGTATCCGTGTGCCAGGGATATTCGGTGGCCGTCAGTC TTGGAGGCTGGGAGAGTGATCAATGAGCCCAACAGCTTAATGGACATCTATCCGACGC TGTCTTATATAGCGGAGGGATCTTGTCCCAGGACAGAGTGATTGACGGCCAGAACCT AATGCCCTGCTGGAAGGAAGGGCGTCCCACTCCGACCAAGAGTTCTCTTCCACTAC TGTGGGGTCTATCTGCACACGGTCAGGTGGCATCAGAAGGACACTGTGTGGAAGCTC ATTATGTGACTCTTAAATTCTACCCTGAAGGAACAGGTGCTGTCTATGGGAGTGGAA ATGTTTATGTTTGGGGATGTAACCTACCACGACCCCACTCCTCTTTGACATCTCA AGAGACCCCTCAGAAGCCCTTCCACTGAACCTGACAATGAGCCATTATTTGACTCCG TGATCAAAAAGATGGAGGCAGCCATAAGAGAGCATCGTAGGACACTAACACCTGTCCC ACAGCAGTTCTCTGTGTTCAACACAATTGGAAACCATGGCTGCAGCCTTGCTGTGGG ACCTTCCCCTTCTGTGGGTGTGACAAGGAAGATGACATCCTTCCCATGGCTCCCTGAG ACCATGCGGACCACGTGTTACCCACCACAACTTACTGTTACAATGGTCATAGGAGCA GAGCTCACCTGACTGATTCAATCCATTG		
	ORF Start: ATG at 122	ORF Stop: TGA at 1853	
	SEQ ID NO: 338	577 aa	MW at 65099.5kD
NOV121a, CG59938-01 Protein Sequence	MSLVCALLNTQAHVRVHDDKPNIVLIMVDDLIGIDLGCYGNMTMRTPHIDRLAREGVR LTQHISAASLCSPSRSAFLTGRYPISGMVSSGNRRVIQNLAVPAGLPLNETTLAALL KKQGYSTGLIGLKGWHLGLSCASRNDHCYHPLNHGFHYFYGVFPGLLSDCQASKTPE LHRWLRIKLWISTVALALVPFLLLI PKFARWFSVPWKVIFVFALLAFLFTTSWYSSYG FTRRWNCILMRNHEIIQQPMKEEKVASLMLKEALAFIERYKREPLFFSFLHVHTPL ISKKKFVGRSKYGRYDNVEEMDWMVGGKILDALDQERLANHTLVYFTSDNGGHLEPL DGA VQLGWNNGIYKGGKMGWEGGIRVPGIFRWPSVLEAGRVINEPTSLMDIYPTLS YIGGGILSQDRVIDQNLMPLLEGRASHSDHEFLFHYCGVYLHTVRWHQKDTVWKAHY VTPKFYPEGTGACYGSGICSCSGDVTYHDPPLLFDISRDPSEALPLNPNEPLFDSVI KKMEAAIREHRRTLTPVPQQFSVFNTIWKPLWQPCGTFPFCGCKEDDILPMAP		

Further analysis of the NOV121a protein yielded the following properties shown in Table 121B.

Table 121B. Protein Sequence Properties NOV121a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV121a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 121C.

Table 121C. Geneseq Results for NOV121a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV121a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM78688	Human protein SEQ ID NO 1350 - Homo sapiens, 590 aa. [WO200157190-A2, 09-AUG-2001]	1..572 10..580	388/576 (67%) 449/576 (77%)	0.0
AAM39343	Human polypeptide SEQ ID NO 2488 - Homo sapiens, 589 aa. [WO200153312-A1, 26-JUL-2001]	20..571 37..587	331/555 (59%) 404/555 (72%)	0.0
AAM41129	Human polypeptide SEQ ID NO 6060 - Homo sapiens, 646 aa. [WO200153312-A1, 26-JUL-2001]	20..571 94..644	331/555 (59%) 404/555 (72%)	0.0
AAY39920	Human steroid sulphatase protein sequence - Homo sapiens, 583 aa. [WO9950453-A1, 07-OCT-1999]	20..569 26..575	295/559 (52%) 374/559 (66%)	e-166
AAB51185	Human sulfatase protein C SEQ ID NO:14 - Homo sapiens, 583 aa. [US6153188-A, 28-NOV-2000]	20..569 26..575	294/559 (52%) 372/559 (65%)	e-165

In a BLAST search of public sequence databases, the NOV121a protein was found to have homology to the proteins shown in the BLASTP data in Table 121D.

Table 121D. Public BLASTP Results for NOV121a				
Protein Accession Number	Protein/Organism/Length	NOV121a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P54793	Arylsulfatase F precursor (EC 3.1.6.-) (ASF) - Homo sapiens (Human), 591 aa.	1..572 10..581	379/577 (65%) 441/577 (75%)	0.0
AAH20229	HYPOTHETICAL 64.9 KDA PROTEIN - Homo sapiens (Human), 593 aa.	4..574 24..593	358/574 (62%) 440/574 (76%)	0.0
P51689	Arylsulfatase D precursor (EC 3.1.6.-) (ASD) - Homo sapiens (Human), 593 aa.	4..574 24..593	349/574 (60%) 429/574 (73%)	0.0
P51690	Arylsulfatase E precursor (EC 3.1.6.-) (ASE) - Homo sapiens (Human), 589 aa.	20..571 37..587	334/555 (60%) 405/555 (72%)	0.0
P08842	Steryl-sulfatase precursor (EC 3.1.6.2) (Steroid sulfatase) (Steryl- sulfate sulfohydrolase) (Arylsulfatase C) (ASC) - Homo sapiens (Human), 583 aa.	20..569 26..575	295/559 (52%) 374/559 (66%)	e-166

PFam analysis predicts that the NOV121a protein contains the domains shown in the Table 121E.

Table 121E. Domain Analysis of NOV121a			
Pfam Domain	NOV121a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Sulfatase: domain 1 of 1	21..504	231/530 (44%) 410/530 (77%)	1e-187

Example 122.

The NOV122 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 122A.

Table 122A. NOV122 Sequence Analysis

	SEQ ID NO: 339	3005 bp
NOV122a, CG59746-01 DNA Sequence	<p> ATTTCCTTGGTGTGTCTTCACAGCTGAACTTGCAAAACAGATTGGAACCTCAAGATT ATCAATAATCGGAGATACGTATATTTTATTGTAAAGAAAACATGGCTGCCCTATTCC TACGTGGTTTTGTCCAAATAGGGAACTGCAAGACTGGGATATCTAAGTCAAAAGAAGC ATTCAATTGAAGCAGTGGAAAGAAAGAAAGATAGACTGGTGCTGTATTTCAAAGT GGAAAAATATAGCACTTTTCGGCTAAGTGATAATTCAAATGTAGTCCCTTAAATCCT ATAGAGGAAACCAAATCACCTGCATTTAACTTTACAAAATAAATAGGCTTGTATAT TGAAGGATTATCTCCACAGATGCTGAACAATTGAAGATATTCTTGACAGAGTTCAT CAAAACGAGGTTTCAGCCACCTGTGAGACCTGGTAAGGGTGGGAGTGCTTTTCTAGCA CAACACAGAAGGAAATCAACAAAACCTTCATTCCACAAAGTTGATGAGAAATCAAGTAG CAAATCTTTGAGATAGCAAAAGGAAGTGGACAGGTGCTCTTCAGAGGATGCCTTTG CTTACATCAAAATTGACACTTACTTGCGGAGAGTTATCAGAAAATCAGCACAAGAGA GGAAAAGAATGCTCTCATCTAGCTCAGAGATGAATGAGGAATCTTGAAAGAAAATAA TTCTGTAGAATACAAGAAATCCAAGGCAGATTGTTGAGGTTGTAGATATAATCGA GAGAAACAATTGAAGTTAAAGAGTTAGAAGAGAATAAGAAATGGAAATGTGAATCTT CATGCATCATGAACGCCACTGGAATCCTTACCTAGATGACATTGGTCTTCTCCAAGC TCTCACTGAGAAAATGGTTTTGGTATTTCTGTTACAACAAGGTATAGTGACGGTTAC ACAAAGTGGGATAAAATAAACTATTTTTTGAATTATTTCCAGAGAAAATATGCCAGC GCCTCCCAATTGGGAAACACCTGTATATGAATGCAGTGTACAGTCTCTACTTTTC AATCCCATCGTTTGTGATGATTACTTAATCAGAGTTTCCCATGGGGTAAATTTCCC CTTAATGCTCTTACCATGTGCTTGCGACGGCTACTTTTCTTAAAGATACCTATATA TAGAAATCAAGGAGATGTTACTCTGAATCTTAAAGGCCATTTCAGCAGCTGCAGA GATATTCATGGCAATGCACAGAAGCATGCTCATGAGTTTTAGCTCACTGTTTAGAT CAACTGAAAGATAACATGGAATAACTCAACACAATTTGGAAGCCTAAAAGTGAATTTG GGGAAGATAATTTCTTAACAGGTTTTTGTGATGATCCTGACACAGTGGGTTTTTC TTGCCCTGTCTTACTAATTTTGAAGTTAGAGTTGTTGCACTCCATTGCTGTAAAGCT TGTGGTCAGGTTATTCTCAAGACAGAACTGAATAATTACCTCTCCATCAACCTTCCCC AAAGAATAAAGCACATCCTTCATCTATTCAGTCTACTTTTGAATCTTTTGGAGC AGAAGAGCTTGAGTATAATGTGCAAAATGTGAGCACAAGACTTCCGTTGGAGTGCAC TCATTCACTAGTACTCTAGAAATCCTTATGTTTCACTCAACGCTATAGCTTGAATG AGTTTTGTGCATTAAGAAGAATGACCAGGAAGTCATCATTCCAAATATTTAAAGGT GTCTTCTCATTGCAATGAAGGCACAGACCACTCTTCCCTGAGTGAGGATGGAGAA ATTACAGATTTCAATTATTTAAAGTTATTCGAAAGATGACTTCTGGAACATCAGTG TATCATGGCCTGCAACAAAGGAATCCAAGATATCCTGGCTCCACACATTGGATCAGA TAAGGAGTCTGAACAAAAAAGGCCAGACAGTCTTTAAAGGGCAAGCAGAAGACAG CAGCAAAAGTACCTTGGAATAAATTTCAACCAATGAGCTAGATCTGTATCTCAG GAGATCGAGCATTCTTGAAGAAACCGTTAGCTCACTTAATGACGTATCTGGAAGA TACCTCACTTTGTGAGTTCCACAAAGCTGGAGGTAAACCTGCCAGCAGCCAGGCACA CCTCTCTCAAAAGTTGACTTTCAACAGTGCCCGAAAATCCTTAAGACCTACAAAATATG TGAAAAACAGTAAGTTGTAGCTTTTGTAGGATTATCAATCTACTAAAGATTGTGA TGAAGATAAAATATCAGAAATCCAGAAAGATTCCAAAAGTGTCTGAACAGACTCAG CAGTGTGACGGTATGAGAATCTGTGAACAAGCCCTCAGCAGGCACTGCCTCAAAGCT TTCCAAAGCCAGGCACCCAGGGGCACACAAAGAACCTCTAAGACCTACAAAATATAA TCTACAGAAGTCTAACAGGAATCCCTACTTGCACTGGGTTCCAATAAGATCCAAGA AACAAAGACATTTAGATAAGATAAAATCTAAAGCCAAAGGAAACAAAAGAAATGATG ATAAGGGAGATCATACCTACCGGCTCATTAGTGTGTGTCAGGCATCTTGGGAAGACTCT AAAGTCAGGCCATTATATCTGTGATGCCTATGACTTTGAGAAACAGATCTGGTCACT TACGATGATATGCGGTGTGTAGGTATCCAGGAGGCCAGATGCAGGAGGATAGGCGTT GCACTGGGTACATCTCTTTTACATGCATAATGAGATCTTTGAAGAGATGTTGAAAG AGAAGAGAATGCCAGCTTAATAGCAAGGAGGTAGAGGAGACCTTCAGAAGGAATAA GAGGAACGTACTCCTCTGTACAGATCTGCCTGACTGTCTCACTCGATACCACCTTCC TCCATGGAAGGAAACCTGTGAACCTTATCCAGAGATGAAAATGCAATTAGTCTAGGAC CAAAGGTCAAACAGAAACACTTAATGGGGAGATCTGCATTCTAATCC </p>	
	ORF Start: ATG at 101	ORF Stop: TAA at 2840
	SEQ ID NO: 340	913 aa MW at 104046.0kD
NOV122a, CG59746-01 Protein Sequence	<p> MAALFLRGFVQIGNCKTGISKSEAFIEAVERKKDRLVLVYFKSGKYSTFRLSDNIQ VVLKSYRGNQNLHLTLQNNGLFIEGLSSTDAEQLKIFLDRVHQNEVQPPVRPGKG SVFSSTTQKEINKTSPHKVDEKSSSKSFEIAKSGSGTVLQRMPLLTSLKLTLCGE LSE NQHKRRKRLSSSSSENEEFLEKENSVEYKSKADCSRCSVYNREQLKLEENK LECESSIMNATGNPYLDDIGLLQALTEKMLVFLVLLQGYSDGYTKWDKLLFFELFP EKICHLPLNLTGYMNAVLSLLSIPSFADLLNQSPFWGKILPLNALTMLCLRLFF KDTYNIEIKEMLLNLKKAISAAEIPHGNAQNDAHEFLAHLCDQLKDNMEKLTNIWK PKSEFGEDNFPKQVFPDDPDTSGFSCPVTITNFELELLHSIACKACGVILKTELNNYL SINLPQRIKAHPSSIQSTFDLFFGAEELEYKCAKEHKTSGVHSFRLPRLILIVHLK RYSLNFEKALKNDQEVISKYLVSSHNEGTPLPLSEDEGIEITGFQLLKVIRKMT SGNISVSWPATKESKDILAPHIGSDKESEKKGQTVFKGASRRQQQYKLGKNSKPNEL ESVYSGDRAPIEKEPLAHLMTYLEDTSLCQFHKAGGKPASSPGTPLSKVDFQTPVNP </p>	

	KRKKYVKTSTKVFADRIINPTKDLVEDKNIRIPERFQKVSEQTQQCDGMRICEQAPQO ALPQSFPPKPGTQGHTKNLLRPTKLNQKSNRNSLLALGSNNKPNKIDLDKIKSKAKE TKRNDKGDHTYRLISVVSHLGTKLSGHYICDAYDFEKQIWFTYDDMRVLGIQEAQM QEDRRCTGYIFFYMHNEIFEMLKREENAQLNSKEVEETLQKE
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Further analysis of the NOV122a protein yielded the following properties shown in Table 122B.

Table 122B. Protein Sequence Properties NOV122a	
PSort analysis:	0.7000 probability located in nucleus; 0.4270 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1047 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 16 and 17

A search of the NOV122a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 122C.

Table 122C. Geneseq Results for NOV122a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV122a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU07888	Polypeptide sequence for human hspG25 - Homo sapiens, 913 aa. [WO200166752-A2, 13-SEP-2001]	1..913 1..913	913/913 (100%) 913/913 (100%)	0.0
AAB75607	Human cancer associated antigen precursor HOM-TES-84/6 SEQ ID NO:6 - Homo sapiens, 912 aa. [WO200100874-A2, 04-JAN-2001]	1..905 1..904	429/920 (46%) 566/920 (60%)	0.0
AAU07869	Polypeptide sequence for mammalian SpG25 - Mammalia, 835 aa. [WO200166752-A2, 13-SEP-2001]	1..904 1..834	335/921 (36%) 504/921 (54%)	e-147
AAG75460	Human colon cancer antigen protein SEQ ID NO:6224 - Homo sapiens, 109 aa. [WO200122920-A2, 05-APR-2001]	810..912 3..107	61/105 (58%) 79/105 (75%)	3e-28
AAB39364	Gene 8 human secreted protein homologous amino acid sequence #113 - Bos taurus, 64 aa. [WO200057903-A2, 05-OCT-2000]	810..871 1..64	39/64 (60%) 48/64 (74%)	5e-15

In a BLAST search of public sequence databases, the NOV122a protein was found to have homology to the proteins shown in the BLASTP data in Table 122D.

Table 122D. Public BLASTP Results for NOV122a				
Protein Accession Number	Protein/Organism/Length	NOV122a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BXU7	Ubiquitin carboxyl-terminal hydrolase 26 (EC 3.1.2.15) (Ubiquitin thiolesterase 26) (Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26) - Homo sapiens (Human), 913 aa.	1..913 1..913	913/913 (100%) 913/913 (100%)	0.0
Q9HBJ7	UBIQUITIN-SPECIFIC PROCESSING PROTEASE - Homo sapiens (Human), 922 aa.	1..905 1..904	429/920 (46%) 566/920 (60%)	0.0
Q9HCH8	KIAA1594 PROTEIN - Homo sapiens (Human), 931 aa (fragment).	50..912 3..929	393/932 (42%) 535/932 (57%)	e-171
Q99MX1	Ubiquitin carboxyl-terminal hydrolase 26 (EC 3.1.2.15) (Ubiquitin thiolesterase 26) (Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26) - Mus musculus (Mouse), 835 aa.	1..904 1..834	335/921 (36%) 504/921 (54%)	e-147
Q9ES63	UBIQUITIN-SPECIFIC PROCESSING PROTEASE - Mus musculus (Mouse), 869 aa.	1..908 1..848	341/933 (36%) 480/933 (50%)	e-131

PFam analysis predicts that the NOV122a protein contains the domains shown in the Table 122E.

Table 122E. Domain Analysis of NOV122a			
Pfam Domain	NOV122a Match Region	Identities/ Similarities for the Matched Region	Expect Value
UCH-1: domain 1 of 1	295..326	21/32 (66%) 29/32 (91%)	8.8e-12
UCH-2: domain 1 of 1	820..885	20/72 (28%) 47/72 (65%)	2.2e-11

Example 123.

The NOV123 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 123A.

Table 123A. NOV123 Sequence Analysis			
	SEQ ID NO: 341	2146 bp	
NOV123a, CG88613-01 DNA Sequence	GAAGGAGCGGGCATGAGGCGCTGCCCGTGCCGTGGGAGCCTGAACGAGGCGGAGGGCGG GGGCGCTGCCCGCGGCGGCCCGCATGGGACTGGAGGCGCCGCGAGGAGGGCGGCGGGCG GCAGCCGGGACAGCAGCGACCTGGGCCCGGCGCAGGGGCCCCGGCGGGGCGGCCGGAG GGGGCGGGCCCTGGGCGCGGACAGAGGGGTCCAGCCTCCACAGCGAGCCTGAGAGGG CCGGCCTCGGGCCTGCGCCGGGGACAGAGAGTCCGCAGGCAGAATTCTGGACAGACGG ACAGACTGAGCCGCGGCAGCTGGCCTTGGAGTAGAGACCGGAGAGGCCAAGCAAAAG ACGGAGCCAGACAGGTCCAGCCTCCGGACGCATCTAGAATGGAGCTGGTCAGAGCTGG AGACGACTTGTCTTTGGACGGAGACCGGGACAGATGGCCTTTGGACTGATCCGACAG GTCCGACCTCCAGTTTCAGCCCGAGGAGGCCAGCCCCCTGGACACAGCCAGGGGTTTCAT GGGCCCTGGACAGAGCTGGAAACGCATGGGTACAGACTCAGCCAGAGAGGGTCAAGT CCTGGGCTGATAACCTCTGGACCCACCAGAACAGTTCAGCCTCCAGACTCAGCCAGAG AGGAGCCTGTCCCTCAAAGAGCCAAAGTGTGATGGCTCTTGGAAGAATTGTATACT GATGGCTCCAGGACACAACAGGATATTGAAGGTCCCTGGACAGAGCCATATACTGATG GCTCCCAAGAAAAACAGGATACTGAAGCAGCCAGGAAACAGCCTGGCACTGTGTGTTT CCAAATACAACAGGATACTGATGGCTCCTGGACACAACCTAGCACTGACGGTTTCCAG ACAGCACCTGGGACAGACTGCCTCTTGGGAGAGCCTGAGGATGGCCCATTAGAGGAAC CAGAGCCTGGAGAATTGCTGACTCACCTGTACTCTCACCTGAAGTGTAGCCCCCTGTG CCCTGTGCCCGCCTCATCATTACCCCTGAGACCCCTGAGCCTGAGGCCACAGCCAGTG GGACCCCTCCCGGTTGAGGGGGCAGCGCGGCTTCTCCTCTGCCTCTTCTTTTCG ACGAGTCTGAGGATGACGTGGTGGCGGGGGCGGAGGTGCCAGCGATCCCGAGGACAG GTCTGGGAGCAACCCTGGAAGAAGCTGAAGACAGTTCTGAAGTATTACCCCTTTGTG GTCTCCTTCCGAAAACACTACCCCTGGGTCCAGCTTCTGGACATGCTGGGAACCTTCC AGGCAGGAGAGGATGGTCGGATTCTGAAACGTTTCTGTAGTGTGAGCAGCGCAGCCT GGAGCAGCTGATGAAGACCCGCTGCGACCTTTCGTGCCTGCCTACTATGGCATGGTG CTGCAGGATGGCCAGACCTTCAACCAGATGGAAGACCTCTGGCTGACTTTGAGGGCC CCTCCATTATGGAAGTGAAGATGGGCAGCAGGACCTATCTGGAAGAGGAGCTAGTGAA GGCAGCGGAACGTCCCGTCCCGGAAGGACATGTATGAGAAGATGGTGGCTGTGGAC CCTGGGCCCCCTACCCCTGAGGAGCATGCCAGGGTGCAGTACCAAGCCCCGCTACA TGCACTGGAGGAAACCATGAGCTCCACCTCTACCCCTGGGCTTCCGGATCGAGGGCAT CAAGAAGGCAGATGGGACCTGTAACACCAACTTCAAGAAGACGCAGGCACTGGAGCAG GTGACAAAAGTCTGGAGGACTTCGTGGATGGAGACACGTCATCTCTGCAAAAGTACG TGGCATGCCTAGAAGAACTTCGTGAAGCTCTGGAGATCTCCCCCTTCTTCAAGACCA CGAGGTGGTAGGCAGTCCCTCCTCTTCGTGCACGACCAACCGGCTGGCCAAGGTC TGGATGATAGACTTCGGCAAGACGGTGGCCTTGCCCGACCAACAGAGCTCAGCCACA GGCTGCCCTGGGCTGAGGGCAACCGTGAGGACGGCTACCTCTGGGGCTGGACAACAT GATCTGCCTCTCGCAGGGGCTGGCACAGAGCTGAGCTGCTCAGCCACCATCAGGTTAA TTGGATGGCGCCAGTCTGGCTGGAGGAGCCCTGAGATGCCATGGGAGGCCCTGAGGTTG		
	ORF Start: ATG at 13	ORF Stop: TGA at 2062	
	SEQ ID NO: 342	683 aa	MW at 75206.8kD
NOV123a, CG88613-01 Protein Sequence	MRRCPCRGSLNEAEAGALPAAARMGLEAPRGRRRQPGQQRPGPAGAPAGRPEGGGP WARTEGSSLSHSEPERAGLGPAPGTESPAEFWTDGQTEPAAAGLVETERPKQKTEPD RSSLRTHLEWSWSELETTCLWTETGTDGLWTDPHRSDLQFPQEEASPTQPGVHPWT ELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKEPSADGSWKELYTDGSR TQQDIEGPWTEPYTDGSQKKQDTEAARKQPGTGGFQIQDQTDGSSWTQPTDGSQTAPG TDCLLGEPEDEPLEEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPAQPVGPPS RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSKPKWKLKTVLKYSFVVSFR KHYPWVQLSGHAGNFQAGEDGRILKRFQCEQSRLEQLMKDPLRPFYAYGMVLQDG QTFNQMEDLLADFEGPSIMDCMGSRTYLEEELVKARERPRPRKDMYKMAVDPGAP TPEEHAQGAVTKPRYMOWRETMSSSTLGFRIEIKKADGTCNTNFKKTQALEQVTKV LEDVFDGDHVLQKYVACLEELREALEISPFFKTHEVVGSSLLFVHDHTGLAKVWMID FGKTVALPDHQTLSHRLPWAEGNREDGYLWGLDNMICLLQGLAQS		

Further analysis of the NOV123a protein yielded the following properties shown in Table 123B.

Table 123B. Protein Sequence Properties NOV123a	
PSort analysis:	0.5663 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV123a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 123C.

Table 123C. Geneseq Results for NOV123a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV123a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41393	Human polypeptide SEQ ID NO 6324 - Homo sapiens, 687 aa. [WO200153312-A1, 26-JUL-2001]	1..683 5..687	682/683 (99%) 682/683 (99%)	0.0
AAM39607	Human polypeptide SEQ ID NO 2752 - Homo sapiens, 711 aa. [WO200153312-A1, 26-JUL-2001]	12..683 36..711	642/680 (94%) 643/680 (94%)	0.0
AAE04364	Human kinase (PKIN)-5 - Homo sapiens, 798 aa. [WO200146397-A2, 28-JUN-2001]	273..682 380..793	219/432 (50%) 285/432 (65%)	e-117

In a BLAST search of public sequence databases, the NOV123a protein was found to have homology to the proteins shown in the BLASTP data in Table 123D.

Table 123D. Public BLASTP Results for NOV123a				
Protein Accession Number	Protein/Organism/Length	NOV123a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96DU7	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE C - Homo sapiens (Human), 683 aa.	1..683 1..683	683/683 (100%) 683/683 (100%)	0.0
Q9Y475	INOSITOL 1,4,5-	83..683 4..604	601/601 (100%) 601/601 (100%)	0.0

	ISOENZYME (EC 2.7.1.127) - Homo sapiens (Human), 604 aa (fragment).			
S17682	1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) B - human, 472 aa.	273..682 54..467	219/432 (50%) 285/432 (65%)	e-117
CAB65055	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE B - Homo sapiens (Human), 946 aa.	273..682 528..941	219/432 (50%) 285/432 (65%)	e-117
Q96JS1	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE, ISOFORM B (EC 2.7.1.127) - Homo sapiens (Human), 946 aa.	273..682 528..941	219/432 (50%) 285/432 (65%)	e-117

Pfam analysis predicts that the NOV123a protein contains the domains shown in the Table 123E.

Table 123E. Domain Analysis of NOV123a			
Pfam Domain	NOV123a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 124.

The NOV124 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 124A.

Table 124A. NOV124 Sequence Analysis		
	SEQ ID NO: 343	1395 bp
NOV124a, CG59993-01 DNA Sequence	GGTAAGACGACCTCTGGATGCTCACCCCTGCCCTCTTCACCTCTCGTCCCCAGCTGTTT CCTCTGCCACCATGAGGAACATTTTCAAGAGGAACCAGGAGCCTATTGTGGCTCCTGC CACCACCACCGCCACGATGCCCATTTGGACCCGTGGACAACCTCACTGAGAGTGGGGGT GCTGGGGAGAGCCAGGAGGACATGTTTGCCAACTGAAGGAGAAGTTATTCAATGAGA TAAACAAGATTCCCTTACCACCCCTGGGCACTGATCGCCATTGCTGTGGTTGCTGGGCT CCTGCTTCTCACCTGCTGCTTCTGCATCTGCAAGAAATGCTGCTGCAAGAAGAAGAAG AACAAGAAGGAGAAGGGCAAGGCATGAAGAATGCCATGAACATGAAGCATGAAG GGGGTCAGGATGACGACGACGACAGACAGGCCTGACTGAGGGGAAGGTGAAGGGGA GGAGGAGAAAGGCCAGAGAACCTGGGCAAACTGCAGTTTTCCTGGACTATGATTTT CAGGCTAATCAGCTTACTGTGGGCGTTCTGCAGGCTGCTGAAGTGCCTGCGCTGGACA TGGGAGGCACCTCAGACCCTTATGTCAAGGTCTTCCTCCTTCTGACAAGAAGAAGAA ATATGAGACCAAGTCCATCGGAAGACACTGAACCCTGCCTTCAATGAAACCTTCAAC TTCAAGGTGCCATACCAGGAGCTTGGGGGCAAACTCTGGTGATGGCCATCTATGACT TTGACCGCTTCTCAAACATGACATCATTGGAGAGGTAAAGGTGCCTATGAACACAGT GGACCTCGGCCAGCCATTGAGGAGTGGAGAGACCTGCAAGGCGGGGAAAAGGAGGAG CCGGAGAAGCTGGGCGACATCTGCACCTCCCTGCGCTATGTGCTCAACGCGCGGAAGC TCACTGTCTGCATCCTGGAGGCTAAGAACCTCAAGAAGATGGACGTGGGCGGCCTTTC AGACCCGTACGTGAAGATCCACCTGATGCAGATGGCAAGAGGCTCAAGAAGAAGAAG ACAACCGTGAAGAAGAAGACCTGAACCATACTTCAACGAGTCTTCAGCTTTTGAGA TCCCCCTCGAGCAGATTCAAGAAAGTCCAGGTAGTGGTCACCGTGCTGGACTATGACAA GCTGGGCAAGAACGAAGCCATAGGCAAGATCTTCGTGGGCAGCAATGCCACGGGCACA GAGCTGCGGCACTGGTCCGACATGCTGGCCAACCCCGGAGGCCATCGCCAGTGGC	

	ACTCGCTCAAGCCTGAGGAGGAGGTGGATGCACTCCTGGGCAAGAACAGTAGACAGC AGCGGCTGGGACCCACACCTTTACGGACACTGACAAGATCCAGAGCTATCAATACC TCA		
	ORF Start: ATG at 70	ORF Stop: TAG at 1327	
	SEQ ID NO: 344	419 aa	MW at 46871.8kD
NOV124a, CG59993-01 Protein Sequence	MRNIFKRNQEPIVAPATTTATMPIGPVDNSTESGGAGESQEDMFAKLKEKLFNEINKI PLPPWALIAIAVVAGLLLLTCCFCICKKCCCKKKKKEKKGKGMKNAMNMKDMKGGQD DDDAETGLTEGEGEGEEKEPENLGLQFSLDYDFQANQLTVGVLQAAELPALDMGGT SDPYVKVFLLPDKKKKYETKVHRKTLNPAFNETFTFKVPYQELGGKTLVMAIYDFDRF SKHDIIGEVKVPMTVDLGQPIEWRDLQGGEGEEPEKLGDICTSLRVVPTAGKLTVC ILEAKNLKMDVGGLSDPYVKIHLMQNGKRLKKKKTTVKKKTLNPFYNESFSFEIPFE QIQKVQVVTVLDYDKLGKNEAIGKIFVGSNATGTCLRHSMDLANPRRPIAQWHSLK PEEEVDALLGKNK		
	SEQ ID NO: 345	1338 bp	
NOV124b, CG59993-02 DNA Sequence	CCACCATGAGGAACATTTTCAAGAGGAACCAGGAGCCTATTGTGGCTCCTGCCACCAC CACCGCCACGATGCCCATTTGGACCCGTGGACAACCTCCACTGAGAGTGGGGGTGCTGGG GAGAGTCAGGAGGACATGTTTGCCTAACTGAAGGAGAAGTTATTCAATGAGATAAACA AGATTCCCTTACCACCTGGGCACTGATCGCCATTGCTGTGGTGTGCTGGGCTCCTGCT TCTCACCTGCTGCTTCTGCATCTGCAAGAAATGCTGCTGCAAGAAGAAGAACAAG AAGGAGAAGGGCAAAGGTATGAAGAATGCCATGAACATGAAGGACATGAAAGGGGGTC AGGATGACGACGACGAGAGACAGGCGCTGACTGAGGGGGAAGGTGAAGGGGAGGAGGA GAAAGAGCCAGAGAACCTGGGCAAACCTGCAGTTTTCCCTGGACTATGATTTTCAGGCT AATCAGCTTACTGTGGCGTCTGCAAGGCTGCTGAACCTGCCTGCCCTGGACATGGGAG GCACCTCAGACCTTATGTCAAGGTCTTCTCCTTCTGACAAGAAGAAGAATATGA GACCAAAGTCCATCGGAAGACACTGAACCTGCCTTCAATGAAACCTTCACCTTCAAG GTGCCATACCAGGAGCTTGGGGGCAAACCTCTGGTGATGGCCATCTATGACTTTGACC GCTTCTCCAACATGACATCATTGGAGAGGTAAAGGTGCCTATGAACACAGTGGACCT CGGCCAGCCCATTTGAGGAGTGGAGAGACCTGCAAGGCGGGGAAAGGAGGAGCGGAG AAGCTGGGCGACATCTGCACCTCCCTGCGCTATGTGCCACGGCGGGAAGCTCACTG TCTGCATCTCAGGAGCTAAGAACCTCAAGAAGATGGACGTGGGCGGCTTTGACAGCC GTACGTGAAGATCCACCTGATGCAGAATGGCAAGAGGCTCAAGAAGAAGAAGACAACC ATGAAGAAGAAGACCTGAACCCATACTTCAACGAGTCCTTCAAGTTGAGATCCCCT TCGAGCAGATTCAAGAGTCCAGGTAGTGGTCACCGTGTGGACTATGACAAGCTGGG CAAGAACGAAGCCATAGGCAAGATCTTCTGGGCGAGCAATGCCACGGGACAGAGCTG CGGCACTGGTCCGACATGCTGGCCAACCCCGGAGGCCATCGCCAGTGGCACTCGC TCAAGCCTGAGGAGGAGGTGGTGCCTCTGGGCAAGAACAGTAGACAGCAGCGGC TGGGACCCACACCTTTCACGGACACTGACAAGATCCAGAGCTATCAATAAGGTGTAG GCGG		
	ORF Start: ATG at 6	ORF Stop: TAG at 1263	
	SEQ ID NO: 346	419 aa	MW at 46845.9kD
NOV124b, CG59993-02 Protein Sequence	MRNIFKRNQEPIVAPATTTATMPIGPVDNSTESGGAGESQEDMFAKLKEKLFNEINKI PLPPWALIAIAVVAGLLLLTCCFCICKKCCCKKKKKEKKGKGMKNAMNMKDMKGGQD DDDAETGLTEGEGEGEEKEPENLGLQFSLDYDFQANQLTVGVLQAAELPALDMGGT SDPYVKVFLLPDKKKKYETKVHRKTLNPAFNETFTFKVPYQELGGKTLVMAIYDFDRF SKHDIIGEVKVPMTVDLGQPIEWRDLQGGEGEEPEKLGDICTSLRVVPTAGKLTVC ILEAKNLKMDVGGLSDPYVKIHLMQNGKRLKKKKTVMKKKTLNPFYNESFSFEIPFE QIQKVQVVTVLDYDKLGKNEAIGKIFVGSNATGTCLRHSMDLANPRRPIAQWHSLK PEEEVGALLGKNK		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 124B.

Table 124B. Comparison of NOV124a against NOV124b.		
Protein Sequence	NOV124a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV124b	1..419 1..419	335/419 (79%) 335/419 (79%)

Further analysis of the NOV124a protein yielded the following properties shown in Table 124C.

Table 124C. Protein Sequence Properties NOV124a	
PSort analysis:	0.8202 probability located in mitochondrial inner membrane; 0.6000 probability located in endoplasmic reticulum (membrane); 0.3500 probability located in nucleus; 0.3034 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV124a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 124D.

Table 124D. Geneseq Results for NOV124a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV124a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAR97722	Mouse inositol polyphosphate binding protein IP4-BP - Mus musculus, 422 aa. [JP08092290-A, 09-APR-1996]	1..419 1..422	412/422 (97%) 414/422 (97%)	0.0
AAU19715	Human novel extracellular matrix protein, Seq ID No 365 - Homo sapiens, 461 aa. [WO200155368-A1, 02-AUG-2001]	128..405 169..447	141/280 (50%) 201/280 (71%)	2e-80
AAU19714	Human novel extracellular matrix protein, Seq ID No 364 - Homo sapiens, 295 aa. [WO200155368-A1, 02-AUG-2001]	141..409 11..281	140/273 (51%) 193/273 (70%)	3e-74
AAW87702	A human membrane fusion protein designated SYNTAX2 - Homo sapiens, 375 aa. [WO9856813-A2, 17-DEC-1998]	59..407 31..364	146/352 (41%) 220/352 (62%)	4e-73
AAO05534	Human polypeptide SEQ ID NO 19426 - Homo sapiens, 149 aa. [WO200164835-A2, 07-SEP-2001]	33..164 15..149	127/135 (94%) 131/135 (96%)	5e-70

In a BLAST search of public sequence databases, the NOV124a protein was found to have homology to the proteins shown in the BLASTP data in Table 124E.

Table 124E. Public BLASTP Results for NOV124a				
Protein Accession Number	Protein/Organism/Length	NOV124a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P29101	Synaptotagmin II (SytII) - Rattus norvegicus (Rat), 422 aa.	1..419 1..422	411/422 (97%) 414/422 (97%)	0.0
A55417	synaptotagmin II - mouse, 422 aa.	1..419 1..422	412/422 (97%) 414/422 (97%)	0.0
P46097	Synaptotagmin II (SytII) - Mus musculus (Mouse), 422 aa.	1..419 1..422	411/422 (97%) 413/422 (97%)	0.0
P24506	Synaptotagmin B (Synaptic vesicle protein O-P65-B) - Discopyge ommata (Electric ray), 439 aa.	10..419 27..439	341/413 (82%) 366/413 (88%)	0.0
P46096	Synaptotagmin I (SytI) (p65) - Mus musculus (Mouse), 421 aa.	10..419 8..421	323/418 (77%) 353/418 (84%)	0.0

PFam analysis predicts that the NOV124a protein contains the domains shown in the Table 124F.

Table 124F. Domain Analysis of NOV124a			
Pfam Domain	NOV124a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Adeno_E3_CR2: domain 1 of 1	62..108	16/50 (32%) 26/50 (52%)	6.5
C2: domain 1 of 2	156..242	54/97 (56%) 81/97 (84%)	1.8e-42
C2: domain 2 of 2	287..375	44/97 (45%) 80/97 (82%)	2.9e-39

Example 125.

The NOV125 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 125A.

Table 125A. NOV125 Sequence Analysis		
	SEQ ID NO: 347	3226 bp

NOV125a, CG59991-01 DNA Sequence	<p>GGACCACTTCTGATGCATCTCTGGGTCCCAACTATCCACTGCAAGGCCTCGAAACA GGGGGCCAGATGGGACCCCATTTAGCACAAAGAGAGACGTCCCACTCTGTGAGCCC AAAGGGAGAGAGGCTCAGGCCACGGCAGAGACGGAACCAGGAAAACGTACAGAAAACA GCCTCAAGTTGCCAGGTCCCTTGCAGGAACAGACAGGCCCTGGGGCCGCCACCTGGG CTCAGAGCTTGGGCTGCATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACC AAATTGCTGAGGAGGAGGTGTACGTCTGTAGTTTGAAGAACACTGCTGCTGACTGGC CGGAAATGCAACGTTGGCTGGTGCTTTTGATTGACACCGGTGGGGCTTCCGGCCTCG CACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATC GTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCTACGTCTTCTTCC TCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTACAGAGTTCATCTCCAG GGAGTGGCCAGACTCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAAGGCTG TTGTTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCTCAACAATGACACAAAGC TCTGCAAGACTGGGCTGAGAAGCAGCCTCCGTTACCCCTCATACGAGTCTGCTGAG GAAGTCTGCTCCCTGAGTCTTCTGATCGTCACCGTCAGAGTGGGCAAGAG AAGCTCAAGTCAGAGGTCGTGTCTCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGG AACAAAGAAATCCACTTGCTCTTGCAGCGGGGATTGGTGAGCATCAGAAGACACAAG GTTGCGTGCATCATGAACAACCGTGAGTGTCTCGACAGTCAGGTCGCGCGCTG GGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGAGAGCGTCGCC CCTTCAACCAACGCTCACAGGCTGCACGCCGCTTTTGTTTTCATAGCTCACCCC TCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGCTCTGAAGCGCTTC TGCCGTATGCTGTGGAGGAGTGTGGAATAGGAAGTCAGTGTGTGACGGTGACGACC TCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTGTGTTTACATGAACATCCT TCTCCAGACAGCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGAC TTCTGTGCCGCTTGTACTACGTGTAGAGGGCTGGAATCGAGCCAGCTCTCTGCC CTCTGTCAGTTGAGAAGACAAAGAGTCCATGGAGCTTAAACAGCAGGCTTCCATAT CCACTCGCTTGGATGAAGCGTTTCTGTTTGGCCTCGTGAGCGAAGAGCTAAGGAGG CCACTGGAGGTCTGCTGGGCTGTCCCGTTCCCTGGGGGTGAAGCAGAAGCTTCTGC ACTGGGTCTCTGTTGGGTGACGAGCTAATGCCACCCACCCAGGAGACCTCTGGA CGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTGTTGCTTGGCATTAAAC AGCTTCCAAGAAAGTGTGGCTTCCGATTAACCAGAACTGGACTTGATAGCATCTTCTCT TCTGCCCTCCAGCACTGTCCGTATTTCGGGAAAATTCGGGTGGATGTCAAAGGATCTT CCCAAGAGATGAGTCCGCTGAGGCATGTCTGTGGTCCCTCTATGGATCGGGATAAG ACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACC TGCGGCAGCTGGACCTGGGCAGCAGCATCTGACAGAGCGGGCCATGAAGACCTGTG TGCCAAGCTGAGGCATCCACCTGCAAGATACAGACCTGATGTTTAGAAATGCACAG ATTACCCCTGGTGTGAGCACCTCTGGAGAATCGTCATGGCCAACTAACATGAAGT CCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGAAGGATGGCGTGTGAAGC CTTAAACACCCAAATGTTTGTGGAGTCTTTGAGGCTGGATGCTGTGGATTGACC CATGCTGTACTGAAGATCTCCAAATCCTTACGACCTCCCCAGCTGGAATCTC TGAGCTTGGCAGGAAACAAGGTGACAGACAGGGAGTAATGCCTCTCAGTGATGCCTT GAGAGTCTCCAGTGCGCCCTGCAGAAGCTGATCTGGAGGACTGTGGCATCACAGCC ACGGGTGGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGT GCCTATCCAACAACAGCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAG GCTTCCCACTGTAGTCTGAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCT GGCTGTGGTTTTCTTGCACTTGCCTTATGGGTAACTCATGGCTGACGCACCTGAGCC TTAGCATGAACCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTGATGAGAGA ACCATCTTGTCTCTCCAGGACCTGGAGTTGGTAAAGTGTCTACCCGCGCGCTG TGTGAGAGTCTGCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCA CGGACAATGCCCTGGGTGACGGTGGGGTGTCTGCACTGTGCGAGGAGTGAAGCAAAA GAACAGTGTCTGACGAGACTCGGGTGAAGGCATGTGGACTGACTTCTGATTGCTGT GAGGCACTCTCTTGGCCCTTCTGCAACCGGCATCTGACCACTTAAACCTGGTGC AGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCCGCCCTTTCCTGTCCCAC GTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAATAAGGAAG CTGCTGGAGGAAGTGACGCTACTCAAGCCCCGAGTCGTAATTGACGGTGTGGCATT CTTTTGATGAAGATGACCGGTACTGGTGGAAAACTGAAGATACGGAAACCTGCCCA CTCACCCCATCTGATGGAGGAACTTAAACGCTGT</p>
	ORF Start: ATG at 69 ORF Stop: TGA at 3168
	SEQ ID NO: 348 1033 aa MW at 116310.7kD
NOV125a, CG59991-01 Protein Sequence	<p>MGPPFSTRETSTLCEPKGRRLRPRQRNQNENVTKNSLKLPGPLQEQTGLGPPHLSSEL GLHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAAGFSDRWGFRPRTVV LHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREW DSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAQKQPFPTLIRSLLRKVL LPESFLIVTVRDVGTGLKSEVVSPLYLLVRGISGEQRIHLLBERGIGHQKQTGLRA IMNRELDDQCQVPAVGLICVALQLQDVVGESVAFNQTLTGLHAAPVFHQLTGRV VRRCLNLEERVVLKRFRCRMAVEGVNKRKSVFDGDDLMVQGLGSELRLALFHMNILLPD SHCEEYTFPHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSL WMKRFLLFGLVSEDVRRPLEVLGLCPVPLGVKQLLHWVSLGQQPNATTPGDTLDAFH CLFETQDKFVRLALNSFQEVNLPINQNLDLIASSFCLOHCPYLKIRVDVKGIFPRD ESAEACPVVPLWMDKTLIEEQWEDFCMLGTHPHLRQLDLGSSILTERAMKTLCAKL RHPTCKIQTLMFRNAQITPGVQHLWIRVIMANRNLRLSLNLGGTHLKEEDVRMACEALKH PKCLLESRLDCCGLTHACYLKIISQILTTSPSLKSLSLAGNKVTDQGVMLPSDALRVS QCALQKLILEDGITATGCSLASALVSNRSLTHLCLSNLSNEGVLNLLCRSMRLPH CSLQRLMLNQCHLDTAGCGFLALALMGNLWTHLSLSMNPVEDNGVKLLCEVMREPS HLQDLELVKCHLTAACCESLSCVISRSHLKSLLDLDNALGDDGVAALCEGLKQKNSV</p>

LTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMLCSAFACPTSNL QIIGLWKWQYPVQIRKLLQVQLLKPRVVIDGSWHSFDEDDRYWKN
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Further analysis of the NOV125a protein yielded the following properties shown in Table 125B.

Table 125B. Protein Sequence Properties NOV125a	
PSort analysis:	0.7600 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV125a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 125C.

Table 125C. Geneseq Results for NOV125a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV125a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE07514	Human PYRIN-1 protein - Homo sapiens, 1034 aa. [WO200161005-A2, 23-AUG-2001]	103..934 207..1003	276/843 (32%) 445/843 (52%)	e-126
AAE07513	Human nucleotide binding site 1 (NBS-1) protein - Homo sapiens, 1033 aa. [WO200161005-A2, 23-AUG-2001]	114..935 180..990	281/839 (33%) 431/839 (50%)	e-120
AAU07878	Polypeptide sequence for mammalian Spg65 - Mammalia, 748 aa. [WO200166752-A2, 13-SEP-2001]	207..963 9..748	218/766 (28%) 380/766 (49%)	7e-95
AAE06758	Human G-protein coupled receptor-8 (GCREC-8) protein - Homo sapiens, 1473 aa. [WO200157085-A2, 09-AUG-2001]	21..764 219..959	235/772 (30%) 380/772 (48%)	3e-88
AAB62571	Human CARD-7 polypeptide - Homo sapiens, 1429 aa. [WO200130813-A1, 03-MAY-2001]	21..764 219..959	235/772 (30%) 380/772 (48%)	3e-88

In a BLAST search of public sequence databases, the NOV125a protein was found to have homology to the proteins shown in the BLASTP data in Table 125D.

Table 125D. Public BLASTP Results for NOV125a				
Protein Accession Number	Protein/Organism/Length	NOV125a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JLR2	MATERNAL-ANTIGEN-THAT-EMBRYOS-REQUIRE PROTEIN - Mus musculus (Mouse), 1111 aa.	24..1033 104..1111	548/1019 (53%) 716/1019 (69%)	0.0
Q9R1M5	MATER PROTEIN - Mus musculus (Mouse), 1111 aa.	24..1033 104..1111	547/1019 (53%) 716/1019 (69%)	0.0
AAL35293	NALP4 - Homo sapiens (Human), 994 aa.	63..958 94..981	291/907 (32%) 473/907 (52%)	e-133
Q96MN2	CDNA FLJ32126 FIS, CLONE PEBLM2000112, WEAKLY SIMILAR TO HOMO SAPIENS NUCLEOTIDE-BINDING SITE PROTEIN 1 MRNA - Homo sapiens (Human), 919 aa.	63..958 19..906	291/907 (32%) 473/907 (52%)	e-133
AAL12497	CRYOPYRIN - Homo sapiens (Human), 1034 aa.	103..934 207..1003	276/843 (32%) 445/843 (52%)	e-125

PFam analysis predicts that the NOV125a protein contains the domains shown in the Table 125E.

Table 125E. Domain Analysis of NOV125a			
Pfam Domain	NOV125a Match Region	Identities/ Similarities for the Matched Region	Expect Value
LRR: domain 1 of 6	671..695	6/25 (24%) 16/25 (64%)	1.6e+02
LRR: domain 2 of 6	728..752	7/27 (26%) 17/27 (63%)	2.3e+02
LRR: domain 3 of 6	785..809	7/26 (27%) 19/26 (73%)	1.6e+02
LRR: domain 4 of 6	814..836		4.3e+02

		14/25 (56%)	
LRR: domain 5 of 6	899..923	8/26 (31%) 20/26 (77%)	27
LRR: domain 6 of 6	956..977	7/25 (28%) 16/25 (64%)	2.9e+02

Example 126.

The NOV126 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 126A.

Table 126A. NOV126 Sequence Analysis			
	SEQ ID NO: 349	2310 bp	
NOV126a, CG59987-01 DNA Sequence	CCGCGCCTCAGTCCGCGCTCCGCCCTCCGCGCCCGCGCCGCTAGCATGACCGACGCGC TGTTGCCCGCGGCCCGCCAGCGCTGGAGAAGGAGAACGACGGCTACTTTCGGAAGGG CTGTAATCCCTTGCACAAACCGGCCGAGTAAATTGCAGAAATCAAAGAGCTGCTTTG AATCAGCAGATCCTGAAAGCCGTGCGGATGAGGACCGGAGCGGAAAACCTTCTGAAAG TGGCCACAAACTCAAAGGTGCGGGAGCAAGTGGCTGGAGCTGAGCTTCGTCAACTC AGACCTGCAGATGCTCAAGGAAGAGCTGGAGGGGTGAACATCTCGGTGGGCGTCTAT CAGAACACAGAGGAGGCATTTACGATTCCCTGATTCTCTTGGCCTGAAGGAAACGA AAGACGTCGACTTTGCAGTCCTCAAGGATTTATCCTGGAACATTACAGTGAAGA TGGCTATTTATATGAAGATGAAATTGCAGATCTTATGGATCTGAGACAAGCTTGTCGG ACGCTAGCCGGGATGAGGCCGGGTGGAAGTCTGATGACATACTTCATCCAGCTGG GCTTTGTCGAGAGTCGATTCTTCCCGCCACACGGCAGATGGGACTCCTGTTACCTG GTATGACTCTCTACCGGGGTTCCGGTCAGCCAGCAGAACCTGCTGCTGGAGAAGGCC AGTGTCTCTGTTCAACACTGGGGCCCTTACACCCAGATTGGGACCCGGTGTGATCGGC AGACGACGGCTGGGCTGGAGAGTGCCATAGATGCCTTTCAGAGAGCCGAGGGGTTT AAATTACCTGAAAGACACATTTACCCATACTCCAAGTTACGACATGAGCCCTGCCATG CTCAGCGTGCTCGTCAAATGATGCTTGCAACAAGCCCAAGAAAGCGTGTGAGAAAA TCAGCCTTCTGGGATCCGGAATGAATCTTCATGCTGGTGAAGGTGGCTCAGGAGGC TGCTAAGGTGGGAGAGGTCTACCAACAGCTACACGAGCCATGAGCCAGGCGCGGTG AAAGAGAACATCCCTACTCTGGGCCAGCTTAGCCTGCGTGAAGGCCACCACTACG CGGCCCTGGCCACTACTTCACTGCCATCCTCCTCATCGACCACAGGTGAAGCCAGG CAGGATCTGGACCACCAGGAGAAGTGCTGTCCAGCTCTACGACCATATGCCAGAG GGGCTGACACCCCTTGCCCACTGAAGAATGATCAGCAGCGCCGACAGCTGGGGAAGT CCCCTTGCGCAGAGCCATGGCTCATCAGGAGGAGTCGGTGGCGGAGGCCAGCCTCTG CAAGAAGCTGGCGAGCATTGAGGTGCTACAGAAGGTGCTGTGTGCCGACAGGAACGC TCCCGGCTCAGTACGCCAGCACCAGGAGGAGGATGACCTGCTGAACCTGATCGAGC CCCCAGAGTGTGTTGCTAAAACTGAGCAAGAGGTTGACATTATATTGCCCCAGTTC TCCAGCTGACAGTCACGGACTTCTTCCAGAAGCTGGGCCCTTATCTGTGCTGTGCGGT AACAAGCGGTGGACGCCTCTCGAAGCATCCGCTTCACTGCAGAAGAAGGGGACTTGG GGTTCACTTGAAGAGGAACGCCCCGTTCAAGTTCACTTCTGGATCTTACTGCTC TGCTCTCGTGGCAGGAGCCCGGAAGGAGATTATATTGCTCCATTACGCTTGTGGAT TGTAAGTGGCTGACGCTGAGTGAGGTTATGAAGCTGCTGAAGAGCTTTGGCGAGGACG AGATCGAGATGAAAGTCGTGAGCCTCTGGACTCCACATCATCCATGCATAATAAGAG TGCCACATACTCCGTGGGAATGCAGAAAACGTACTCCATGATCTGCTAGCCATTGAT GATGACGACAAAACGTATAAAACCAAGAAAATCTCCAAGAAGCTTTCTTCTCTGAGTT GGGGCACCAACAAGAACAGACAGAAGTCAGCCAGCACCTTGTGCTCCCATCGGTGCG GGCTGCACGGCCTCAGGTCAAGAAGAAGCTGCCCTCCCTTTCAGCCTTCTCAACTCA GACAGTTCTTGGTACTAATGTGAGGAAACAAACATGTTCAAGGCCCAACATTTCGGG TGCTGACTCGGCCTTAAACGTTTGTGCCATAATGGAAAATATCTATCTATCTGTTCTC AAATCCTGTTTTTCTCATAGTGTAAACTCACATTTGATGTGTTTTATGAAGGAAAGT AACCAAGAAACCTCTAGGAATTAGTGAAAAAAGAACTTTTTTGAGGTG		
	ORF Start: ATG at 46	ORF Stop: TAA at 2104	
	SEQ ID NO: 350	686 aa	MW at 76812.3kD
NOV126a, CG59987-01 Protein Sequence	MTDALLPAAPQPLEKENDGYFRKGCNPLAQTGRSKLQNRRAALNQILKAVRMRTGAE NLLKVATNSKVRQVRLELSFVNSDLQMLKEELEGNIISVGVIYQNTTEAFTIPLIPLG LKETKDVDFAVVLKDFILEHYSDEGDYIEDEIADLMDLRQACRTPSRDEAGVELLMY FIQLGFVESRFFPPTRQMGLLFTWYDSLTPVPSVQNNLLEKASVLFNTGALYTIQIGT RCDRQTQAGLESAIDAFQRAAGVLNLYKDTFTHTPSYDMSPAFLSVLVKMMLAQAQES VFEKISLPGIRNEFFMLVKVAQEAQVGEVYQQLHAAMSQAPVKENIPYSWASLACVK AHHYAALAHYFTAILLIDHQVKGPTDLHQEKLSQLYDHMEPEGLTPLATLKNDDQRR QLGKSHLRRAMAHHEESVREASLCKKLRSIEVLQKVLCAAQERSRLTYAQHQEEDDLL NLIDAPRVLLLLKSLRLTLCPSSPADSHGLLPEAGPLSVLSANKRWTPPRSIRFTAE		

	EGDLGFTLRGNAPVQVHFLDPYCSASVAGAREGDYIVSIQLVDCWKWLTSEVMKLLKS FGEDEIEMKVSVLLDSTSSMHNKSATYSVGMQKTYSMICLAIDDDDKTDKTKKISKKL SFLSWGTHNQRKSASTLCLPSVGAARPQVKKLPSFLLNSDSSWY		
	SEQ ID NO: 351	2109 bp	
NOV126b, CG59987-02 DNA Sequence	CGCCGCTAGCATGACCGACGCGCTGTTGCCCGCGGCCCCAGCCGCTGGAGAAGGAG AACGACGGCTACTTTTCGGAAGGGCTGTAATCCCCTTGACAAAACGGCCGGAGTAAAT TGCAGAATCAAAGAGCTGCTTTGAATCAGCAGATCCTGAAAGCCGTGCGGATGAGGAC CGGAGCGGAAAACCTTCTGAAAGTGGCCACAACTCAAAGGTGCGGGAGCAAGTGCGG CTGGAGCTGAGCTTCGTCAACTCAGACCTGCAGATGCTCAAGGAAGAGCTGGAGGGG TGAACATCTCGGTGGGCGTCTATCAGAACACAGAGGAGGCATTATCAGATTCCCCTGAT TCCTCTTGGCCCTGAAGGAAACGAAAGACGTCGACTTTGCAGTCGTCTCAAGGATTTT ATCCTGGAACATTACAGTGAAGATGGCTATTATATGAAGATGAAATGCAGATCTTA TGGATCTGAGACAAGCTTGTGCGACGCTAGCCGGGATGAGGCCGGGTGGAACTGCT GATGACATACTTCATCCAGCTGGGCTTTGTGCGAGAGTCGATTCTTCCGCCCCACACGG CAGATGGGACTCCTGTTCACTTGGTATGACTCTCTCACCGGGGTTCCGGTCAGCCAGC AGAACCCTGCTGCTGGAGAAGGCCAGTGTCTGTTCAACACTGGGGCCCTCTACACCCA GATTGGGACCCGGTGCATCGGCAGACGCGAGGCTGGGCTGGAGAGTGCCATAGATGCC TTTCAGAGAGCCGACGGGTTTAAATTACCTGAAAGACACATTTACCCATACTCCAA GTTACGACATGAGCCCTGCCATGCTCAGCGTGCTCGTCAAAATGATGCTTGCACAAGC CCAAGAAAGCGTGTTTGAGAAAATCAGCCTTCTCGGATCCGGAATGAATTCTTCATG CTGGTGAAGGTGGCTCAGGAGGCTGCTAAGGTGGGAGAGGTCTACCAACAGCTACACG CAGCCATGAGCCAGGCGCCGGTGAAAGAGAACATCCCTACTCTCTGGGCCAGCTTAGC CTGCGTGAAGGCCACCACTACGCGGCCCTGGCCCACTACTTCACTGCCATCTCTCTC ATCGACCACAGGTGAAGCCAGGCACGGATCTGGACCACAGGAGAAGTGCCCTGTCCC AGCTCTACGACCACATGCCAGAGGGGCTGACACCCCTTGGCCCACTGAAGAATGATCA GCAGCGCCGACAGCTGGGGAAGTCCCACTTGCGCAGAGCCATGGCTCATCAGGAGGAG TCGGTGCAGGAGCAAGCCTCTGCAAGAAGCTGCGGAGCATTGAGGTGCTACAGAAGG TGCTGTGTGCCGCACAGGAACGCTCCCGGCTCACGTACGCCACAGCAGGAGGAGGA TGACCTGCTGAACCTGATCGACGCCCCAGTGTGTTGCTAAACTGAGCAAGAGGTT GACATTATATTGCCCACTTCTCAAGCTGACAGTACCGGACTTCTTCCAGAAGCTGG GCCCTTATCTGTGTTTTCGGCTAAACAAGCGGTGGACGCTCCTCGAAGCATCCGCTT CACTGCAGAAGAAGGGGACTTGGGGTTCACTTGAGAGGGAACGCCCCCGTTCAAGTT CACTTCCTGGATCCTTACTGCTCTGCCTCGGTGGCAGGAGCCGGGAAGGAGATTATA TTGTCTCCATTAGCTTGTGGATTGTAAGTGGCTGACGCTGAGTGAGGTTATGAAGCT GCTGAAGAGCTTTGGCAGGAGCAGATCGAGATGAAAGTCGTGAGCCTCTCGGACTCC ACATCATCCATGCATAATAAGAGTGCCACATACTCCGTGGGAATGTAGAAAACGTACT CCATGATCTGCTTAGCCATTGATGATGACGACAAAACCTGATAAAACCAAGAAAATCTC CAAGAAGCTTTCCTTCTGAGTTGGGGCACCAACAAGAACAGACAGAAGTACGCCAGC ACCTTGTGCTCCCATCGGTGGGGCTGCACGGCCTCAGGTCAAGAAGAAGCTGCCCT CCCCCTTTCAGCCTTCTCAACTCAGACAGTTCTTGGTACTAATGTGAGGAAACAAACAT GTTCAGGCCCCGAACATTTCC		
	ORF Start: ATG at 11	ORF Stop: TAG at 1844	
	SEQ ID NO: 352	611 aa	MW at 68613.9kD
NOV126b, CG59987-02 Protein Sequence	MTDALLPAAPQPLEKENDGYFRKGCNPLAQTRSKLQNRALNQIILKAVRMRTGAE NLLKVATNSKVRQVRLELSFVNSDLQMLKEELEGNIISVGVIQNTTEAFTIPLIPLG LKETKDVDFAVVLKDFILEHSEDGYLYEDEIADLMDLRQACRTPSRDEAGVELLMTY FIQLGFVESRFFPPTROMGLLFTWYDSLTVGPVVSQNLLEKASVLFNTGALYTOIGT RCDRQTQAGLESIDAQRAAGVNLNLYKDTFTHTPSYDMSFAMLSVLVKMMLAQAES VFEKISLPGIRNEFFMLVKVAQEAQVGEVYQQLHAAMSQAPVKENIPYSWASLACVK AHHYAALAHYFTAILLDHQQVPGTDLDHQEKCLSQLYDHMPGLTPLATLKNDDQRR QLGKSHLRAMAHHEESVREASLCKKLRSIEVLQKVLCAAQERSRLTYAQHQEEDLL NLIDAPSVVAKTEQEVDIILPQFSKLTVTDFQKLGPLSVFSANKRWTTPRSIRFTA EGDLGFTLRGNAPVQVHFLDPYCSASVAGAREGDYIVSIQLVDCWKWLTSEVMKLLKS FGEDEIEMKVSVLLDSTSSMHNKSATYSVGM		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 126B.

Table 126B. Comparison of NOV126a against NOV126b.		
Protein Sequence	NOV126a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV126b	1..611 1..611	585/612 (95%) 590/612 (95%)

Further analysis of the NOV126a protein yielded the following properties shown in Table 126C.

Table 126C. Protein Sequence Properties NOV126a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV126a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 126D.

Table 126D. Geneseq Results for NOV126a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV126a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU10192	Human prostate specific protein PSL22 - Homo sapiens, 686 aa. [WO200172962-A2, 04-OCT-2001]	1..686 1..686	660/687 (96%) 665/687 (96%)	0.0
AAB68561	Human GTP-binding associated protein #61 - Homo sapiens, 666 aa. [WO200105970-A2, 25-JAN-2001]	27..686 7..666	626/661 (94%) 633/661 (95%)	0.0
AAG64579	Human transcription termination factor binding protein 54 - Homo sapiens, 488 aa. [CN1297918-A, 06-JUN-2001]	201..686 3..488	458/487 (94%) 464/487 (95%)	0.0
AAB29661	Human histidine domain-protein tyrosine phosphatase, SEQ ID NO:2 -	110..357 7..253	82/252 (32%) 135/252 (53%)	3e-28

	[WO200063392-A1, 26-OCT-2000]			
AAU00869	Human cancer related protein 5 - Homo sapiens, 257 aa. [WO200118014-A1, 15-MAR-2001]	409..597 8..196	70/189 (37%) 102/189 (53%)	2e-27

In a BLAST search of public sequence databases, the NOV126a protein was found to have homology to the proteins shown in the BLASTP data in Table 126E.

Table 126E. Public BLASTP Results for NOV126a				
Protein Accession Number	Protein/Organism/Length	NOV126a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96RU1	RHOPHILIN-LIKE PROTEIN - Homo sapiens (Human), 685 aa.	1..686 1..685	627/688 (91%) 640/688 (92%)	0.0
Q9DBN2	1300002E07RIK PROTEIN - Mus musculus (Mouse), 686 aa.	1..686 1..686	573/687 (83%) 616/687 (89%)	0.0
Q61085	GTP-RHO binding protein 1 (Rhopilin) - Mus musculus (Mouse), 643 aa.	16..596 20..580	273/583 (46%) 361/583 (61%)	e-135
Q9XYY9	RHOPHILIN - Drosophila melanogaster (Fruit fly), 718 aa.	21..615 31..674	248/654 (37%) 363/654 (54%)	e-110
Q96PV9	KIAA1929 PROTEIN - Homo sapiens (Human), 410 aa (fragment).	23..366 17..362	178/346 (51%) 241/346 (69%)	1e-93

PFam analysis predicts that the NOV126a protein contains the domains shown in the Table 126F.

Table 126F. Domain Analysis of NOV126a			
Pfam Domain	NOV126a Match Region	Identities/ Similarities for the Matched Region	Expect Value
HR1: domain 1 of 1	38..110	19/87 (22%) 53/87 (61%)	1.2e-05
BRO1: domain 1 of 1	111..263	60/172 (35%) 125/172 (73%)	3.8e-56
PDZ: domain 1 of 1	516..593	20/84 (24%) 53/84 (63%)	0.46

Example 127.

The NOV127 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 127A.

Table 127A. NOV127 Sequence Analysis			
	SEQ ID NO: 353		3351 bp
NOV127a, CG59971-01 DNA Sequence	CGTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTGTTGTGGAAGCTCGCGGGT TGCTGCGGGAGTCCGGTGATGTGGTCTGTCTGGCTGTAGCACCTGAGCCTGCTGAC TCCCACTGCAACAGCTGAACACGATTTTCTGAGCTGCACCTGGGGCCATGGGGCCCT GGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCTGCCGACTCCCTGTTATTCTTC AGCTTCAGTTTCTCTCGATGTGCTGCAGAAAACACTTTCACTCAAGCTGGTCCATGT TGCTGGTCTTGGCCCCACAGGGCCCATCAAGATTTTCCCTTCAAATCCCTTCGGCAC CTGGAGCTCCGAGGTGTTCCCTCCACTGTCTGCATGGCTCCGAGGCATCTACTCCC AGCTGGAGACCTGATTTGCAGCAGGAGCCTCCAGGCATTAGAGGAGCTCCTCTCAGC CTGCGGCGGGCACTTCTGCTCTGCCCTCCCTTGGCTGGCTCTGCTTTCTGCCAACTTC AGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTTGTGAGCTCTGCGTT TCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTCAAGGATTCTGATGGATTGTG TGAGCTCCACCATCTGGACATCTCTATAATCGCTGCAATTTGGTGCCAAGAATGGGA CCCTCAGGGGCTGCTCTGGGGTCTGATACTGCGAGGCAATGAGCTTCGGAGCCTGC CAGGCCTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTGGCATACAACCTGCTGGA AGGACACCGGGAGCTGTCAACACTGTGGCTGTGGCTGAGCTCCGCAAGCTCTACCTG GAGGGGAACCTCTTTGGTTCCACCCTGAGCACCGAGCAGCACTGCCCACTTGTGT CACCCCGGGCCAGGGATGTGCTACTGGCTTCTTCTCGATGGCAAGGTCTTGTCACT GACAGATTTTCAACAGACTCACACATCTTGGGGCTCAGCCCCATGGGCCACCTTTG CCCTGGCCAGTGGGGAGTACTCTGAAACCTCAGTGGCCCTGACCTGAGTGACAGCC TCTCTCAGGGGTGTTTGTGACCCAGCCCTGCTTCAAGGTTAAGAGCCGAGTCCG TGTGAGGCGGGCAAGCATCTCTGAACCCAGTGATACGGACCCGGAGCCCCGAACCTG AACCCCTCTCCGGCTGGTTGGTTCGTGCAGCAGCACCCGAGCTGGAGCTCATGAGCA GCTTCGGGAACGGTTTCGGCCGCAACTGGCTGCAGTACAGGAGTCACTGGAGCCCTC CGGAAACCTCTGCGGGCCACCCCACTACTTCTGCACCCAGTGACCTCCAGCCAGC TCCAGGGCCCCGCACTGCACCCAGACCTTCACCCCGCAGGAGGAAGCCAGAGGCC CCCAGGAGTCACCACAGAAAATGTCAAGGAGGTCAAGGCGGAGCCACAGGAGGAGGA AGAGGAGAAGGAGGGGAAGGAGGAGAAGGAGGAGGGGGAGATGGTGAACCCAGGAGAA GAGGAGGCAGGAGAGGAGGAAGAAGAGGAGCAGGACCAGAAGGAAGTGAAGCGGAAC TCTGTGCCCCCTTGTGTGTGTGTCTCCCTGGAGGGGCTGAGGGCGTACGGGGCAGGGA ATGCTTTCTCAGGGTCACTTCTGCCACCTGTTTGAGGTGGAACCTCAAGCAGCTCGC ACCTTGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAGATAGAGCCGAGGCC AGGCCAGGGTCCCCCTCTGTCTGCGCAGGGCTCAGATCTGTCTCCTGGAGCCCCAT CCTCAGTCTGCGCTTCTCTACATCTGCCCTGACCGGCAGTTGCGTCTGCTATTGGTG CTGGAGCCTGATGCCCAAGCAGCTGTCCAGGAGCTGCTTGGCTGTGACCCAGTCA CCAATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGGACCTCCTGCTGGGTAGATTCCA GTGTCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCAGGATGGGATTAGACAGT GAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGAATCTCTGCTGTGTGTCTTAAT GTGGTAGTGACCAAGTGGTTCTCTCGCTGTGTCTCGGGGAACCCCAACAGGGAGCG GAAACAGGGAGAGCAGTCTCTGGCTCCTTCTCCGTCTGCCAGCCCTGTCTGCCACCCT CCTGGCCATGTTGACCACTTGACAGGGCCAAGAACAGCCCACTCAGGCACCGAGCA CCCGTGACCATGGTAGTTGGAGCCTCAGTCCCGCCCTGAGCGCTGTGGCTCCGCTC TGTGGACCAACCGACTCCGGCTCTTCTGATGTGTGAGGTGTTCAGCGATGCCAGGAG GAGTTCCAGTGTGCTCAAGGTCCAGTGGCATTGGCAGGCCACACTGGGGAGTTCA TGTGCCCTGTGGTTGTGTCTGACCGCAGGCTGTACCTGTTGAAGGTGACTGGGGAGAT GAGTGAGCCTCCAGCTAGCTGGCTGCAGCTGACCTGGCTGTTCCTGACAGGATCTG AGTGGCATAGAGCTGGGCTGGCAGGCCAGAGCCTGCGGCTAGAGTGGGAGCTGGGG CGGGCCGCTGTGTGTGTGTGCCCCGAGATGCCAGGCATTGCCGGGCTTCTTAGAGGA GCTCCTTGGTGTCTTGAGTCTCTGCCCTGCTGGAGAACTGTGTAGTGGCCACA GAGGAGGAGTCAACCCCAAGCAGCGCTCTGGCCATTGCTGGAAAAGACTCATCCT TGGAGGCTCGCCAGTTCTTCACTTCCGGCGTCTCTGGTTGAAGGTGAAGCCTCTGT GCAGCTGATGCTTCCCTCCACTGCGCTCGATCCCTGTTGTGTGACTCCGTCCACCTG TTCTGTTAGATGAGGATGCTGCAGGTCCTCCGCGCAGAGCCCTCTCTCCAGCAGCAT CTGGCGAAGCCTCTGAGAAGGTGCTTCCCTCGGGGCGGGCCCTGCTGTGCTGTGAG GGAGCAGCAGCCACTCAGCAGCCTGAGTCCGTGCTGCTCTACCGCTCAGCCCCGTAG GACTTGGCGTGTCTTCTACGATGAGGTGTCCCGGCTGGAGAGCTTTTGGGCACTCC GTGTGGTGTGTGAGGAGCAGCTGACAGCCCTGCTTGCCTGGATCCGGGAACCATGGGA GGAGCTGTTTTCCATCGGACTCCGGACAGTGATCCAAGAGGCGCTGGCCCTTGACCGA TGAGGGTCCCAGCTGACCTTGGCCCTGACCTCAGGAGCCACGCT		
	ORF Start: ATG at 13		ORF Stop: TGA at 3307
	SEQ ID NO: 354	1098 aa	MW at 121004.1kD
NOV127a,	MTTAQRDSSLWKLGLLRESGDVLSGCSLTLSTPTLQQLNHVFLHLGFWPGQTG		

CG59971-01 Protein Sequence	<p>FVALPSHPADSPVILQLQFLDVLQKTLSLKLVHVAGPGPTGPIKIFPFKSLRHLRLR GVPLHCLHGLRGYISQLETLICSRSLQALELLSACGGDFCSALPWALLSANFSYNA LTALDSSLRLLSALRFLNLSHNQVQDCQGFMDLCELHHLDISYNRLHLVPRMGPSGA ALGVILIRGNELRSLPGLLEQLRNLRLHLDLAYNLEGHRELSPLWLLAELRLKLYLEGNP LWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSTDFQQTHTSLGLSPMGPPLPWPV GSTPETSGGPDLSDLSGGVVTQPLLHKVKSRRVRRASISEPSTDPEPRTLNPSF AGWVQQHPELELMSSFRERFGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGP DTAPRPSPPQEEARGPQESPOKMSSEVRAEPQEEEEKEGKEKEEGEMVEQEEEEAG EEEEEQDQKEVAELCRPLLVCPLGPEGVVRGECFLRVTSAPHLFEVELQAARTLER LELQSLAEAEISEPAQAGPPPLAAQGSDDLPGAPILSLRFSYICPDRLRRYLVEPD AHAAVQELLAVLTPVTNVAREQLGEARDLLGRFQCLRCGHEFKPEEPRMGLDSEEGW RPLFQKTESPAVCPNGSDHVVLLAVSRGTENRERKQGEQSLAPSASPVCHPPGHG DHLDRAKNSPPQAPSTRDHGSWSLSPAPERCLRSVDHRLRLFLDVEVFSDAQEBCFQC CLKVPVALAGHTGEFMCLVVSDRRLLYLLKVTGEMSEPPASWLQTLTAVPLQDLSGIE LGLAQSLRLLEWAAGAGRCVLLPRDARHCRAFLLELLGLVLSFPAPWNCVATSEEV TPQHRLWPLLEKDDSSLEARQFFYLRAFLVEGEASVQLMLPSTCLVSLLLTPSTLFLLD EDAAGSPAEPSPPAASGEASEKVPPSGPGPAVRVREQQLSSLSVLLYRSAPEDLRL LFYDEVSRLESFVALRVVCQEQLTALLAWIREPWEELFSIGLRTVIQEALALDR</p>
	<div>SEQ ID NO: 355</div> <div>3348 bp</div>
NOV127b, CG59971-02 DNA Sequence	<p>CGTCCCCTGGCCATGACGACCGCTCAGAGGACTCCCTGTTGTGGAAGCTCGCGGGGT TGCTGCGGGAGTCCGGTGTATGGTCTGTGCTGTAGCACCTGAGCCTGCTGAC TCCCACTGCAACAGCTGAACACGATTTGAGCTGCACCTGGGGCCATGGGGCCCT GGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCTGCCGACTCCCTGTTATTCTTC AGCTTCAGTTTCTCTCGATGTGCTGCAGAAAACACTTTCACCTCAAGCTGGTCCATGT TGCTGGTCTGGCCACAGGGCCCATCAAGATTTCCCTTCAAATCCCTCGGCAC CTGGAGCTCCGAGGTGTTCCCTCCACTGTCTGCATGGCTCCGAGGCATCTACTCCC AGCTGGAGACCTGATTGACAGCAGGAGCTCCAGGCATTAGAGGAGCTCCTCTCAGC CTGCGGCGGCGACTTCTGCTCTGCCCTCCCTGGCTGGCTGCTGCTTCTGCCAAGCTC AGCTACAACTGACTGACCGCTTAGACAGCTCCCTGCGCTCTTGTGAGCTCTGCGTT TCTTGAACTAAGCCACAATCAAGTCCAGGACTGTGAGGATTCCTGATGGATTTGTG TGAGCTCCACCATCTGGACATCTCTATAATCGCTGCATTGGTGCAAGAAATGGGA CCCTCAGGGGTCTCTGCGGGTCTGATCTGCGAGGCAATGAGCTTCGGAGCCTGC CAGGCCTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTGGCATAACAACCTGCTGGA AGGACACCGGAGCTGTCAACACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTG GAGGGGAACCTCTTTGGTTCACCCCTGAGCACCGAGCAGCACTGCCAGTACTTGT CACCCCGGCGAGGATGCTGCTACTGGCTTCTCTCGATGGCAAGGTCTGTCACT GACAGATTTTCAGCAGACTCACACATCTTGGGGCTCAGCCCCATGGGGCCACCTTG CCCTGGCCAGTGGGAGTACTCCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCC TCTCCTCAGGGGTGTGTGACCCAGCCCTGCTTCATAAGGTTAAGAGCCGAGTCCG TGTGAGGCGGGCAAGCATCTGAAACCCAGTGATACGGACCCGGAGCCCCGAACTCTG AACCCTCTCCGGCTGGTTGGTTCGTGCAGCAGCACCCGAGCTGGAGCTCATGAGCA GCTTCCGGGAACGGTTCGGCCGCAACTGGCTGCAGTACAGGAGTCACTTGAGCCCTC CGAAACCTCTGCGGCGCACCCCACTACTTCTGCACCCAGTGACCTCCAGCCAGC TCCAGGGCCCCGACACTGCACCCAGACCTTCACCCCCGAGGAGGAGCCAGAGCC CCAGGAGTCAACACAGAAATGTGAGAGGAGTCAAGGCGGAGCCACAGGAGGAGGA AGAGGAGAAGGAGGGAAGGAGGAGAAGGAGGAGGAGGAGATGGTGGAAACAGGAGAA GAGGAGGAGGAGGAGGAGGAAGAAGAGGAGCAGGACAGGAAGGAGTGGAAAGCGGAAC TCTGTGCGCCCTTGTGGTGTGTCCCTGGAGGGGCTGAGGGCGTACGGGCGAGGGA ATGCTTTCTCAGGGTCACTTCTGCCACCTGTTTGAGGTGGAACCTCAAGCAGCTCGC ACCTTGAGCGACTGGAGCTCCAGAGTCTGGAGGAGCTGAGATAGAGCCGAGGCCCC AGGCCCCAGAGTCCGCCAGGCCACGGGCTCAGATCTGCTCCCTCAGGCCCCCATCT CAGTCTGCGCTTCTCTACATCTGCCCTGACCGGCAGTTCGCTCGCTATTGGTGTG GAGCCTGATGCCACGAGCTGTCCAGGAGCTGCTGCGGTGTTGACCCAGTCAACA ATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGACCTCCTGCTGGGTAGATTCCAGTG TCTACGCTGTGGCATGAGTTCAAGCCAGAGGAGCCAGGATGGGATTAGACAGTGAG GAAGGCTGGAGGCTCTGTTCCAAAGACAGAACTCTCTGCTGTGTCTTAACCTGTG GTAGTGACACGCTGTTCTCTCTGCTGTCTCGGGGAACCCCCAACAGGGAGCGGAA ACAGGGAGAGCAGTCTCTGGCTCTTCTCTCGTCTGCCAGCCCTGTCTGCCACCTCT GGCCATGGTGACCACTTGACAGGGCCAAGAACAGCCACCTCAGGCACCGAGCAGCC GTGACCATGGTAGTTGGAGCCTCAGTCCCGCCCTGAGCGCTGTGGCTCCGCTCTGT GGACACCGACTCCGCTCTTCTGGATGTTGAGGTGTTACAGCATGCCAGGAGGAG TTCCAGTCTGCCCTCAAGTCCAGTGGCATTGGCAGGCCACACTGGGGAGTTTCAATG GCCTTGTGGTGTGTGCTGACCGCAGGCTGTACCTGTTGAAGGTGACTGGGAGATGAG TGAGCCTCCAGCTAGCTGGCTGCAGCTGACCTGGCTGTTCCCTGCAGGATCTGAGT GGCATAGAGCTGGGCTGGCAGGCCAGAGCCTGCGGCTAGAGTGGGAGCTGGGGCGG GCCGCTGTGTGCTGTGCCCGAGATGCCAGGCATTGCCGGGCTTCTTAGAGGAGCT CCTTGGTGTCTTGACGTCTCTGCCCTGCTGGAGGAACGTGTGCTGCTGACAGAG GAGGAGGTACCCCCAGCACCGGCTCTGGCCATTGCTGGAAAAAGACTCATCTTGG AGGCTGCCAGTCTTCTACCTTCCGGCGTCTCTGGTTGAAGGTGAAGCCTCTGTGCA GCTGATGCTTCCCTCCACCTGCCTCGTATCCCTGTTGCTGACTCCGTCCACCTGTTT CTGTTAGATGAGGATGTGACAGGTCCTCGGCAGAGCCCTCTCTCAGCAGCATCTG CGAAGCCTCTGAGAAGGTGCTCCCTCGGGCGGGCCCTGCTGTGCTGTGTCAGGGA GCAGCAGCACTCAGCAGCCTGAGCTCCGTGCTGCTCTACCGCTCAGCCCTGAGGAC TTGCGGCTGCTCTCTACGATGAGGTGTCCCGCTGGAGAGCTTTTGGGCACTCCGTG TGGTGTGTCAGGAGCAGCTGACAGCCCTGCTGCTGGATCCGGGAACCATGGGAGGA</p>

	GCTGTTTTCCATCGGACTCCGGACAGTGATCCAAGAGGCGCTGGCCCTTGACCGATGA GGGTCCCACGCTGACCTTGGCCCTGACCTCAGGAGCCACGCT		
	ORF Start: ATG at 13		ORF Stop: TGA at 3304
	SEQ ID NO: 356	1097 aa	MW at 121064.1kD
NOV127b, CG59971-02 Protein Sequence	MTTAQRDSLLWKLGLLRESGDVVLSCSTLSLLTPTLQQLNHVFELHLPWGPQGQTG FVALPSHPADSPVILQLQFLFDVLQKTLCLKLVHVAGPGTGPICKIFPFKSLRHLRLR GVPLHCLHGLRGIYSQLETLCRSRLQALEELLSACGGDFCSALPWLALLSANFSYNA LTALDSSRLRLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGA ALGVILIRGNELRSLPGLEQLRNLRLHLDLAYNLLLEGHRELSPLWLLAELRKLYLEGNP LWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSTDFQQTHTSLGLSPMGPPLPWPV GSTPETSGGPDLSDSLSSGGVVTQPLLHKVKSRVRRRASISEPSDTPPEPRLNPNP AGWVFQQHPELELMSSFRERFRGNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGP DTAPRPSPPQEEARGPQESPOKMSSEVRAEPQEEEEKEGKEEKEEGEMVEQGEAEAG EEEEEQDQKEVEAELCRPLLVCPLGPEGVVRGECFLRVTSAPHLFEVELQAARTLER LELQSLAEAEIEPEAQQRSPRPTGSDLLPGAPILSLRFSYICPDRQLRRYLVLEPDA HAAVQELLAVLTPVTNVAREQLGEARDLLGRFQCLRCGHEFKPEEPRMGLDSEEGWR PLFQKTESPAVCPNCGSDHVVLLAVSRGTPNRERKQGEQSLAPSPASPVCHPPGHGD HLDRAKNSPPQAPSTRDHGSWSLSPAPERCLRSVDHRLRLFLDVEVFSDAQEEFQCC LKVPVALAGHTGEFMCLVVVSDRLYLKVTGEMSEPPASWLQTLAVPLQDLSGIEL GLAQSLRLLEWAAGAGRCVLLPRDARHCRAFLEELLGVLSLPPAWRNCVSATEEEVT PQHRLWPLLEKDSSLEARQFFYLRAFLVEGEASVQLMLPSTCLVSLLLTPSTLFLDE DAAGSPAEPSPPAASGEASEKVPSPGPGPAVRVREQQPLSSLSVLLYRSAPEDRLLL FYDEVSRLESFWALRVVCQEQLTALLAWIREPWEELFSIGLRTVIEQALALDR		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 127B.

Table 127B. Comparison of NOV127a against NOV127b.		
Protein Sequence	NOV127a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV127b	1..1098	891/1098 (81%)
	1..1097	891/1098 (81%)

Further analysis of the NOV127a protein yielded the following properties shown in Table 127C.

Table 127C. Protein Sequence Properties NOV127a	
PSort analysis:	0.5163 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.2442 probability located in mitochondrial inner membrane; 0.2442 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV127a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 127D.

Table 127D. Geneseq Results for NOV127a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV127a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM39827	Human polypeptide SEQ ID NO 2972 - Homo sapiens, 169 aa. [WO200153312-A1, 26-JUL-2001]	375..528 14..167	140/154 (90%) 145/154 (93%)	3e-78
AAM41613	Human polypeptide SEQ ID NO 6544 - Homo sapiens, 184 aa. [WO200153312-A1, 26-JUL-2001]	375..528 29..182	140/154 (90%) 145/154 (93%)	4e-78
AAU19764	Human novel extracellular matrix protein, Seq ID No 414 - Homo sapiens, 211 aa. [WO200155368-A1, 02-AUG-2001]	444..647 13..209	157/207 (75%) 160/207 (76%)	2e-75
ABB19833	Protein #1832 encoded by probe for measuring heart cell gene expression - Homo sapiens, 127 aa. [WO200157274-A2, 09-AUG-2001]	409..535 1..127	127/127 (100%) 127/127 (100%)	2e-70
AAM67606	Human bone marrow expressed probe encoded protein SEQ ID NO: 27912 - Homo sapiens, 127 aa. [WO200157276-A2, 09-AUG-2001]	409..535 1..127	127/127 (100%) 127/127 (100%)	2e-70

In a BLAST search of public sequence databases, the NOV127a protein was found to have homology to the proteins shown in the BLASTP data in Table 127E.

Table 127E. Public BLASTP Results for NOV127a				
Protein Accession Number	Protein/Organism/Length	NOV127a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL49726	LKB1-INTERACTING PROTEIN 1 - Homo sapiens (Human), 1099 aa.	1..1098 12..1099	1077/1098 (98%) 1078/1098 (98%)	0.0
Q96PY9	KIAA1898 PROTEIN - Homo sapiens (Human), 1013 aa (fragment).	76..1098 1..1013	1003/1023 (98%) 1003/1023 (98%)	0.0
Q96CN3	SIMILAR TO RIKEN CDNA 1200014D22 GENE - Homo sapiens (Human), 804 aa (fragment).	288..1098 4..804	793/811 (97%) 793/811 (97%)	0.0
Q9DBT7				0.0

	musculus (Mouse), 1072 aa.	1..1072	895/1098 (81%)	
Q9VMK9	CG9044 PROTEIN - Drosophila melanogaster (Fruit fly), 1289 aa.	12..433 8..463	139/459 (30%) 220/459 (47%)	6e-38

Pfam analysis predicts that the NOV127a protein contains the domains shown in the Table 127F.

Table 127F. Domain Analysis of NOV127a			
Pfam Domain	NOV127a Match Region	Identities/ Similarities for the Matched Region	Expect Value
LRR: domain 1 of 5	164..186	7/25 (28%) 15/25 (60%)	2.5e+02
LRR: domain 2 of 5	187..209	6/25 (24%) 16/25 (64%)	2.5e+02
LRR: domain 3 of 5	210..231	8/25 (32%) 13/25 (52%)	83
LRR: domain 4 of 5	233..254	9/25 (36%) 17/25 (68%)	16
LRR: domain 5 of 5	255..279	10/27 (37%) 19/27 (70%)	22
Pkinase_C: domain 1 of 1	620..629	5/11 (45%) 9/11 (82%)	8.9
rubredoxin: domain 1 of 2	669..686	5/18 (28%) 13/18 (72%)	4.6
rubredoxin: domain 2 of 2	708..713	5/6 (83%) 6/6 (100%)	1.2e+03

Example B: Sequencing Methodology and Identification of NOVX Clones

1. **GeneCalling™ Technology:** This is a proprietary method of performing differential gene expression profiling between two or more samples developed at CuraGen and described by Shimkets, et al., "Gene expression analysis by transcript profiling coupled to a gene database query" Nature Biotechnology 17:198-803 (1999). cDNA was derived from various

human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then digested with up to as many as 120 pairs of restriction enzymes and pairs of linker-adaptors specific for each pair of restriction enzymes were ligated to the appropriate end. The restriction digestion generates a mixture of unique cDNA gene fragments. Limited PCR amplification is performed with primers homologous to the linker adapter sequence where one primer is biotinylated and the other is fluorescently labeled. The doubly labeled material is isolated and the fluorescently labeled single strand is resolved by capillary gel electrophoresis. A computer algorithm compares the electropherograms from an experimental and control group for each of the restriction digestions. This and additional sequence-derived information is used to predict the identity of each differentially expressed gene fragment using a variety of genetic databases. The identity of the gene fragment is confirmed by additional, gene-specific competitive PCR or by isolation and sequencing of the gene fragment.

2. SeqCalling™ Technology: cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then sequenced using CuraGen's proprietary SeqCalling technology. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

3. PathCalling™ Technology:

The NOVX nucleic acid sequences are derived by laboratory screening of cDNA library by the two-hybrid approach. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, are sequenced. In silico prediction was based on sequences available in CuraGen Corporation's proprietary sequence databases or in the public human sequence databases, and provided either the full length DNA sequence, or some portion thereof.

The laboratory screening was performed using the methods summarized below:

cDNA libraries were derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then directionally cloned into the appropriate two-hybrid vector (Gal4-activation domain (Gal4-AD) fusion). Such cDNA libraries as well as commercially available cDNA libraries from Clontech (Palo Alto, CA) were then transferred from E.coli into a CuraGen Corporation proprietary yeast strain (disclosed in U. S. Patents 6,057,101 and 6,083,693, incorporated herein by reference in their entireties).

Gal4-binding domain (Gal4-BD) fusions of a CuraGen Corporation proprietary library of human sequences was used to screen multiple Gal4-AD fusion cDNA libraries resulting in the selection of yeast hybrid diploids in each of which the Gal4-AD fusion contains an individual cDNA. Each sample was amplified using the polymerase chain reaction (PCR) using non-specific primers at the cDNA insert boundaries. Such PCR product was sequenced; sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

Physical clone: the cDNA fragment derived by the screening procedure, covering the entire open reading frame is, as a recombinant DNA, cloned into pACT2 plasmid (Clontech) used to make the cDNA library. The recombinant plasmid is inserted into the host and selected by the yeast hybrid diploid generated during the screening procedure by the mating of both CuraGen Corporation proprietary yeast strains N106' and YULH (U. S. Patents 6,057,101 and 6,083,693).

4. **RACE:** Techniques based on the polymerase chain reaction such as rapid amplification of cDNA ends (RACE), were used to isolate or complete the predicted sequence of the cDNA of the invention. Usually multiple clones were sequenced from one or more human samples to derive the sequences for fragments. Various human tissue samples from different donors were used for the RACE reaction. The sequences derived from these procedures were included in the SeqCalling Assembly process described in preceding paragraphs.

5. **Exon Linking:** The NOVX target sequences identified in the present invention were subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. **Table B1** shows the sequences of the PCR primers used for obtaining different clones. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on in silico predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences from other species. These primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain - whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The PCR product derived from exon linking was cloned into the pCR2.1 vector from Invitrogen. The resulting bacterial clone has an insert covering the entire open reading

frame cloned into the pCR2.1 vector. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported herein.

6. Physical Clone:

Exons were predicted by homology and the intron/exon boundaries were determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN, BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the full-length protein.

The PCR product derived by exon linking, covering the entire open reading frame, was cloned into the pCR2.1 vector from Invitrogen to provide clones used for expression and screening purposes.

Example C: Quantitative expression analysis of clones in various cells and tissues

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines and tissues using real time quantitative PCR (RTQ PCR). RTQ PCR was performed on an Applied Biosystems ABI PRISM® 7700 or an ABI PRISM® 7900 HT Sequence Detection System. Various collections of samples are assembled on the plates, and referred to as Panel 1 (containing normal tissues and cancer cell lines), Panel 2 (containing samples derived from tissues from normal and cancer sources), Panel 3 (containing cancer cell lines), Panel 4 (containing cells and cell lines from normal tissues and cells related to inflammatory conditions), Panel 5D/5I (containing human tissues and cell lines with an emphasis on metabolic diseases), AI_comprehensive_panel (containing normal tissue and samples from autoimmune diseases), Panel CNSD.01 (containing central nervous system samples from normal and diseased brains) and CNS_neurodegeneration_panel (containing samples from normal and Alzheimer's diseased brains).

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

First, the RNA samples were normalized to reference nucleic acids such as constitutively expressed genes (for example, β -actin and GAPDH). Normalized RNA (5 μ l) was converted to cDNA and analyzed by RTQ-PCR using One Step RT-PCR Master Mix Reagents (Applied Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions.

In other cases, non-normalized RNA samples were converted to single strand cDNA (sscDNA) using Superscript II (Invitrogen Corporation; Catalog No. 18064-147) and random hexamers according to the manufacturer's instructions. Reactions containing up to 10 μ g of total RNA were performed in a volume of 20 μ l and incubated for 60 minutes at 42°C. This reaction can be scaled up to 50 μ g of total RNA in a final volume of 100 μ l. sscDNA samples are then normalized to reference nucleic acids as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions.

Probes and primers were designed for each assay according to Applied Biosystems Primer Express Software package (version I for Apple Computer's Macintosh Power PC) or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58°-60°C, primer optimal T_m = 59°C, maximum primer difference = 2°C, probe does not have 5'G, probe T_m must be 10°C greater than primer T_m , amplicon size 75bp to 100bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final concentrations were: forward and reverse primers, 900nM each, and probe, 200nM.

PCR conditions: When working with RNA samples, normalized RNA from each tissue and each cell line was spotted in each well of either a 96 well or a 384-well PCR plate (Applied Biosystems). PCR cocktails included either a single gene specific probe and primers set, or two multiplexed probe and primers sets (a set specific for the target clone and another gene-specific set multiplexed with the target probe). PCR reactions were set up using TaqMan® One-Step RT-PCR Master Mix (Applied Biosystems, Catalog No. 4313803) following manufacturer's instructions. Reverse transcription was performed at 48°C for 30 minutes followed by amplification/PCR cycles as follows: 95°C 10 min, then 40 cycles of 95°C for 15 seconds, 60°C for 1 minute. Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA difference and multiplying by 100.

When working with sscDNA samples, normalized sscDNA was used as described previously for RNA samples. PCR reactions containing one or two sets of probe and primers were set up as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions. PCR amplification was performed as follows: 95°C 10 min, then 40 cycles of 95°C for 15 seconds, 60°C for 1 minute. Results were analyzed and processed as described previously.

Panels 1, 1.1, 1.2, and 1.3D

The plates for Panels 1, 1.1, 1.2 and 1.3D include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in these panels are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in these panels are widely available through the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on these panels are comprised of samples derived from all major organ systems from single adult individuals or

fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine, colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose.

In the results for Panels 1, 1.1, 1.2 and 1.3D, the following abbreviations are used:

ca. = carcinoma,
 * = established from metastasis,
 met = metastasis,
 s cell var = small cell variant,
 non-s = non-sm = non-small,
 squam = squamous,
 pl. eff = pl effusion = pleural effusion,
 glio = glioma,
 astro = astrocytoma, and
 neuro = neuroblastoma.

General_screening_panel_v1.4

The plates for Panel 1.4 include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in Panel 1.4 are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in Panel 1.4 are widely available through the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on Panel 1.4 are comprised of pools of samples derived from all major organ systems from 2 to 5 different adult individuals or fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine, colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose. Abbreviations are as described for Panels 1, 1.1, 1.2, and 1.3D.

Panels 2D and 2.2

The plates for Panels 2D and 2.2 generally include 2 control wells and 94 test samples composed of RNA or cDNA isolated from human tissue procured by surgeons working in close cooperation with the National Cancer Institute's Cooperative Human Tissue Network (CHTN) or the National Disease Research Initiative (NDRI). The tissues are derived from human malignancies and in cases where indicated many malignant tissues have "matched margins" obtained from noncancerous tissue just adjacent to the tumor. These are termed normal adjacent tissues and are denoted "NAT" in the results below. The tumor tissue and the "matched margins" are evaluated by two independent pathologists (the surgical pathologists and again by a pathologist at NDRI or CHTN). This analysis provides a gross histopathological assessment of tumor differentiation grade. Moreover, most samples include the original surgical pathology report that provides information regarding the clinical stage of the patient. These matched margins are taken from the tissue surrounding (i.e. immediately proximal) to the zone of surgery (designated "NAT", for normal adjacent tissue, in Table RR). In addition, RNA and cDNA samples were obtained from various human tissues derived from autopsies performed on elderly people or sudden death victims (accidents, etc.). These tissues were ascertained to be free of disease and were purchased from various commercial sources such as Clontech (Palo Alto, CA), Research Genetics, and Invitrogen.

Panel 3D

The plates of Panel 3D are comprised of 94 cDNA samples and two control samples. Specifically, 92 of these samples are derived from cultured human cancer cell lines, 2 samples of human primary cerebellar tissue and 2 controls. The human cell lines are generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: Squamous cell carcinoma of the tongue, breast cancer, prostate cancer, melanoma, epidermoid carcinoma, sarcomas, bladder carcinomas, pancreatic cancers, kidney cancers, leukemias/lymphomas, ovarian/uterine/cervical, gastric, colon, lung and CNS cancer cell lines. In addition, there are two independent samples of cerebellum. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. The cell lines in panel 3D and 1.3D are of the most common cell lines used in the scientific literature.

Panels 4D, 4R, and 4.1D

Panel 4 includes samples on a 96 well plate (2 control wells, 94 test samples) composed of RNA (Panel 4R) or cDNA (Panels 4D/4.1D) isolated from various human cell lines or tissues related to inflammatory conditions. Total RNA from control normal tissues such as colon and lung (Stratagene, La Jolla, CA) and thymus and kidney (Clontech) was employed. Total RNA from liver tissue from cirrhosis patients and kidney from lupus patients was obtained from BioChain (Biochain Institute, Inc., Hayward, CA). Intestinal tissue for RNA preparation from patients diagnosed as having Crohn's disease and ulcerative colitis was obtained from the National Disease Research Interchange (NDRI) (Philadelphia, PA).

Astrocytes, lung fibroblasts, dermal fibroblasts, coronary artery smooth muscle cells, small airway epithelium, bronchial epithelium, microvascular dermal endothelial cells, microvascular lung endothelial cells, human pulmonary aortic endothelial cells, human umbilical vein endothelial cells were all purchased from Clonetics (Walkersville, MD) and grown in the media supplied for these cell types by Clonetics. These primary cell types were activated with various cytokines or combinations of cytokines for 6 and/or 12-14 hours, as indicated. The following cytokines were used; IL-1 beta at approximately 1-5ng/ml, TNF alpha at approximately 5-10ng/ml, IFN gamma at approximately 20-50ng/ml, IL-4 at approximately 5-10ng/ml, IL-9 at approximately 5-10ng/ml, IL-13 at approximately 5-10ng/ml. Endothelial cells were sometimes starved for various times by culture in the basal media from Clonetics with 0.1% serum.

Mononuclear cells were prepared from blood of employees at CuraGen Corporation, using Ficoll. LAK cells were prepared from these cells by culture in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco/Life Technologies, Rockville, MD), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) and Interleukin 2 for 4-6 days. Cells were then either activated with 10-20ng/ml PMA and 1-2µg/ml ionomycin, IL-12 at 5-10ng/ml, IFN gamma at 20-50ng/ml and IL-18 at 5-10ng/ml for 6 hours. In some cases, mononuclear cells were cultured for 4-5 days in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) with PHA (phytohemagglutinin) or PWM (pokeweed mitogen) at approximately 5µg/ml. Samples were taken at 24, 48 and 72 hours for RNA preparation. MLR (mixed lymphocyte reaction) samples were obtained by taking blood from two donors, isolating the mononuclear cells using Ficoll and mixing the isolated mononuclear cells 1:1 at a final concentration of approximately 2×10^6 cells/ml in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM

sodium pyruvate (Gibco), mercaptoethanol ($5.5 \times 10^{-5} \text{M}$) (Gibco), and 10mM Hepes (Gibco). The MLR was cultured and samples taken at various time points ranging from 1- 7 days for RNA preparation.

Monocytes were isolated from mononuclear cells using CD14 Miltenyi Beads, +ve VS selection columns and a Vario Magnet according to the manufacturer's instructions. Monocytes were differentiated into dendritic cells by culture in DMEM 5% fetal calf serum (FCS) (Hyclone, Logan, UT), 100 μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), and 10mM Hepes (Gibco), 50ng/ml GMCSF and 5ng/ml IL-4 for 5-7 days. Macrophages were prepared by culture of monocytes for 5-7 days in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), 10mM Hepes (Gibco) and 10% AB Human Serum or MCSF at approximately 50ng/ml. Monocytes, macrophages and dendritic cells were stimulated for 6 and 12-14 hours with lipopolysaccharide (LPS) at 100ng/ml. Dendritic cells were also stimulated with anti-CD40 monoclonal antibody (Pharmingen) at 10 $\mu\text{g/ml}$ for 6 and 12-14 hours.

CD4 lymphocytes, CD8 lymphocytes and NK cells were also isolated from mononuclear cells using CD4, CD8 and CD56 Miltenyi beads, positive VS selection columns and a Vario Magnet according to the manufacturer's instructions. CD45RA and CD45RO CD4 lymphocytes were isolated by depleting mononuclear cells of CD8, CD56, CD14 and CD19 cells using CD8, CD56, CD14 and CD19 Miltenyi beads and positive selection. CD45RO beads were then used to isolate the CD45RO CD4 lymphocytes with the remaining cells being CD45RA CD4 lymphocytes. CD45RA CD4, CD45RO CD4 and CD8 lymphocytes were placed in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), and 10mM Hepes (Gibco) and plated at 10^6cells/ml onto Falcon 6 well tissue culture plates that had been coated overnight with 0.5 $\mu\text{g/ml}$ anti-CD28 (Pharmingen) and 3 $\mu\text{g/ml}$ anti-CD3 (OKT3, ATCC) in PBS. After 6 and 24 hours, the cells were harvested for RNA preparation. To prepare chronically activated CD8 lymphocytes, we activated the isolated CD8 lymphocytes for 4 days on anti-CD28 and anti-CD3 coated plates and then harvested the cells and expanded them in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), and 10mM Hepes (Gibco) and IL-2. The expanded CD8 cells were then activated again with plate bound anti-CD3 and anti-CD28 for 4 days and expanded as before. RNA was isolated 6 and 24 hours after the second activation and after 4

days of the second expansion culture. The isolated NK cells were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10⁻⁵M (Gibco), and 10mM Hepes (Gibco) and IL-2 for 4-6 days before RNA was prepared.

To obtain B cells, tonsils were procured from NDRI. The tonsil was cut up with sterile dissecting scissors and then passed through a sieve. Tonsil cells were then spun down and resuspended at 10⁶ cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10⁻⁵M (Gibco), and 10mM Hepes (Gibco). To activate the cells, we used PWM at 5 μ g/ml or anti-CD40 (Pharmingen) at approximately 10 μ g/ml and IL-4 at 5-10ng/ml. Cells were harvested for RNA preparation at 24, 48 and 72 hours.

To prepare the primary and secondary Th1/Th2 and Tr1 cells, six-well Falcon plates were coated overnight with 10 μ g/ml anti-CD28 (Pharmingen) and 2 μ g/ml OKT3 (ATCC), and then washed twice with PBS. Umbilical cord blood CD4 lymphocytes (Poietic Systems, German Town, MD) were cultured at 10⁵-10⁶ cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10⁻⁵M (Gibco), 10mM Hepes (Gibco) and IL-2 (4ng/ml). IL-12 (5ng/ml) and anti-IL4 (1 μ g/ml) were used to direct to Th1, while IL-4 (5ng/ml) and anti-IFN gamma (1 μ g/ml) were used to direct to Th2 and IL-10 at 5ng/ml was used to direct to Tr1. After 4-5 days, the activated Th1, Th2 and Tr1 lymphocytes were washed once in DMEM and expanded for 4-7 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10⁻⁵M (Gibco), 10mM Hepes (Gibco) and IL-2 (1ng/ml). Following this, the activated Th1, Th2 and Tr1 lymphocytes were re-stimulated for 5 days with anti-CD28/OKT3 and cytokines as described above, but with the addition of anti-CD95L (1 μ g/ml) to prevent apoptosis. After 4-5 days, the Th1, Th2 and Tr1 lymphocytes were washed and then expanded again with IL-2 for 4-7 days. Activated Th1 and Th2 lymphocytes were maintained in this way for a maximum of three cycles. RNA was prepared from primary and secondary Th1, Th2 and Tr1 after 6 and 24 hours following the second and third activations with plate bound anti-CD3 and anti-CD28 mAbs and 4 days into the second and third expansion cultures in Interleukin 2.

The following leukocyte cells lines were obtained from the ATCC: Ramos, EOL-1, KU-812. EOL cells were further differentiated by culture in 0.1mM dbcAMP at 5x10⁵ cells/ml

for 8 days, changing the media every 3 days and adjusting the cell concentration to 5×10^5 cells/ml. For the culture of these cells, we used DMEM or RPMI (as recommended by the ATCC), with the addition of 5% FCS (Hyclone), $100 \mu\text{M}$ non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), 10mM Hepes (Gibco). RNA was either prepared from resting cells or cells activated with PMA at 10ng/ml and ionomycin at $1 \mu\text{g/ml}$ for 6 and 14 hours. Keratinocyte line CCD106 and an airway epithelial tumor line NCI-H292 were also obtained from the ATCC. Both were cultured in DMEM 5% FCS (Hyclone), $100 \mu\text{M}$ non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), and 10mM Hepes (Gibco). CCD1106 cells were activated for 6 and 14 hours with approximately 5 ng/ml TNF alpha and 1 ng/ml IL-1 beta, while NCI-H292 cells were activated for 6 and 14 hours with the following cytokines: 5 ng/ml IL-4, 5 ng/ml IL-9, 5 ng/ml IL-13 and 25 ng/ml IFN gamma.

For these cell lines and blood cells, RNA was prepared by lysing approximately 10^7 cells/ml using Trizol (Gibco BRL). Briefly, 1/10 volume of bromochloropropane (Molecular Research Corporation) was added to the RNA sample, vortexed and after 10 minutes at room temperature, the tubes were spun at $14,000 \text{ rpm}$ in a Sorvall SS34 rotor. The aqueous phase was removed and placed in a 15 ml Falcon Tube. An equal volume of isopropanol was added and left at -20°C overnight. The precipitated RNA was spun down at $9,000 \text{ rpm}$ for 15 min in a Sorvall SS34 rotor and washed in 70% ethanol. The pellet was redissolved in $300 \mu\text{l}$ of RNase-free water and $35 \mu\text{l}$ buffer (Promega) $5 \mu\text{l}$ DTT, $7 \mu\text{l}$ RNasin and $8 \mu\text{l}$ DNase were added. The tube was incubated at 37°C for 30 minutes to remove contaminating genomic DNA, extracted once with phenol chloroform and re-precipitated with 1/10 volume of 3M sodium acetate and 2 volumes of 100% ethanol. The RNA was spun down and placed in RNase free water. RNA was stored at -80°C .

AI_comprehensive panel_v1.0

The plates for AI_comprehensive panel_v1.0 include two control wells and 89 test samples comprised of cDNA isolated from surgical and postmortem human tissues obtained from the Backus Hospital and Clinomics (Frederick, MD). Total RNA was extracted from tissue samples from the Backus Hospital in the Facility at CuraGen. Total RNA from other tissues was obtained from Clinomics.

Joint tissues including synovial fluid, synovium, bone and cartilage were obtained from patients undergoing total knee or hip replacement surgery at the Backus Hospital. Tissue samples were immediately snap frozen in liquid nitrogen to ensure that isolated RNA was of optimal quality and not degraded. Additional samples of osteoarthritis and rheumatoid arthritis joint tissues were obtained from Clinomics. Normal control tissues were supplied by Clinomics and were obtained during autopsy of trauma victims.

Surgical specimens of psoriatic tissues and adjacent matched tissues were provided as total RNA by Clinomics. Two male and two female patients were selected between the ages of 25 and 47. None of the patients were taking prescription drugs at the time samples were isolated.

Surgical specimens of diseased colon from patients with ulcerative colitis and Crohn's disease and adjacent matched tissues were obtained from Clinomics. Bowel tissue from three female and three male Crohn's patients between the ages of 41-69 were used. Two patients were not on prescription medication while the others were taking dexamethasone, phenobarbital, or tylenol. Ulcerative colitis tissue was from three male and four female patients. Four of the patients were taking lebid and two were on phenobarbital.

Total RNA from post mortem lung tissue from trauma victims with no disease or with emphysema, asthma or COPD was purchased from Clinomics. Emphysema patients ranged in age from 40-70 and all were smokers, this age range was chosen to focus on patients with cigarette-linked emphysema and to avoid those patients with alpha-1 anti-trypsin deficiencies. Asthma patients ranged in age from 36-75, and excluded smokers to prevent those patients that could also have COPD. COPD patients ranged in age from 35-80 and included both smokers and non-smokers. Most patients were taking corticosteroids, and bronchodilators.

In the labels employed to identify tissues in the AI_comprehensive panel_v1.0 panel, the following abbreviations are used:

AI = Autoimmunity
Syn = Synovial
Normal = No apparent disease
Rep22 /Rep20 = individual patients
RA = Rheumatoid arthritis
Backus = From Backus Hospital
OA = Osteoarthritis
(SS) (BA) (MF) = Individual patients

Adj = Adjacent tissue
 Match control = adjacent tissues
 -M = Male
 -F = Female
 COPD = Chronic obstructive pulmonary disease

Panels 5D and 5I

The plates for Panel 5D and 5I include two control wells and a variety of cDNAs isolated from human tissues and cell lines with an emphasis on metabolic diseases. Metabolic tissues were obtained from patients enrolled in the Gestational Diabetes study. Cells were obtained during different stages in the differentiation of adipocytes from human mesenchymal stem cells. Human pancreatic islets were also obtained.

In the Gestational Diabetes study subjects are young (18 - 40 years), otherwise healthy women with and without gestational diabetes undergoing routine (elective) Caesarean section. After delivery of the infant, when the surgical incisions were being repaired/closed, the obstetrician removed a small sample (<1 cc) of the exposed metabolic tissues during the closure of each surgical level. The biopsy material was rinsed in sterile saline, blotted and fast frozen within 5 minutes from the time of removal. The tissue was then flash frozen in liquid nitrogen and stored, individually, in sterile screw-top tubes and kept on dry ice for shipment to or to be picked up by CuraGen. The metabolic tissues of interest include uterine wall (smooth muscle), visceral adipose, skeletal muscle (rectus) and subcutaneous adipose. Patient descriptions are as follows:

Patient 2	Diabetic Hispanic, overweight, not on insulin
Patient 7-9	Nondiabetic Caucasian and obese (BMI>30)
Patient 10	Diabetic Hispanic, overweight, on insulin
Patient 11	Nondiabetic African American and overweight
Patient 12	Diabetic Hispanic on insulin

Adipocyte differentiation was induced in donor progenitor cells obtained from Osirus (a division of Clonetics/BioWhittaker) in triplicate, except for Donor 3U which had only two replicates. Scientists at Clonetics isolated, grew and differentiated human mesenchymal stem cells (HuMSCs) for CuraGen based on the published protocol found in Mark F. Pittenger, et al., Multilineage Potential of Adult Human Mesenchymal Stem Cells Science Apr 2 1999: 143-147. Clonetics provided Trizol lysates or frozen pellets suitable for mRNA isolation and ds cDNA production. A general description of each donor is as follows:

Donor 2 and 3 U: Mesenchymal Stem cells, Undifferentiated Adipose
Donor 2 and 3 AM: Adipose, AdiposeMidway Differentiated
Donor 2 and 3 AD: Adipose, Adipose Differentiated

Human cell lines were generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: kidney proximal convoluted tubule, uterine smooth muscle cells, small intestine, liver HepG2 cancer cells, heart primary stromal cells, and adrenal cortical adenoma cells. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. All samples were processed at CuraGen to produce single stranded cDNA.

Panel 5I contains all samples previously described with the addition of pancreatic islets from a 58 year old female patient obtained from the Diabetes Research Institute at the University of Miami School of Medicine. Islet tissue was processed to total RNA at an outside source and delivered to CuraGen for addition to panel 5I.

In the labels employed to identify tissues in the 5D and 5I panels, the following abbreviations are used:

GO Adipose = Greater Omentum Adipose
SK = Skeletal Muscle
UT = Uterus
PL = Placenta
AD = Adipose Differentiated
AM = Adipose Midway Differentiated
U = Undifferentiated Stem Cells

Panel CNSD.01

The plates for Panel CNSD.01 include two control wells and 94 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center. Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains two brains from each of the following diagnoses: Alzheimer's disease, Parkinson's disease, Huntington's disease, Progressive Supranuclear Palsy, Depression, and "Normal controls". Within each of these brains, the following regions are represented: cingulate gyrus, temporal pole, globus

palladus, substantia nigra, Brodman Area 4 (primary motor strip), Brodman Area 7 (parietal cortex), Brodman Area 9 (prefrontal cortex), and Brodman area 17 (occipital cortex). Not all brain regions are represented in all cases; e.g., Huntington's disease is characterized in part by neurodegeneration in the globus palladus, thus this region is impossible to obtain from confirmed Huntington's cases. Likewise Parkinson's disease is characterized by degeneration of the substantia nigra making this region more difficult to obtain. Normal control brains were examined for neuropathology and found to be free of any pathology consistent with neurodegeneration.

In the labels employed to identify tissues in the CNS panel, the following abbreviations are used:

PSP = Progressive supranuclear palsy
Sub Nigra = Substantia nigra
Glob Palladus= Globus palladus
Temp Pole = Temporal pole
Cing Gyr = Cingulate gyrus
BA 4 = Brodman Area 4

Panel CNS_Neurodegeneration_V1.0

The plates for Panel CNS_Neurodegeneration_V1.0 include two control wells and 47 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center (McLean Hospital) and the Human Brain and Spinal Fluid Resource Center (VA Greater Los Angeles Healthcare System). Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains six brains from Alzheimer's disease (AD) patients, and eight brains from "Normal controls" who showed no evidence of dementia prior to death. The eight normal control brains are divided into two categories: Controls with no dementia and no Alzheimer's like pathology (Controls) and controls with no dementia but evidence of severe Alzheimer's like pathology, (specifically senile plaque load rated as level 3 on a scale of 0-3; 0 = no evidence of plaques, 3 = severe AD senile plaque load). Within each of these brains, the following regions are represented: hippocampus, temporal cortex (Brodman Area 21), parietal cortex (Brodman area 7), and occipital cortex (Brodman area 17). These regions were chosen to encompass all levels of

neurodegeneration in AD. The hippocampus is a region of early and severe neuronal loss in AD; the temporal cortex is known to show neurodegeneration in AD after the hippocampus; the parietal cortex shows moderate neuronal death in the late stages of the disease; the occipital cortex is spared in AD and therefore acts as a "control" region within AD patients. Not all brain regions are represented in all cases.

In the labels employed to identify tissues in the CNS_Neurodegeneration_V1.0 panel, the following abbreviations are used:

AD = Alzheimer's disease brain; patient was demented and showed AD-like pathology upon autopsy

Control = Control brains; patient not demented, showing no neuropathology

Control (Path) = Control brains; patient not demented but showing severe AD-like pathology

SupTemporal Ctx = Superior Temporal Cortex

Inf Temporal Ctx = Inferior Temporal Cortex

A. CG58522-01: HUMAN PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA

Expression of gene CG58522-01 was assessed using the primer-probe set Ag3365, described in Table AA. Results of the RTQ-PCR runs are shown in Table AB.

Table AA. Probe Name Ag3365

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cagaatgaaccaaggagactca-3'	22	3	357
Probe	TET-5'-ctactccgcacatgcggcagaagacatt-3'-TAMRA	26	35	358
Reverse	5'-cacatccatctgtcatctcctt-3'	22	62	359

Table AB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3365, Run 216709759	Tissue Name	Rel. Exp.(%) Ag3365, Run 216709759
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma*	0.0	Colon ca. SW-948	0.0

LOXIMVI			
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	10.7	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	4.9	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	7.9	Stomach Pool	0.0
Ovarian ca. OVCAR-8	26.8	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	1.7	Lymph Node Pool	16.5
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	3.3	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	4.5	CNS cancer (glio) SNB-19	6.2
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	25.7

Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	100.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	4.8
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	1.8
Liver	0.0	Brain (Thalamus) Pool	3.6
Fetal Liver	0.0	Brain (whole)	6.9
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3365 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3365 - Significant expression of this gene is seen only in the lung cancer cell line NCI-H23 (CT=33.1). Therefore, expression of this gene may be used to distinguish this sample from the other samples on this panel.

Panel 4D Summary: Ag3365 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

B. CG58520-01: GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1

Expression of gene CG58520-01 was assessed using the primer-probe set Ag3364, described in Table BA.

Table BA. Probe Name Ag3364

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ttcttctgcggaggtcaaagtag-3'	22	43	360
Probe	TET-5'-ttggtcttcttgttactgacctgca-3'-TAMRA	26	75	361
Reverse	5'-tcattctgccttatcaacgtttc-3'	22	106	362

CNS_neurodegeneration_v1.0 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel CNS_1 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

C. CG58520-03: GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR)

Expression of gene CG58520-03 was assessed using the primer-probe set Ag5092, described in Table CA.

Table CA. Probe Name Ag5092

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gaacattcctgtccactgga-3'	20	625	363
Probe	TET-5'-atTTTcaagcgatggataccctaaaa-3'- TAMRA	26	645	364
Reverse	5'-cacttctacggagggtttt-3'	20	692	365

CNS_neurodegeneration_v1.0 Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.5 Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

D. CG58518-01: GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-3 -

Expression of gene CG58518-01 was assessed using the primer-probe sets Ag3363, Ag1130, Ag1198, Ag1253 and Ag1603, described in Tables DA, DB, DC, DD and DE. Results of the RTQ-PCR runs are shown in Tables DF, DG and DH.

Table DA. Probe Name Ag3363

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tggtcttccagttagtctcctt-3'	22	14	366
Probe	TET-5'-cacctacatctggatcatattgaaacca-3'- TAMRA	28	36	367
Reverse	5'-ttgatgttagaagcagcacaaa-3'	22	68	368

Table DB. Probe Name Ag1130

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcctggcttccagttagtct-3'	22	10	369
Probe	TET-5'-tcacctacatctggatcatattgaaacca-3'- TAMRA	29	35	370
Reverse	5'-ttgatgttagaagcagcacaaa-3'	22	68	371

Table DC. Probe Name Ag1198

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcctggcttccagttagtct-3'	22	10	372
Probe	TET-5'-tcacctacatctggatcatattgaaacca-3'- TAMRA	29	35	373
Reverse	5'-ttgatgttagaagcagcacaaa-3'	22	68	374

Table DD. Probe Name Ag1253

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atctgggtgcctgatattctttt-3'	22	466	375
Probe	TET-5'-tgtccactctaaaagatccttcatccatga-3'- TAMRA	30	489	376
Reverse	5'-cgagcatgatattctccatag-3'	22	524	377

Table DE. Probe Name Ag1603

Primers	Sequences	Length	Start Position	SEQ ID NO:
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Forward	5'-gtcctggctttccagtttagtct-3'	22	10	378
Probe	TET-5'-tcacctacatctggatcatattgaaacca-3'- TAMRA	29	35	379
Reverse	5'-ttgatgttagaagcagcacaaa-3'	22	68	380

Table DF. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3363, Run 216709559	Tissue Name	Rel. Exp.(%) Ag3363, Run 216709559
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	6.6
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	16.7	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV- 1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA- MB-231	0.0	Lymph Node Pool	6.8
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0

Breast ca. T47D	6.4	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	8.5
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	10.9
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	77.9	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	100.0	CNS cancer (glio) SF- 295	11.4
Lung ca. A549	10.1	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	34.4	Brain (fetal)	0.0
Lung ca. NCI-H460	30.6	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	5.1
Fetal Liver	0.0	Brain (whole)	50.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	3.0	Adrenal Gland	0.0
Fetal Kidney	8.4	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table DG. Panel 1.2

Tissue Name	Rel. Exp.(%) Ag1130, Run 125117140	Rel. Exp.(%) Ag1130, Run 126566764	Rel. Exp.(%) Ag1198, Run 129140506	Tissue Name	Rel. Exp.(%) Ag1130, Run 125117140	Rel. Exp.(%) Ag1130, Run 126566764	Rel. Exp.(%) Ag1198, Run 129140506
Endothelial cells	0.0	0.0	0.0	Renal ca. 786-0	0.0	0.0	0.0

Heart (Fetal)	0.0	0.0	0.0	Renal ca. A498	7.3	4.7	0.0
Pancreas	0.0	0.0	0.0	Renal ca. RXF 393	0.0	0.0	0.0
Pancreatic ca. CAPAN 2	9.0	0.0	0.0	Renal ca. ACHN	0.0	0.0	0.0
Adrenal Gland	0.0	2.6	0.0	Renal ca. UO-31	3.9	0.0	0.0
Thyroid	0.0	0.0	0.0	Renal ca. TK-10	0.0	0.0	0.0
Salivary gland	0.0	0.0	0.0	Liver	26.6	0.0	0.0
Pituitary gland	0.0	0.0	0.0	Liver (fetal)	25.3	0.0	0.0
Brain (fetal)	0.0	0.0	0.0	Liver ca. (hepatoblast) HepG2	0.0	0.0	0.0
Brain (whole)	2.6	20.0	0.0	Lung	0.0	0.0	0.0
Brain (amygdala)	1.3	32.1	0.0	Lung (fetal)	0.0	0.0	0.0
Brain (cerebellum)	1.5	3.8	0.0	Lung ca. (small cell) LX-1	3.4	0.0	0.0
Brain (hippocampus)	0.0	27.0	0.0	Lung ca. (small cell) NCI-H69	28.5	74.2	0.0
Brain (thalamus)	9.9	22.5	9.8	Lung ca. (s.cell var.) SHP-77	3.8	9.7	0.0
Cerebral Cortex	0.0	0.0	0.0	Lung ca. (large cell) NCI-H460	8.8	4.1	5.3
Spinal cord	4.4	0.0	0.0	Lung ca. (non-sm. cell) A549	51.4	9.5	7.2
glio/astro U87-MG	0.0	0.0	0.0	Lung ca. (non-s.cell) NCI-H23	0.0	0.0	0.0
glio/astro U-118-MG	0.0	0.0	0.0	Lung ca. (non-s.cell)	8.4	2.7	9.6

				HOP-62			
astrocytoma SW1783	2.9	0.0	0.0	Lung ca. (non-s.cl) NCI-H522	0.0	0.0	0.0
neuro*; met SK-N-AS	0.0	0.0	0.0	Lung ca. (squam.) SW 900	3.2	8.7	0.0
astrocytoma SF-539	5.1	0.0	0.0	Lung ca. (squam.) NCI-H596	2.3	15.9	0.0
astrocytoma SNB-75	2.3	0.0	0.0	Mammary gland	0.0	0.0	0.0
glioma SNB-19	6.3	20.7	9.0	Breast ca.* (pl.ef) MCF-7	0.0	0.0	0.0
glioma U251	1.4	0.0	1.8	Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0	0.0
glioma SF-295	0.0	0.0	0.0	Breast ca.* (pl.ef) T47D	14.1	37.4	0.0
Heart	0.0	0.0	0.0	Breast ca. BT-549	12.5	21.0	12.3
Skeletal Muscle	2.3	0.0	0.0	Breast ca. MDA-N	0.0	0.0	0.0
Bone marrow	0.0	0.0	0.0	Ovary	0.0	0.0	0.0
Thymus	0.0	0.0	0.0	Ovarian ca. OVCAR-3	0.0	0.0	0.0
Spleen	2.2	0.0	0.0	Ovarian ca. OVCAR-4	0.0	0.0	0.0
Lymph node	0.0	0.0	0.0	Ovarian ca. OVCAR-5	66.9	35.4	4.4
Colorectal Tissue	11.3	27.7	21.8	Ovarian ca. OVCAR-	2.7	0.0	0.0

				8			
Stomach	0.0	0.0	0.0	Ovarian ca. IGROV-1	6.0	0.0	0.0
Small intestine	5.4	0.0	0.0	Ovarian ca. (ascites) SK-OV-3	30.8	0.0	0.0
Colon ca. SW480	3.2	0.0	0.0	Uterus	0.0	0.0	0.0
Colon ca.* SW620 (SW480 met)	0.0	0.0	0.0	Placenta	0.0	0.0	0.0
Colon ca. HT29	1.9	14.4	0.0	Prostate	6.9	0.0	0.0
Colon ca. HCT-116	0.0	0.0	0.0	Prostate ca.* (bone met) PC-3	100.0	0.0	0.0
Colon ca. CaCo-2	0.0	0.0	0.0	Testis	54.7	100.0	36.9
Colon ca. Tissue (ODO3866)	72.2	75.8	100.0	Melanom a Hs688(A). T	4.2	0.0	0.0
Colon ca. HCC-2998	5.3	4.8	0.0	Melanom a* (met) Hs688(B). T	2.7	34.2	13.3
Gastric ca.* (liver met) NCI-N87	50.3	0.0	0.0	Melanom a UACC- 62	0.0	0.0	0.0
Bladder	6.0	22.1	0.0	Melanom a M14	31.4	36.3	20.2
Trachea	0.0	0.0	0.0	Melanom a LOX IMVI	0.0	0.0	0.0
Kidney	2.0	0.0	0.0	Melanom a* (met) SK-MEL- 5	2.4	0.0	0.0
Kidney (fetal)	1.1	2.5	0.0				

Table DH. Panel 4R

Tissue Name	Rel. Exp.(%)	Tissue Name	Rel. Exp.(%)
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	Ag1198, Run 142014937		Ag1198, Run 142014937
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	2.5	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1 _anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	16.4
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0

Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	0.0	IBD Colitis 1	100.0
Monocytes rest	0.0	IBD Colitis 2	0.0
Monocytes LPS	0.0	IBD Crohn's	0.0
Macrophages rest	0.0	Colon	0.0
Macrophages LPS	0.0	Lung	0.0
HUVEC none	0.0	Thymus	0.0
HUVEC starved	0.0	Kidney	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3363 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3363 - Significant expression is seen in lung cancer cell line NCI-H146 (CT=34.5) and lung cancer cell line SHP-77 (CT=34.2). Therefore, expression of this can be used to distinguish these samples from the rest of the samples on this panel.

Panel 1.2 Summary: Ag1130/Ag1198 - Three different runs using the same primer sequences yield similar results. Significant expression of this gene is seen in testis and a colon cancer sample. Therefore, expression of this gene can be used to differentiate these samples

from other samples on these panels. Results from a third experiment using the probe and primer set Ag1253 show low/undetectable levels of expression in all the samples on this panel.

Panel 1.3D Summary: Ag1253 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 2D Summary: Ag1603 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag1130/Ag1198/Ag1253/Ag3363 - Two experiments showed possible experimental difficulties, while the other three runs showed expression of this gene as low/undetectable (CTs > 35) across all of the samples on the panel.

Panel 4R Summary: Ag1198 - Significant expression of this gene is seen only in the IBD colitis 1 sample (CT=34.2). Therefore, expression of this gene can be used to differentiate this sample from others on the panel.

Panel CNS_1 Summary: Ag1253/Ag1603 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

E. CG58516-01: G-protein beta WD-40 repeats

Expression of gene CG58516-01 was assessed using the primer-probe set Ag3362, described in Table EA. Results of the RTQ-PCR runs are shown in Tables EB and EC.

Table EA. Probe Name Ag3362

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcgggcaggacctttact-3'	19	1474	381
Probe	TET-5'-tcctacagctaattctgcagggcaca-3'-TAMRA	26	1498	382
Reverse	5'-tacgctttactcccgttaagtca-3'	22	1543	383

Table EB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3362, Run 210153738	Tissue Name	Rel. Exp.(%) Ag3362, Run 210153738
AD 1 Hippo	9.9	Control (Path) 3 Temporal Ctx	0.0

AD 2 Hippo	33.2	Control (Path) 4 Temporal Ctx	24.3
AD 3 Hippo	4.3	AD 1 Occipital Ctx	2.0
AD 4 Hippo	16.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	96.6	AD 3 Occipital Ctx	5.4
AD 6 Hippo	43.2	AD 4 Occipital Ctx	24.7
Control 2 Hippo	29.1	AD 5 Occipital Ctx	24.5
Control 4 Hippo	16.6	AD 6 Occipital Ctx	31.9
Control (Path) 3 Hippo	3.8	Control 1 Occipital Ctx	0.9
AD 1 Temporal Ctx	7.1	Control 2 Occipital Ctx	89.5
AD 2 Temporal Ctx	23.2	Control 3 Occipital Ctx	12.6
AD 3 Temporal Ctx	5.6	Control 4 Occipital Ctx	6.3
AD 4 Temporal Ctx	20.0	Control (Path) 1 Occipital Ctx	65.1
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	15.8
AD 5 Sup Temporal Ctx	43.8	Control (Path) 3 Occipital Ctx	2.0
AD 6 Inf Temporal Ctx	30.8	Control (Path) 4 Occipital Ctx	11.6
AD 6 Sup Temporal Ctx	69.7	Control 1 Parietal Ctx	2.8
Control 1 Temporal Ctx	9.0	Control 2 Parietal Ctx	39.2
Control 2 Temporal Ctx	59.0	Control 3 Parietal Ctx	23.5
Control 3 Temporal Ctx	11.7	Control (Path) 1 Parietal Ctx	69.7
Control 4 Temporal Ctx	8.2	Control (Path) 2 Parietal Ctx	14.9
Control (Path) 1 Temporal Ctx	56.3	Control (Path) 3 Parietal Ctx	0.9
Control (Path) 2 Temporal Ctx	34.2	Control (Path) 4 Parietal Ctx	38.7

Table EC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3362, Run 216523482	Tissue Name	Rel. Exp.(%) Ag3362, Run 216523482
Adipose	6.3	Renal ca. TK-10	44.1

Melanoma* Hs688(A).T	17.6	Bladder	9.4
Melanoma* Hs688(B).T	18.3	Gastric ca. (liver met.) NCI-N87	21.6
Melanoma* M14	17.1	Gastric ca. KATO III	17.6
Melanoma* LOXIMVI	13.6	Colon ca. SW-948	5.8
Melanoma* SK- MEL-5	19.6	Colon ca. SW480	34.6
Squamous cell carcinoma SCC-4	14.6	Colon ca.* (SW480 met) SW620	14.2
Testis Pool	4.0	Colon ca. HT29	7.2
Prostate ca.* (bone met) PC-3	90.8	Colon ca. HCT-116	14.3
Prostate Pool	4.0	Colon ca. CaCo-2	19.8
Placenta	11.4	Colon cancer tissue	3.6
Uterus Pool	2.1	Colon ca. SW1116	9.4
Ovarian ca. OVCAR-3	17.4	Colon ca. Colo-205	8.8
Ovarian ca. SK-OV- 3	47.0	Colon ca. SW-48	13.2
Ovarian ca. OVCAR-4	14.7	Colon Pool	5.7
Ovarian ca. OVCAR-5	31.6	Small Intestine Pool	10.2
Ovarian ca. IGROV- 1	12.9	Stomach Pool	6.2
Ovarian ca. OVCAR-8	6.7	Bone Marrow Pool	1.3
Ovary	12.5	Fetal Heart	1.1
Breast ca. MCF-7	75.8	Heart Pool	3.4
Breast ca. MDA- MB-231	30.4	Lymph Node Pool	8.7
Breast ca. BT 549	65.5	Fetal Skeletal Muscle	2.3
Breast ca. T47D	100.0	Skeletal Muscle Pool	9.4
Breast ca. MDA-N	33.4	Spleen Pool	4.6
Breast Pool	4.6	Thymus Pool	7.3
Trachea	7.7	CNS cancer (glio/astro) U87-MG	33.9
Lung	4.9	CNS cancer (glio/astro) U-118-MG	27.2
Fetal Lung	7.1	CNS cancer (neuro;met) SK-N-AS	16.0
Lung ca. NCI-N417	9.3	CNS cancer (astro) SF- 539	14.3

Lung ca. LX-1	15.8	CNS cancer (astro) SNB-75	60.7
Lung ca. NCI-H146	4.9	CNS cancer (glio) SNB-19	13.8
Lung ca. SHP-77	16.5	CNS cancer (glio) SF- 295	28.5
Lung ca. A549	27.2	Brain (Amygdala) Pool	5.3
Lung ca. NCI-H526	4.1	Brain (cerebellum)	5.0
Lung ca. NCI-H23	15.0	Brain (fetal)	16.4
Lung ca. NCI-H460	9.5	Brain (Hippocampus) Pool	5.5
Lung ca. HOP-62	7.6	Cerebral Cortex Pool	8.7
Lung ca. NCI-H522	18.2	Brain (Substantia nigra) Pool	8.3
Liver	0.0	Brain (Thalamus) Pool	6.3
Fetal Liver	7.3	Brain (whole)	7.0
Liver ca. HepG2	29.5	Spinal Cord Pool	5.6
Kidney Pool	17.7	Adrenal Gland	6.3
Fetal Kidney	4.6	Pituitary gland Pool	0.8
Renal ca. 786-0	17.2	Salivary Gland	5.6
Renal ca. A498	5.1	Thyroid (female)	9.7
Renal ca. ACHN	17.3	Pancreatic ca. CAPAN2	11.7
Renal ca. UO-31	11.1	Pancreas Pool	9.2

CNS_neurodegeneration_v1.0 Summary: Ag3362 Highest expression of the CG58516-01 gene is seen in the occipital cortex of a control patient and the temporal cortex of an Alzheimer's patient. While the CG58516-01 gene does not appear to be preferentially expressed in Alzheimer's disease, this panel confirms expression of the CG58516-01 gene at moderate/high levels in the brain in an additional set of individuals. Please see Panel 1.4 for discussion of potential utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3362 The CG58516-01 gene is widely expressed in this panel, with highest expression in the breast cancer cell line T47D (CT=29). Significant expression is also seen in cell lines derived from prostate, breast and ovarian cancers. In general, expression of the CG58516-01 gene appears to be greater in the cancer cell lines than in normal tissue. Thus, the expression of this gene could be used to distinguish these cell line types from others in the panel.

Among tissues involved in central nervous system function, this gene is expressed at low but significant levels in all brain regions examined. This gene encodes a protein with a

putative zinc-finger motif. Since these proteins are known to interact with nucleic acids, this suggests that this gene product may play a potential role in transcription. Thus, therapeutic modulation of the CG58516-01 gene product may be used to regulate the transcription of disease-related proteins such as ataxin, huntingtin, or various apoptosis cascade proteins.

Among tissues with metabolic function, this gene is expressed at low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, skeletal muscle, heart, and fetal liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

References:

1. Zhu W, Chan EK, Li J, Hemmerich P, Tan EM. (2001) Transcription activating property of autoantigen SG2NA and modulating effect of WD-40 repeats. *Exp Cell Res.* 269(2):312-21

Panel 4D Summary: Ag3362 Results from one experiment with the CG58516-01 gene are not included because the amp plot corresponding to the run indicates that there were problems with the experiment.

F. CG58473-01: PROTEIN KINASE

Expression of gene CG58473-01 was assessed using the primer-probe set Ag3357, described in Table FA. Results of the RTQ-PCR runs are shown in Tables FB and FC.

Table FA. Probe Name Ag3357

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcaaggtggccctaaaattc-3'	21	853	384
Probe	TET-5'-ccaggacctcatctccaagctgctta-3'-TAMRA	26	897	385
Reverse	5'-agccgttctgaggggttat-3'	19	926	386

Table FB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3357, Run 216523477	Tissue Name	Rel. Exp.(%) Ag3357, Run 216523477
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Adipose	0.0	Renal ca. TK-10	13.2
Melanoma* Hs688(A).T	0.0	Bladder	7.2
Melanoma* Hs688(B).T	1.1	Gastric ca. (liver met.) NCI-N87	5.4
Melanoma* M14	50.0	Gastric ca. KATO III	49.0
Melanoma* LOXIMVI	33.0	Colon ca. SW-948	14.9
Melanoma* SK- MEL-5	24.7	Colon ca. SW480	95.9
Squamous cell carcinoma SCC-4	11.6	Colon ca.* (SW480 met) SW620	53.6
Testis Pool	8.2	Colon ca. HT29	10.3
Prostate ca.* (bone met) PC-3	3.2	Colon ca. HCT-116	76.3
Prostate Pool	0.0	Colon ca. CaCo-2	14.1
Placenta	2.4	Colon cancer tissue	6.3
Uterus Pool	0.0	Colon ca. SW1116	18.6
Ovarian ca. OVCAR-3	51.1	Colon ca. Colo-205	24.3
Ovarian ca. SK-OV- 3	53.2	Colon ca. SW-48	26.1
Ovarian ca. OVCAR-4	10.4	Colon Pool	4.6
Ovarian ca. OVCAR-5	12.3	Small Intestine Pool	1.7
Ovarian ca. IGROV- 1	10.1	Stomach Pool	1.2
Ovarian ca. OVCAR-8	13.4	Bone Marrow Pool	1.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	20.3	Heart Pool	0.0
Breast ca. MDA- MB-231	65.1	Lymph Node Pool	1.4
Breast ca. BT 549	100.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	34.2	Skeletal Muscle Pool	1.6
Breast ca. MDA-N	36.3	Spleen Pool	3.4
Breast Pool	1.3	Thymus Pool	4.7
Trachea	0.0	CNS cancer (glio/astro) U87-MG	7.8
Lung	0.0	CNS cancer (glio/astro) U-118-MG	54.0
Fetal Lung	5.0	CNS cancer (neuro;met) SK-N-AS	7.9

Lung ca. NCI-N417	17.9	CNS cancer (astro) SF-539	22.4
Lung ca. LX-1	28.5	CNS cancer (astro) SNB-75	19.2
Lung ca. NCI-H146	74.7	CNS cancer (glio) SNB-19	14.6
Lung ca. SHP-77	40.6	CNS cancer (glio) SF-295	3.0
Lung ca. A549	64.6	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	23.8	Brain (cerebellum)	0.0
Lung ca. NCI-H23	63.7	Brain (fetal)	0.0
Lung ca. NCI-H460	0.8	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	2.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	34.4	Brain (Substantia nigra) Pool	2.6
Liver	0.0	Brain (Thalamus) Pool	9.3
Fetal Liver	0.0	Brain (whole)	2.5
Liver ca. HepG2	11.4	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	3.1	Pituitary gland Pool	1.4
Renal ca. 786-0	20.0	Salivary Gland	0.0
Renal ca. A498	3.6	Thyroid (female)	0.0
Renal ca. ACHN	18.9	Pancreatic ca. CAPAN2	20.4
Renal ca. UO-31	10.4	Pancreas Pool	1.3

Table FC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3357, Run 165231196	Tissue Name	Rel. Exp.(%) Ag3357, Run 165231196
Secondary Th1 act	9.0	HUVEC IL-1beta	9.5
Secondary Th2 act	43.2	HUVEC IFN gamma	6.3
Secondary Tr1 act	46.0	HUVEC TNF alpha + IFN gamma	7.3
Secondary Th1 rest	6.7	HUVEC TNF alpha + IL4	25.3
Secondary Th2 rest	12.2	HUVEC IL-11	13.1
Secondary Tr1 rest	1.9	Lung Microvascular EC none	3.3
Primary Th1 act	6.1	Lung Microvascular EC TNFalpha + IL-1beta	7.1
Primary Th2 act	21.8	Microvascular Dermal EC none	10.9
Primary Tr1 act	33.0	Microvascular Dermal EC	7.3

		TNFalpha + IL-1beta	
Primary Th1 rest	28.1	Bronchial epithelium TNFalpha + IL1beta	1.9
Primary Th2 rest	12.1	Small airway epithelium none	3.6
Primary Tr1 rest	29.7	Small airway epithelium TNFalpha + IL-1beta	36.3
CD45RA CD4 lymphocyte act	28.5	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	39.8	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	18.6	Astrocytes rest	1.4
Secondary CD8 lymphocyte rest	26.8	Astrocytes TNFalpha + IL-1beta	1.2
Secondary CD8 lymphocyte act	19.2	KU-812 (Basophil) rest	18.2
CD4 lymphocyte none	10.6	KU-812 (Basophil) PMA/ionomycin	30.4
2ry Th1/Th2/Tr1 _anti- CD95 CH11	15.6	CCD1106 (Keratinocytes) none	18.3
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	7.7
LAK cells IL-2	42.6	Liver cirrhosis	25.7
LAK cells IL-2+IL-12	24.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	24.8	NCI-H292 none	7.8
LAK cells IL-2+ IL-18	40.3	NCI-H292 IL-4	26.4
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	29.7
NK Cells IL-2 rest	23.5	NCI-H292 IL-13	20.7
Two Way MLR 3 day	13.7	NCI-H292 IFN gamma	27.9
Two Way MLR 5 day	13.2	HPAEC none	8.6
Two Way MLR 7 day	11.7	HPAEC TNF alpha + IL-1 beta	2.4
PBMC rest	0.0	Lung fibroblast none	5.5
PBMC PWM	52.1	Lung fibroblast TNF alpha + IL-1 beta	2.2
PBMC PHA-L	14.6	Lung fibroblast IL-4	0.0
Ramos (B cell) none	16.5	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	14.7	Lung fibroblast IL-13	0.0
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	10.4	Dermal fibroblast CCD1070 rest	40.1

EOL-1 dbcAMP	9.9	Dermal fibroblast CCD1070 TNF alpha	43.8
EOL-1 dbcAMP PMA/ionomycin	13.2	Dermal fibroblast CCD1070 IL-1 beta	23.5
Dendritic cells none	4.7	Dermal fibroblast IFN gamma	3.7
Dendritic cells LPS	1.1	Dermal fibroblast IL-4	4.6
Dendritic cells anti- CD40	0.0	IBD Colitis 2	0.0
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	28.1
Macrophages rest	4.3	Lung	59.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	28.3	Kidney	10.0
HUVEC starved	25.3		

CNS_neurodegeneration_v1.0 Summary: Ag3357 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3357 This gene is primarily expressed in cancer cell lines, with highest expression in a breast cancer cell line BT 549(CT=32.8). This gene is expressed in the following cell lines but not the corresponding healthy tissue: gastric, brain, colon, lung, breast, ovarian cancer and melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

Panel 4D Summary: Ag3357 Highest expression of the CG58473-01 gene is seen in pokeweed mitogen-activated purified peripheral blood B lymphocytes (CT=33.2). In addition, no expression of the transcript is seen in PBMC that contain normal B cells, but the transcript is induced when PBMC are treated with the B cell selective pokeweed mitogen. The transcript is not seen in the B cell lymphoma cell line Ramos regardless of stimulation. Thus, the putative protein encoded by this gene could potentially be used diagnostically to identify activated B cells. Therefore, therapeutics that antagonize the function of this gene product may be useful as therapeutic drugs to reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as lupus erythematosus, Crohn's disease, ulcerative

colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

G. CG58470-01: UDP-N-ACETYLHEXOSAMINE PYROPHOSPHORYLASE

Expression of gene CG58470-01 was assessed using the primer-probe set Ag5940, described in Table GA.

Table GA. Probe Name Ag5940

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atatcctgaagctacaacagtttagct-3'	26	422	387
Probe	TET-5'-tggcaacaaatgcattattccatattacg-3'-TAMRA	29	459	388
Reverse	5'-gagtgaactcgctgggtcatg-3'	20	489	389

General_screening_panel_v1.5 Summary: Ag5940 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 5 Islet Summary: Ag5940 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

H. CG58593-01: UBIQUITIN-52

Expression of gene CG58593-01 was assessed using the primer-probe set Ag3421, described in Table HA.

Table HA. Probe Name Ag3421

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atctgctgcaagtgctatgc-3'	20	291	390
Probe	TET-5'-cggtgctatcaactgccacaagaaga-3'-TAMRA	26	323	391
Reverse	5'-tgaccttcttcctgggggtac-3'	20	371	392

CNS_neurodegeneration_v1.0 Summary: Ag3421 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3421 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3421 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

I. CG57871-01: TOUSLED-LIKE KINASE

Expression of gene CG57871-01 was assessed using the primer-probe set Ag3351, described in Table IA. Results of the RTQ-PCR runs are shown in Tables IB and IC.

Table IA. Probe Name Ag3351

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gatcctcactgcaacattcttt-3'	22	346	393
Probe	TET-5'-aatcccttaccgcgacgagtagaaca-3'- TAMRA	26	372	394
Reverse	5'-gcactgccatctaaccataga-3'	22	403	395

Table IB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3351, Run 210141594	Tissue Name	Rel. Exp.(%) Ag3351, Run 210141594
AD 1 Hippo	10.4	Control (Path) 3 Temporal Ctx	3.0
AD 2 Hippo	33.4	Control (Path) 4 Temporal Ctx	65.1
AD 3 Hippo	5.5	AD 1 Occipital Ctx	20.2
AD 4 Hippo	8.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	3.8
AD 6 Hippo	33.4	AD 4 Occipital Ctx	45.1
Control 2 Hippo	29.9	AD 5 Occipital Ctx	15.2
Control 4 Hippo	6.7	AD 6 Occipital Ctx	46.7
Control (Path) 3 Hippo	3.7	Control 1 Occipital Ctx	2.7
AD 1 Temporal Ctx	16.8	Control 2 Occipital Ctx	52.5
AD 2 Temporal Ctx	45.1	Control 3 Occipital Ctx	45.4
AD 3 Temporal Ctx	6.9	Control 4 Occipital Ctx	6.3
AD 4 Temporal Ctx	54.0	Control (Path) 1 Occipital Ctx	79.0
AD 5 Inf Temporal Ctx	92.0	Control (Path) 2 Occipital Ctx	34.4

AD 5 SupTemporal Ctx	13.0	Control (Path) 3 Occipital Ctx	0.8
AD 6 Inf Temporal Ctx	48.6	Control (Path) 4 Occipital Ctx	40.6
AD 6 Sup Temporal Ctx	56.6	Control 1 Parietal Ctx	6.9
Control 1 Temporal Ctx	6.2	Control 2 Parietal Ctx	48.0
Control 2 Temporal Ctx	29.3	Control 3 Parietal Ctx	26.1
Control 3 Temporal Ctx	32.8	Control (Path) 1 Parietal Ctx	73.7
Control 4 Temporal Ctx	13.9	Control (Path) 2 Parietal Ctx	57.4
Control (Path) 1 Temporal Ctx	79.6	Control (Path) 3 Parietal Ctx	3.4
Control (Path) 2 Temporal Ctx	97.3	Control (Path) 4 Parietal Ctx	78.5

Table IC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3351, Run 165222896	Tissue Name	Rel. Exp.(%) Ag3351, Run 165222896
Secondary Th1 act	16.5	HUVEC IL-1beta	15.4
Secondary Th2 act	26.4	HUVEC IFN gamma	13.5
Secondary Tr1 act	23.3	HUVEC TNF alpha + IFN gamma	17.0
Secondary Th1 rest	6.0	HUVEC TNF alpha + IL4	11.0
Secondary Th2 rest	10.7	HUVEC IL-11	5.4
Secondary Tr1 rest	2.1	Lung Microvascular EC none	12.4
Primary Th1 act	19.2	Lung Microvascular EC TNFalpha + IL-1beta	9.6
Primary Th2 act	17.6	Microvascular Dermal EC none	14.7
Primary Tr1 act	36.1	Microvascular Dermal EC TNFalpha + IL-1beta	14.8
Primary Th1 rest	55.5	Bronchial epithelium TNFalpha + IL1beta	14.1
Primary Th2 rest	43.8	Small airway epithelium none	7.7
Primary Tr1 rest	15.9	Small airway epithelium TNFalpha + IL-1beta	50.3
CD45RA CD4	13.0	Coronary artery SMC rest	15.6

lymphocyte act			
CD45RO CD4 lymphocyte act	21.0	Coronary artery SMC TNFalpha + IL-1beta	6.1
CD8 lymphocyte act	12.9	Astrocytes rest	11.5
Secondary CD8 lymphocyte rest	14.9	Astrocytes TNFalpha + IL-1beta	11.8
Secondary CD8 lymphocyte act	14.8	KU-812 (Basophil) rest	19.2
CD4 lymphocyte none	10.7	KU-812 (Basophil) PMA/ionomycin	54.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	12.7	CCD1106 (Keratinocytes) none	12.2
LAK cells rest	17.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	9.0
LAK cells IL-2	22.4	Liver cirrhosis	7.4
LAK cells IL-2+IL-12	20.4	Lupus kidney	3.4
LAK cells IL-2+IFN gamma	37.9	NCI-H292 none	47.6
LAK cells IL-2+ IL-18	18.6	NCI-H292 IL-4	42.3
LAK cells PMA/ionomycin	10.5	NCI-H292 IL-9	30.4
NK Cells IL-2 rest	17.8	NCI-H292 IL-13	15.7
Two Way MLR 3 day	33.2	NCI-H292 IFN gamma	25.5
Two Way MLR 5 day	10.6	HPAEC none	13.5
Two Way MLR 7 day	9.9	HPAEC TNF alpha + IL-1 beta	17.7
PBMC rest	12.8	Lung fibroblast none	11.5
PBMC PWM	63.3	Lung fibroblast TNF alpha + IL-1 beta	12.4
PBMC PHA-L	18.0	Lung fibroblast IL-4	31.2
Ramos (B cell) none	14.0	Lung fibroblast IL-9	22.2
Ramos (B cell) ionomycin	77.9	Lung fibroblast IL-13	27.4
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	44.8
B lymphocytes CD40L and IL-4	30.8	Dermal fibroblast CCD1070 rest	33.7
EOL-1 dbcAMP	11.3	Dermal fibroblast CCD1070 TNF alpha	50.0
EOL-1 dbcAMP PMA/ionomycin	13.7	Dermal fibroblast CCD1070 IL-1 beta	13.4
Dendritic cells none	14.7	Dermal fibroblast IFN gamma	14.3
Dendritic cells LPS	19.8	Dermal fibroblast IL-4	25.7

Dendritic cells anti-CD40	14.2	IBD Colitis 2	2.0
Monocytes rest	22.5	IBD Crohn's	3.2
Monocytes LPS	32.8	Colon	26.8
Macrophages rest	31.0	Lung	14.6
Macrophages LPS	30.8	Thymus	28.7
HUVEC none	18.3	Kidney	45.4
HUVEC starved	45.7		

CNS_neurodegeneration_v1.0 Summary: Ag3351 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. While no differential expression of this gene is detected between Alzheimer's diseased postmortem brains and those of non-demented controls, the widespread expression of this gene in the brain suggests that therapeutic modulation of the expression or function of this gene may be effective in the treatment of neurologic disorders such as Parkinson's disease, epilepsy, stroke and multiple sclerosis.

General_screening_panel_v1.4 Summary: Ag3351 - Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 4D Summary: Ag3351 The CG57871-01 gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

J. CG58590-01 and CG58590-02: PALS Guanylate kinase

Expression of gene CG58590-01 and CG58590-02 was assessed using the primer-probe set Ag3380, described in Table JA. Results of the RTQ-PCR runs are shown in Tables

JB, JC and JD. Please note that CG58590-02 represents a full-length physical clone of the CG58590-01 gene, validating the prediction of the gene sequence.

Table JA. Probe Name Ag3380

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tttgatacggcaattgtgaatt-3'	22	1931	396
Probe	TET-5'-ccgatcttgataaagcctatcaggaa-3'- TAMRA	26	1953	397
Reverse	5'-cccactgaggttcagtatcaag-3'	22	2000	398

Table JB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3380, Run 210153753	Tissue Name	Rel. Exp.(%) Ag3380, Run 210153753
AD 1 Hippo	12.9	Control (Path) 3 Temporal Ctx	4.7
AD 2 Hippo	27.7	Control (Path) 4 Temporal Ctx	24.3
AD 3 Hippo	4.8	AD 1 Occipital Ctx	15.6
AD 4 Hippo	7.7	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	7.5
AD 6 Hippo	64.2	AD 4 Occipital Ctx	19.1
Control 2 Hippo	25.5	AD 5 Occipital Ctx	29.5
Control 4 Hippo	9.9	AD 6 Occipital Ctx	40.1
Control (Path) 3 Hippo	8.4	Control 1 Occipital Ctx	4.2
AD 1 Temporal Ctx	17.6	Control 2 Occipital Ctx	65.5
AD 2 Temporal Ctx	25.3	Control 3 Occipital Ctx	13.4
AD 3 Temporal Ctx	4.9	Control 4 Occipital Ctx	6.4
AD 4 Temporal Ctx	17.4	Control (Path) 1 Occipital Ctx	78.5
AD 5 Inf Temporal Ctx	81.8	Control (Path) 2 Occipital Ctx	9.4
AD 5 Sup Temporal Ctx	42.9	Control (Path) 3 Occipital Ctx	3.2
AD 6 Inf Temporal Ctx	48.6	Control (Path) 4 Occipital Ctx	9.9
AD 6 Sup Temporal	53.6	Control 1 Parietal	6.0

Ctx		Ctx	
Control 1 Temporal Ctx	5.7	Control 2 Parietal Ctx	37.1
Control 2 Temporal Ctx	34.6	Control 3 Parietal Ctx	16.5
Control 3 Temporal Ctx	10.2	Control (Path) 1 Parietal Ctx	67.4
Control 4 Temporal Ctx	7.1	Control (Path) 2 Parietal Ctx	18.7
Control (Path) 1 Temporal Ctx	41.5	Control (Path) 3 Parietal Ctx	3.3
Control (Path) 2 Temporal Ctx	29.5	Control (Path) 4 Parietal Ctx	34.4

Table JC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3380, Run 217043276	Tissue Name	Rel. Exp.(%) Ag3380, Run 217043276
Adipose	9.0	Renal ca. TK-10	25.5
Melanoma* Hs688(A).T	18.9	Bladder	15.9
Melanoma* Hs688(B).T	16.8	Gastric ca. (liver met.) NCI-N87	52.5
Melanoma* M14	14.9	Gastric ca. KATO III	34.6
Melanoma* LOXIMVI	21.6	Colon ca. SW-948	4.9
Melanoma* SK- MEL-5	27.0	Colon ca. SW480	82.4
Squamous cell carcinoma SCC-4	28.7	Colon ca.* (SW480 met) SW620	20.6
Testis Pool	5.1	Colon ca. HT29	9.2
Prostate ca.* (bone met) PC-3	59.9	Colon ca. HCT-116	20.6
Prostate Pool	8.6	Colon ca. CaCo-2	22.8
Placenta	3.9	Colon cancer tissue	10.1
Uterus Pool	1.9	Colon ca. SW1116	6.2
Ovarian ca. OVCAR-3	32.5	Colon ca. Colo-205	4.9
Ovarian ca. SK-OV- 3	57.4	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	14.7	Colon Pool	11.4
Ovarian ca. OVCAR-5	59.5	Small Intestine Pool	9.8
Ovarian ca. IGROV-	13.1	Stomach Pool	7.4

1			
Ovarian ca. OVCAR-8	19.2	Bone Marrow Pool	4.2
Ovary	5.9	Fetal Heart	6.3
Breast ca. MCF-7	35.1	Heart Pool	4.9
Breast ca. MDA-MB-231	58.2	Lymph Node Pool	11.4
Breast ca. BT 549	26.8	Fetal Skeletal Muscle	3.3
Breast ca. T47D	100.0	Skeletal Muscle Pool	8.1
Breast ca. MDA-N	8.7	Spleen Pool	5.6
Breast Pool	10.4	Thymus Pool	6.3
Trachea	5.5	CNS cancer (glio/astro) U87-MG	39.2
Lung	3.8	CNS cancer (glio/astro) U-118-MG	54.7
Fetal Lung	11.8	CNS cancer (neuro;met) SK-N-AS	19.6
Lung ca. NCI-N417	3.2	CNS cancer (astro) SF-539	12.2
Lung ca. LX-1	20.7	CNS cancer (astro) SNB-75	29.7
Lung ca. NCI-H146	3.8	CNS cancer (glio) SNB-19	13.4
Lung ca. SHP-77	17.9	CNS cancer (glio) SF-295	28.9
Lung ca. A549	30.6	Brain (Amygdala) Pool	11.8
Lung ca. NCI-H526	3.6	Brain (cerebellum)	6.0
Lung ca. NCI-H23	29.3	Brain (fetal)	8.4
Lung ca. NCI-H460	14.8	Brain (Hippocampus) Pool	14.5
Lung ca. HOP-62	19.5	Cerebral Cortex Pool	16.2
Lung ca. NCI-H522	28.7	Brain (Substantia nigra) Pool	16.0
Liver	0.4	Brain (Thalamus) Pool	22.7
Fetal Liver	11.9	Brain (whole)	5.9
Liver ca. HepG2	12.9	Spinal Cord Pool	16.0
Kidney Pool	18.4	Adrenal Gland	5.1
Fetal Kidney	22.8	Pituitary gland Pool	3.8
Renal ca. 786-0	28.5	Salivary Gland	2.1
Renal ca. A498	5.0	Thyroid (female)	8.2
Renal ca. ACHN	22.4	Pancreatic ca. CAPAN2	51.4
Renal ca. UO-31	36.9	Pancreas Pool	12.3

Table JD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3380, Run 165296532	Tissue Name	Rel. Exp.(%) Ag3380, Run 165296532
Secondary Th1 act	13.1	HUVEC IL-1beta	15.0
Secondary Th2 act	14.6	HUVEC IFN gamma	19.6
Secondary Tr1 act	15.2	HUVEC TNF alpha + IFN gamma	28.3
Secondary Th1 rest	4.6	HUVEC TNF alpha + IL4	26.1
Secondary Th2 rest	4.7	HUVEC IL-11	7.8
Secondary Tr1 rest	8.0	Lung Microvascular EC none	25.5
Primary Th1 act	14.9	Lung Microvascular EC TNFalpha + IL-1beta	19.5
Primary Th2 act	13.2	Microvascular Dermal EC none	37.9
Primary Tr1 act	20.7	Microvascular Dermal EC TNFalpha + IL-1beta	24.8
Primary Th1 rest	35.6	Bronchial epithelium TNFalpha + IL1beta	37.1
Primary Th2 rest	24.0	Small airway epithelium none	15.0
Primary Tr1 rest	16.2	Small airway epithelium TNFalpha + IL-1beta	100.0
CD45RA CD4 lymphocyte act	23.3	Coronary artery SMC rest	30.1
CD45RO CD4 lymphocyte act	18.2	Coronary artery SMC TNFalpha + IL-1beta	13.6
CD8 lymphocyte act	7.4	Astrocytes rest	22.5
Secondary CD8 lymphocyte rest	13.4	Astrocytes TNFalpha + IL-1beta	21.2
Secondary CD8 lymphocyte act	4.4	KU-812 (Basophil) rest	17.9
CD4 lymphocyte none	8.0	KU-812 (Basophil) PMA/ionomycin	68.3
2ry Th1/Th2/Tr1_anti- CD95 CH11	10.7	CCD1106 (Keratinocytes) none	22.1
LAK cells rest	13.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	9.2
LAK cells IL-2	12.9	Liver cirrhosis	3.1
LAK cells IL-2+IL-12	13.2	Lupus kidney	2.9
LAK cells IL-2+IFN gamma	15.6	NCI-H292 none	48.6
LAK cells IL-2+ IL-18	17.0	NCI-H292 IL-4	66.9
LAK cells PMA/ionomycin	9.5	NCI-H292 IL-9	59.5

NK Cells IL-2 rest	7.0	NCI-H292 IL-13	36.6
Two Way MLR 3 day	15.2	NCI-H292 IFN gamma	42.6
Two Way MLR 5 day	7.0	HPAEC none	14.3
Two Way MLR 7 day	9.6	HPAEC TNF alpha + IL-1 beta	25.9
PBMC rest	6.4	Lung fibroblast none	12.5
PBMC PWM	60.7	Lung fibroblast TNF alpha + IL-1 beta	11.0
PBMC PHA-L	18.8	Lung fibroblast IL-4	25.9
Ramos (B cell) none	31.9	Lung fibroblast IL-9	20.6
Ramos (B cell) ionomycin	94.0	Lung fibroblast IL-13	18.8
B lymphocytes PWM	42.9	Lung fibroblast IFN gamma	23.3
B lymphocytes CD40L and IL-4	24.7	Dermal fibroblast CCD1070 rest	59.5
EOL-1 dbcAMP	12.9	Dermal fibroblast CCD1070 TNF alpha	64.2
EOL-1 dbcAMP PMA/ionomycin	10.4	Dermal fibroblast CCD1070 IL-1 beta	32.8
Dendritic cells none	19.6	Dermal fibroblast IFN gamma	10.7
Dendritic cells LPS	10.7	Dermal fibroblast IL-4	21.6
Dendritic cells anti-CD40	18.8	IBD Colitis 2	2.0
Monocytes rest	15.0	IBD Crohn's	3.6
Monocytes LPS	13.8	Colon	36.9
Macrophages rest	25.3	Lung	19.3
Macrophages LPS	8.1	Thymus	72.2
HUVEC none	19.9	Kidney	24.5
HUVEC starved	35.8		

CNS_neurodegeneration_v1.0 Summary: Ag3380 This panel does not show differential expression of the CG58590-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3380 - This gene is expressed at low to moderate levels in all samples on this pattern. The highest level of expression is seen in breast cancer cell line T47D (CT=27.8). Based on expression in this panel, this gene may be involved in brain, colon, renal, lung, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers.

Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and fetal liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes. Furthermore, this gene is more highly expressed in fetal (CT=30.9) liver when compared to expression in the adult (CT>35) and may be useful for the differentiation of the fetal and adult sources of this tissue.

In addition, this gene is expressed at moderate levels in the all regions of the CNS examined. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3380 - This gene is expressed from moderate to low levels across all of the samples on this panel. The highest expression is seen in small airway epithelium treated with TNFalpha and IL-1beta (CT=28.7). Interestingly, expression is much lower in untreated small airway epithelium (CT=31.5). There is also a significant difference between mononuclear cells treated with PWM (CT=29.5) and untreated cells (CT=32.7). Therefore, expression of this gene can be used to differentiate treated and untreated samples.

Expression of this gene is detected at a moderate level (CT=30.2) in normal colon (similar levels for colon are seen on panel 1.4 (CT=30.9), but is significantly lower in the IBD Colitis 2 (CT=34.4) and IBD Crohn's (CT=33.5) samples. Therefore, therapies designed with the protein encoded for by this gene may potentially modulate colon function and play a role in the identification and treatment of inflammatory or autoimmune diseases which effect the colon including Crohn's disease and ulcerative colitis.

K. CG58572-01 and CG58572-02: GLUCOSAMINE-PHOSPHATE N-ACETYLTRANSFERASE

Expression of gene CG58572-01 and full length clone CG58572-02 was assessed using the primer-probe set Ag3375, described in Table KA. Results of the RTQ-PCR runs are shown in Tables KB, KC and KD.

Table KA. Probe Name Ag3375

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-aagaagtggactggagtcagaa-3'	22	58	399
Probe	TET-5'-tacattttctccagccatttccccc-3'- TAMRA	26	86	400
Reverse	5'-agcagtacaaagaggcctcaa-3'	21	135	401

Table KB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3375, Run 210154239	Tissue Name	Rel. Exp.(%) Ag3375, Run 210154239
AD 1 Hippo	17.1	Control (Path) 3 Temporal Ctx	4.8
AD 2 Hippo	19.3	Control (Path) 4 Temporal Ctx	27.5
AD 3 Hippo	7.4	AD 1 Occipital Ctx	11.5
AD 4 Hippo	4.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	72.2	AD 3 Occipital Ctx	5.9
AD 6 Hippo	53.6	AD 4 Occipital Ctx	12.7
Control 2 Hippo	20.3	AD 5 Occipital Ctx	26.6
Control 4 Hippo	6.8	AD 6 Occipital Ctx	19.8
Control (Path) 3 Hippo	5.5	Control 1 Occipital Ctx	3.2
AD 1 Temporal Ctx	11.6	Control 2 Occipital Ctx	36.1
AD 2 Temporal Ctx	23.8	Control 3 Occipital Ctx	7.4
AD 3 Temporal Ctx	5.5	Control 4 Occipital Ctx	4.1
AD 4 Temporal Ctx	16.5	Control (Path) 1 Occipital Ctx	66.0
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	8.2
AD 5 Sup Temporal Ctx	55.9	Control (Path) 3 Occipital Ctx	1.9
AD 6 Inf Temporal Ctx	37.9	Control (Path) 4 Occipital Ctx	12.2
AD 6 Sup Temporal Ctx	59.5	Control 1 Parietal Ctx	2.4
Control 1 Temporal Ctx	3.5	Control 2 Parietal Ctx	31.6
Control 2 Temporal	25.3	Control 3 Parietal	11.7

Ctx		Ctx	
Control 3 Temporal Ctx	8.2	Control (Path) 1 Parietal Ctx	49.7
Control 3 Temporal Ctx	4.0	Control (Path) 2 Parietal Ctx	15.4
Control (Path) 1 Temporal Ctx	52.9	Control (Path) 3 Parietal Ctx	4.2
Control (Path) 2 Temporal Ctx	26.6	Control (Path) 4 Parietal Ctx	32.5

Table KC. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3375, Run 165674233	Tissue Name	Rel. Exp.(%) Ag3375, Run 165674233
Liver adenocarcinoma	51.8	Kidney (fetal)	9.7
Pancreas	9.3	Renal ca. 786-0	19.6
Pancreatic ca. CAPAN 2	52.1	Renal ca. A498	26.2
Adrenal gland	8.9	Renal ca. RXF 393	15.7
Thyroid	6.3	Renal ca. ACHN	8.2
Salivary gland	18.3	Renal ca. UO-31	35.4
Pituitary gland	15.1	Renal ca. TK-10	9.8
Brain (fetal)	15.5	Liver	20.4
Brain (whole)	34.6	Liver (fetal)	16.5
Brain (amygdala)	16.0	Liver ca. (hepatoblast) HepG2	49.0
Brain (cerebellum)	34.2	Lung	4.5
Brain (hippocampus)	12.1	Lung (fetal)	5.4
Brain (substantia nigra)	12.8	Lung ca. (small cell) LX-1	32.3
Brain (thalamus)	17.9	Lung ca. (small cell) NCI-H69	17.3
Cerebral Cortex	10.4	Lung ca. (s.cell var.) SHP-77	30.1
Spinal cord	13.3	Lung ca. (large cell) NCI-H460	66.4
glio/astro U87-MG	14.8	Lung ca. (non-sm. cell) A549	19.1
glio/astro U-118-MG	95.3	Lung ca. (non-s.cell) NCI-H23	13.8
Astrocytoma SW1783	42.0	Lung ca. (non-s.cell) HOP-62	18.7
neuro*; met SK-N-AS	47.0	Lung ca. (non-s.cl) NCI-H522	19.5

Astrocytoma SF-539	11.4	Lung ca. (squam.) SW 900	9.9
Astrocytoma SNB-75	15.6	Lung ca. (squam.) NCI-H596	19.6
glioma SNB-19	11.8	Mammary gland	14.6
glioma U251	40.9	Breast ca.* (pl.ef) MCF-7	81.2
glioma SF-295	10.1	Breast ca.* (pl.ef) MDA-MB-231	91.4
Heart (fetal)	1.3	Breast ca.* (pl.ef) T47D	35.4
Heart	4.7	Breast ca. BT-549	97.9
Skeletal muscle (fetal)	1.2	Breast ca. MDA-N	14.8
Skeletal muscle	38.7	Ovary	1.6
Bone marrow	4.6	Ovarian ca. OVCAR-3	39.2
Thymus	2.7	Ovarian ca. OVCAR-4	23.0
Spleen	7.9	Ovarian ca. OVCAR-5	13.8
Lymph node	13.0	Ovarian ca. OVCAR-8	8.5
Colorectal	3.3	Ovarian ca. IGROV-1	5.6
Stomach	27.7	Ovarian ca.* (ascites) SK-OV-3	44.8
Small intestine	19.3	Uterus	19.5
Colon ca. SW480	16.5	Placenta	2.6
Colon ca.* SW620(SW480 met)	29.1	Prostate	15.6
Colon ca. HT29	13.8	Prostate ca.* (bone met)PC-3	56.6
Colon ca. HCT-116	27.7	Testis	40.6
Colon ca. CaCo-2	17.4	Melanoma Hs688(A).T	5.5
Colon ca. tissue(ODO3866)	26.4	Melanoma* (met) Hs688(B).T	8.9
Colon ca. HCC-2998	32.1	Melanoma UACC-62	17.8
Gastric ca.* (liver met) NCI-N87	100.0	Melanoma M14	27.7
Bladder	28.7	Melanoma LOX IMVI	6.6
Trachea	9.4	Melanoma* (met) SK-MEL-5	13.0
Kidney	9.0	Adipose	8.0

Table KD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3375, Run 165296547	Tissue Name	Rel. Exp.(%) Ag3375, Run 165296547
Secondary Th1 act	14.6	HUVEC IL-1beta	24.5
Secondary Th2 act	13.0	HUVEC IFN gamma	24.5
Secondary Tr1 act	17.3	HUVEC TNF alpha + IFN gamma	24.0
Secondary Th1 rest	0.9	HUVEC TNF alpha + IL4	23.2
Secondary Th2 rest	1.5	HUVEC IL-11	12.1
Secondary Tr1 rest	2.9	Lung Microvascular EC none	21.3
Primary Th1 act	16.0	Lung Microvascular EC TNFalpha + IL-1beta	24.1
Primary Th2 act	12.1	Microvascular Dermal EC none	27.4
Primary Tr1 act	25.0	Microvascular Dermal EC TNFalpha + IL-1beta	24.0
Primary Th1 rest	10.4	Bronchial epithelium TNFalpha + IL1beta	20.3
Primary Th2 rest	6.1	Small airway epithelium none	11.3
Primary Tr1 rest	9.0	Small airway epithelium TNFalpha + IL-1beta	54.0
CD45RA CD4 lymphocyte act	14.6	Coronary artery SMC rest	23.5
CD45RO CD4 lymphocyte act	13.6	Coronary artery SMC TNFalpha + IL-1beta	12.0
CD8 lymphocyte act	14.2	Astrocytes rest	5.3
Secondary CD8 lymphocyte rest	14.4	Astrocytes TNFalpha + IL-1beta	5.4
Secondary CD8 lymphocyte act	5.8	KU-812 (Basophil) rest	19.5
CD4 lymphocyte none	2.4	KU-812 (Basophil) PMA/ionomycin	56.3
2ry Th1/Th2/Tr1_anti- CD95 CH11	2.6	CCD1106 (Keratinocytes) none	26.6
LAK cells rest	5.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	7.8
LAK cells IL-2	10.7	Liver cirrhosis	2.6
LAK cells IL-2+IL-12	12.5	Lupus kidney	0.8
LAK cells IL-2+IFN gamma	20.2	NCI-H292 none	28.7
LAK cells IL-2+ IL-18	16.6	NCI-H292 IL-4	54.7

LAK cells PMA/ionomycin	12.5	NCI-H292 IL-9	45.7
NK Cells IL-2 rest	7.1	NCI-H292 IL-13	24.3
Two Way MLR 3 day	6.8	NCI-H292 IFN gamma	33.2
Two Way MLR 5 day	8.9	HPAEC none	17.8
Two Way MLR 7 day	6.0	HPAEC TNF alpha + IL-1 beta	30.1
PBMC rest	0.8	Lung fibroblast none	10.2
PBMC PWM	42.3	Lung fibroblast TNF alpha + IL-1 beta	6.3
PBMC PHA-L	11.6	Lung fibroblast IL-4	27.2
Ramos (B cell) none	30.6	Lung fibroblast IL-9	26.8
Ramos (B cell) ionomycin	100.0	Lung fibroblast IL-13	21.8
B lymphocytes PWM	77.4	Lung fibroblast IFN gamma	29.5
B lymphocytes CD40L and IL-4	12.2	Dermal fibroblast CCD1070 rest	42.3
EOL-1 dbcAMP	13.0	Dermal fibroblast CCD1070 TNF alpha	51.4
EOL-1 dbcAMP PMA/ionomycin	6.9	Dermal fibroblast CCD1070 IL-1 beta	22.5
Dendritic cells none	4.5	Dermal fibroblast IFN gamma	11.1
Dendritic cells LPS	3.8	Dermal fibroblast IL-4	19.5
Dendritic cells anti- CD40	2.9	IBD Colitis 2	0.7
Monocytes rest	2.2	IBD Crohn's	0.9
Monocytes LPS	1.3	Colon	7.6
Macrophages rest	6.6	Lung	6.2
Macrophages LPS	2.7	Thymus	9.4
HUVEC none	17.4	Kidney	4.2
HUVEC starved	37.4		

CNS_neurodegeneration_v1.0 Summary: Ag3375 This panel does not show differential expression of the CG58572-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

Panel 1.3D Summary: Ag3375 - This gene is expressed at moderate to low levels in all samples on this panel, with the highest expression in gastric cancer cell line NCI-N87 (CT=28.8). Based on expression in this panel, this gene may be involved in gastric, pancreatic,

brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene is expressed at moderate levels in the CNS. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3375 The CG58572-01 gene is ubiquitously expressed on this panel, with highest expression in the B cell line Ramos treated with ionomycin (CT=26.2). Significant levels of expression are also seen in pokeweed mitogen-activated B lymphocytes. Therefore, therapies that antagonize the function of this gene product may be useful as therapeutic drugs to reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

Interestingly, there is a difference between the levels of expression in resting and activated secondary T cells. The level in activated secondary T cells (CT=28.7-29.2) appears to be higher than in resting T cells (CT=31.3-33.1). Therefore, therapeutics designed with the protein encoded by this transcript could be important in the regulation of T cell function.

L. CG58564-01 and CG58564-02: PROTEIN TYROSINE PHOSPHATASE -

Expression of gene CG58564-01 and full length clone CG58564-02 was assessed using the primer-probe sets Ag3023 and Ag3373, described in Tables LA and LB. Results of the RTQ-PCR runs are shown in Tables LC, LD, LE and LF.

Table LA. Probe Name Ag3023

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctaagtctggatttgtccatca-3'	22	492	402
Probe	TET-5'-tcaggaatatgaagccatctacctagca-3'-TAMRA	28	517	403
Reverse	5'-tggagtgggtgacatcatctgta-3'	22	555	404

Table LB. Probe Name Ag3373

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atttgtccatcaacttcaggaa-3'	22	502	405
Probe	TET-5'-tgaagccatctacctagcaaaattaaca-3'-TAMRA	28	526	406
Reverse	5'-tggagtgggtgacatcatctgta-3'	22	555	407

Table LC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071	Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071
AD 1 Hippo	10.9	16.8	Control (Path) 3 Temporal Ctx	9.1	8.0
AD 2 Hippo	34.2	37.6	Control (Path) 4 Temporal Ctx	40.6	65.5
AD 3 Hippo	12.0	15.8	AD 1 Occipital Ctx	24.7	29.1
AD 4 Hippo	13.8	10.3	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	60.7	57.8	AD 3 Occipital Ctx	14.7	15.0
AD 6 Hippo	80.7	72.2	AD 4 Occipital Ctx	35.4	22.4
Control 2 Hippo	35.8	38.4	AD 5 Occipital Ctx	3.9	30.4
Control 4	16.5	11.7	AD 6	46.0	37.4

Hippo			Occipital Ctx		
Control (Path) 3 Hippo	13.1	15.4	Control 1 Occipital Ctx	9.9	10.7
AD 1 Temporal Ctx	39.0	31.4	Control 2 Occipital Ctx	39.0	38.4
AD 2 Temporal Ctx	38.7	73.2	Control 3 Occipital Ctx	23.0	20.6
AD 3 Temporal Ctx	9.5	13.2	Control 4 Occipital Ctx	13.3	13.3
AD 4 Temporal Ctx	27.9	34.9	Control (Path) 1 Occipital Ctx	80.1	76.3
AD 5 Inf Temporal Ctx	59.0	100.0	Control (Path) 2 Occipital Ctx	17.3	20.0
AD 5 Sup Temporal Ctx	33.2	44.1	Control (Path) 3 Occipital Ctx	8.4	8.7
AD 6 Inf Temporal Ctx	100.0	73.2	Control (Path) 4 Occipital Ctx	21.2	20.6
AD 6 Sup Temporal Ctx	79.6	80.1	Control 1 Parietal Ctx	12.1	16.3
Control 1 Temporal Ctx	10.2	13.7	Control 2 Parietal Ctx	48.0	40.9
Control 2 Temporal Ctx	41.2	31.9	Control 3 Parietal Ctx	17.9	16.3
Control 3 Temporal Ctx	20.3	20.0	Control (Path) 1 Parietal Ctx	74.7	64.2
Control 4 Temporal Ctx	9.7	9.9	Control (Path) 2 Parietal Ctx	28.9	59.9
Control (Path) 1 Temporal Ctx	59.9	68.3	Control (Path) 3 Parietal Ctx	10.2	9.0
Control (Path) 2 Temporal Ctx	40.3	41.2	Control (Path) 4	44.8	43.8

		Parietal Ctx	
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Table LD. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119	Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119
Adipose	12.0	Renal ca. TK-10	20.3
Melanoma* Hs688(A).T	30.8	Bladder	23.2
Melanoma* Hs688(B).T	69.3	Gastric ca. (liver met.) NCI-N87	25.3
Melanoma* M14	15.0	Gastric ca. KATO III	30.8
Melanoma* LOXIMVI	26.6	Colon ca. SW-948	9.7
Melanoma* SK- MEL-5	21.5	Colon ca. SW480	35.1
Squamous cell carcinoma SCC-4	33.0	Colon ca.* (SW480 met) SW620	13.9
Testis Pool	19.8	Colon ca. HT29	8.5
Prostate ca.* (bone met) PC-3	100.0	Colon ca. HCT-116	36.9
Prostate Pool	9.2	Colon ca. CaCo-2	42.9
Placenta	3.8	Colon cancer tissue	9.0
Uterus Pool	7.4	Colon ca. SW1116	5.8
Ovarian ca. OVCAR-3	28.5	Colon ca. Colo-205	4.3
Ovarian ca. SK-OV- 3	40.3	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	20.0	Colon Pool	20.7
Ovarian ca. OVCAR-5	35.1	Small Intestine Pool	12.2
Ovarian ca. IGROV- 1	10.9	Stomach Pool	9.9
Ovarian ca. OVCAR-8	9.2	Bone Marrow Pool	11.6
Ovary	9.7	Fetal Heart	20.7
Breast ca. MCF-7	37.6	Heart Pool	10.6
Breast ca. MDA- MB-231	37.1	Lymph Node Pool	17.9
Breast ca. BT 549	62.4	Fetal Skeletal Muscle	12.3
Breast ca. T47D	61.1	Skeletal Muscle Pool	16.0
Breast ca. MDA-N	10.0	Spleen Pool	11.6
Breast Pool	17.3	Thymus Pool	12.2

Trachea	12.0	CNS cancer (glio/astro) U87-MG	29.1
Lung	6.7	CNS cancer (glio/astro) U-118-MG	69.3
Fetal Lung	34.2	CNS cancer (neuro;met) SK-N-AS	34.9
Lung ca. NCI-N417	5.4	CNS cancer (astro) SF- 539	19.1
Lung ca. LX-1	17.2	CNS cancer (astro) SNB-75	35.8
Lung ca. NCI-H146	3.0	CNS cancer (glio) SNB-19	11.3
Lung ca. SHP-77	18.6	CNS cancer (glio) SF- 295	26.4
Lung ca. A549	29.1	Brain (Amygdala) Pool	4.5
Lung ca. NCI-H526	4.6	Brain (cerebellum)	8.1
Lung ca. NCI-H23	31.6	Brain (fetal)	13.2
Lung ca. NCI-H460	18.2	Brain (Hippocampus) Pool	5.3
Lung ca. HOP-62	14.1	Cerebral Cortex Pool	5.4
Lung ca. NCI-H522	31.6	Brain (Substantia nigra) Pool	4.8
Liver	1.2	Brain (Thalamus) Pool	8.0
Fetal Liver	32.3	Brain (whole)	6.2
Liver ca. HepG2	14.6	Spinal Cord Pool	6.6
Kidney Pool	22.1	Adrenal Gland	8.1
Fetal Kidney	26.1	Pituitary gland Pool	3.0
Renal ca. 786-0	28.7	Salivary Gland	4.7
Renal ca. A498	11.3	Thyroid (female)	4.4
Renal ca. ACHN	12.2	Pancreatic ca. CAPAN2	17.3
Renal ca. UO-31	24.1	Pancreas Pool	17.1

Table LE. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931	Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931
Liver adenocarcinoma	51.1	Kidney (fetal)	26.2
Pancreas	6.1	Renal ca. 786-0	34.2
Pancreatic ca. CAPAN 2	17.7	Renal ca. A498	17.6
Adrenal gland	3.8	Renal ca. RXF 393	17.2
Thyroid	3.0	Renal ca. ACHN	13.5
Salivary gland	3.9	Renal ca. UO-31	0.0